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OM protein - protein search, using sw model

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(without alignments)  
246.399 Million cell updates/sec

Title: US-10-059-395-142

Sequence: 1 MKIPVLPVAVTLISLVLSHA.....LNMDFPKLKGKRSATPDAQ 99

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size: 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/1aa/PCITUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/1aa/backfilest.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description          |
|------------|-------|-------------|--------|----|----------------------|
| 1          | 99    | 100.0       | 99     | 4  | US-09-996-243-201    |
| 2          | 9     | 9.1         | 344    | 4  | US-09-253-991A-22286 |
| 3          | 8     | 8.1         | 61     | 2  | US-08-359-222-2      |
| 4          | 8     | 8.1         | 61     | 3  | US-09-094-563-2      |
| 5          | 8     | 8.1         | 146    | 4  | US-09-107-532A-5900  |
| 6          | 7     | 7.1         | 72     | 4  | US-09-205-258-333    |
| 7          | 7     | 7.1         | 80     | 2  | US-08-747-121-7      |
| 8          | 7     | 7.1         | 133    | 4  | US-09-152-060-75     |
| 9          | 7     | 7.1         | 254    | 4  | US-09-107-532A-4795  |
| 10         | 7     | 7.1         | 257    | 4  | US-09-252-991A-26002 |
| 11         | 7     | 7.1         | 312    | 2  | US-08-518-862C-2     |
| 12         | 7     | 7.1         | 373    | 4  | US-09-066-281B-19    |
| 13         | 7     | 7.1         | 407    | 3  | US-08-948-997-3      |
| 14         | 7     | 7.1         | 410    | 3  | US-09-348-817A-3     |
| 15         | 7     | 7.1         | 410    | 4  | US-09-722-297-3      |
| 16         | 7     | 7.1         | 457    | 2  | US-08-847-900-3      |
| 17         | 7     | 7.1         | 648    | 4  | US-09-198-452A-594   |
| 18         | 7     | 7.1         | 814    | 4  | US-09-813-819-4      |
| 19         | 7     | 7.1         | 814    | 4  | US-09-920-048-4      |
| 20         | 7     | 7.1         | 855    | 3  | US-09-813-819-2      |
| 21         | 7     | 7.1         | 855    | 4  | US-09-920-048-2      |
| 22         | 6     | 6.1         | 9      | 2  | US-08-747-121-15     |
| 23         | 6     | 6.1         | 18     | 1  | US-08-295-085-3      |
| 24         | 6     | 6.1         | 18     | 1  | US-08-295-085-4      |
| 25         | 6     | 6.1         | 18     | 1  | US-08-295-085-5      |
| 26         | 6     | 6.1         | 18     | 5  | PCT-US95-10741-3     |
| 27         | 6     | 6.1         | 18     | 5  | PCT-US95-10741-4     |

|    |   |     |     |   |                    |                   |
|----|---|-----|-----|---|--------------------|-------------------|
| 28 | 6 | 6.1 | 18  | 5 | PCT-US95-10741-5   | Sequence 5, Appl  |
| 29 | 6 | 6.1 | 26  | 4 | US-09-504-633-2    | Sequence 2, Appl  |
| 30 | 6 | 6.1 | 29  | 4 | US-09-227-357-176  | Sequence 176, App |
| 31 | 6 | 6.1 | 33  | 4 | US-09-205-258-295  | Sequence 295, App |
| 32 | 6 | 6.1 | 45  | 4 | US-08-469-260A-483 | Sequence 483, App |
| 33 | 6 | 6.1 | 45  | 4 | US-08-488-446-483  | Sequence 483, App |
| 34 | 6 | 6.1 | 45  | 4 | US-08-467-344A-483 | Sequence 14, Appl |
| 35 | 6 | 6.1 | 50  | 3 | US-09-346-860-14   | Sequence 14, Appl |
| 36 | 6 | 6.1 | 50  | 4 | US-09-735-685-14   | Sequence 14, Appl |
| 37 | 6 | 6.1 | 63  | 4 | US-09-504-633-4    | Sequence 4, Appl  |
| 38 | 6 | 6.1 | 73  | 4 | US-09-345-236B-88  | Sequence 88, Appl |
| 39 | 6 | 6.1 | 97  | 4 | US-08-973-544-4    | Sequence 4, Appl  |
| 40 | 6 | 6.1 | 98  | 1 | US-08-375-346A-2   | Sequence 2, Appl  |
| 41 | 6 | 6.1 | 98  | 1 | US-08-467-123B-2   | Sequence 2, Appl  |
| 42 | 6 | 6.1 | 98  | 3 | US-08-943-336A-2   | Sequence 2, Appl  |
| 43 | 6 | 6.1 | 98  | 4 | US-09-635-899-2    | Sequence 2, Appl  |
| 44 | 6 | 6.1 | 98  | 5 | PCT-US95-01780-2   | Sequence 2, Appl  |
| 45 | 6 | 6.1 | 104 | 4 | US-08-973-544-3    | Sequence 3, Appl  |

## ALIGNMENTS

## RESULT 1

US-09-996-243-201

Sequence 201, Application US/09996243

Patent No. 6479825

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Baton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P27301C13

CURRENT APPLICATION NUMBER: US/09/996,243

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

09/440443





PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 99; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.8e-93;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVPAVLLSLVLSAQAATLGGPEESTIENYASRPAFNTPTLNIDKLSAFYA 60  
DB 1 MKIPVPAVLLSLVLSAQAATLGGPEESTIENYASRPAFNTPTLNIDKLSAFYA 60

QY 61 DEFLNMHALFESIKRKLPLFNMNAPFKLKLSRATPDAQ 99  
DB 61 DEFLNMHALFESIKRKLPLFNMNAPFKLKLSRATPDAQ 99

RESULT 2  
US-09-252-991A-22286  
Sequence 22286; Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 22286  
LENGTH: 344  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-22286

Query Match 9.1%; Score 9; DB 4; Length 344;  
Best Local Similarity 100.0%; Pred. No. 0.27;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 GLRSATPDA 98  
DB 210 GLRSATPDA 218

RESULT 3  
US-08-359-222-2  
Sequence 2; Application US/08359222  
Patent No. 5824648  
GENERAL INFORMATION:  
APPLICANT: YANG, Mabel M.  
TITLE OF INVENTION: RNASE-CV (CORIOLUS VERSICOLOR)  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jerome J. No. 5824648ris  
STREET: 1919 18th Street, N.W., Suite 750  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/359,222  
FILING DATE: 19-DEC-1994  
CLASSIFICATION: 330  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5824648ris, Jerome J.  
REGISTRATION NUMBER: 24,696  
REFERENCE/DOCKET NUMBER: 599.31757PX1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-737-4410  
TELEFAX: 202-737-3315  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bos taurus ribonuclease  
TISSUE TYPE: Pancreas  
US-08-359-222-2

Query Match 8.1%; Score 8; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 0.55;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLSLVL 17  
DB 8 VLSLVL 15

RESULT 4  
US-09-094-563-2  
Sequence 2; Application US/09094563  
Patent No. 6087335  
GENERAL INFORMATION:  
APPLICANT: YANG, Mabel M.  
APPLICANT: CHEN, George  
TITLE OF INVENTION: RNASE-CV (CORIOLUS VERSICOLOR)  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jerome J. No. 6087335ris  
STREET: 1919 Pennsylvania Avenue, N.W., Suite 200  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/094,563  
FILING DATE: 15-JUN-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6087335ris, Jerome J.  
REGISTRATION NUMBER: 24,696  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-737-4410  
TELEFAX: 202-737-3315  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bos taurus ribonuclease  
TISSUE TYPE: Pancreas  
US-09-094-563-2

Query Match  
Best Local Similarity 8.1%; Score 8; DB 3; Length 61;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 VLLSLVL 17  
| | | | |  
Db 8 VLLSLVL 15

RESULT 5  
US-09-107-532A-5900  
Sequence 5900, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSER: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:  
NAME: Arinello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 5900:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 146 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (8) LOCATION 1..146  
SEQUENCE DESCRIPTION: SEQ ID NO: 5900:  
US-09-107-532A-5900

Query Match  
Best Local Similarity 8.1%; Score 8; DB 4; Length 146;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 VLLSLVL 17  
| | | | |  
Db 42 VLLSLVL 49

RESULT 6  
US-09-205-258-333  
Sequence 333, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: P2007P1

CURRENT APPLICATION NUMBER: US/09/205,258  
CURRENT FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883

EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 333  
LENGTH: 72  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (58)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (72)  
OTHER INFORMATION: Xaa equals stop translation  
US-09-205-258-333

Query Match  
Best Local Similarity 7.1%; Score 7; DB 4; Length 72;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLSLVL 17  
Db 10 LLSLVL 16

RESULT 7  
US-08-747-121-7  
Sequence 7, Application US/08747121  
Patent No. 5874290  
GENERAL INFORMATION:  
APPLICANT: Murphy, Gerald  
APPLICANT: Boynton, Alton  
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID  
TITLE OF INVENTION: SEQUENCES OF A D2-2 GENE ASSOCIATED WITH  
TITLE OF INVENTION: BRAIN TUMORS AND METHODS BASED THEREON  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,121  
FILING DATE: 08-NOV-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:

APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Baldwin, Geraldine F  
REGISTRATION NUMBER: 31,232  
REFERENCE/DOCKET NUMBER: 8511-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)7909090  
TELEFAX: (212)8698864  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
US-08-747-121-7

Query Match  
Best Local Similarity 7.1%; Score 7; DB 2; Length 80;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLSLVL 17  
Db 11 LLSLVL 17

RESULT 8  
US-09-152-060-75  
Sequence 75, Application US/09152060  
Patent No. 6448230  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 28 Human Secreted Proteins  
FILE REFERENCE: P2003pl US  
CURRENT APPLICATION NUMBER: US/09/152,060  
CURRENT FILING DATE: 1998-09-11  
EARLIER APPLICATION NUMBER: PCT/US98/04858  
EARLIER FILING DATE: 1998-03-12  
EARLIER APPLICATION NUMBER: 60/040,762  
EARLIER FILING DATE: 1997-03-14  
EARLIER APPLICATION NUMBER: 60/040,710  
EARLIER FILING DATE: 1997-03-14  
EARLIER APPLICATION NUMBER: 60/050,934  
EARLIER FILING DATE: 1997-05-30  
EARLIER APPLICATION NUMBER: 60/048,100  
EARLIER FILING DATE: 1997-05-30  
EARLIER APPLICATION NUMBER: 60/048,357  
EARLIER FILING DATE: 1997-05-30  
EARLIER APPLICATION NUMBER: 60/048,189  
EARLIER FILING DATE: 1997-05-30  
EARLIER APPLICATION NUMBER: 60/057,765  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/068,368  
EARLIER FILING DATE: 1997-12-19  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 75  
LENGTH: 133  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-152-060-75

Query Match  
Best Local Similarity 7.1%; Score 7; DB 4; Length 133;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLSLVL 17  
Db 11 LLSLVL 17

Db 6 LSLVL 12

RESULT 9  
US-09-107-532A-4795  
; Sequence 4795, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Maitham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arinello, Pamela Dencke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 4795:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 254 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...254  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4795:  
US-09-107-532A-4795

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Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 KKKLPTL 80  
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Db 33 KKKLPTL 39

RESULT 10  
US-09-252-991A-26002  
; Sequence 26002, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 26002  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-26002

Query Match 7.1%; Score 7; DB 4; Length 257;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 LKGLRSA 94  
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Db 247 LKGLRSA 253

RESULT 11  
US-08-518-862C-2  
; Sequence 2, Application US/0851862C  
; Patent No. 5843757  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth W.  
; APPLICANT: Nicolaides, Nicholas C.  
; TITLE OF INVENTION: Human JTV1 Gene Overlaps PMS2 Gene  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff, Ltd.  
; STREET: 1001 G Street, N.W.  
; CITY: Washington, D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/518,862C  
; FILING DATE: 24-AUG-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kagan, Sarah A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 01107.49697  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-508-9100  
; TELEFAX: 202-508-9299  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 312 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-518-862C-2

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Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LSLVTLH 18  
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Db 133 LSLVTLH 139

RESULT 12  
US-09-066-281B-19  
; Sequence 19, Application US/09066281B

Patent No. 6475783  
GENERAL INFORMATION:  
APPLICANT: LUCAS, Sophie; DE SMET, Charles; BOON-FALLER, Thierry  
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING  
TITLE OF INVENTION: FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGC-C1 AND MAGC-C2  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski L.L.P.  
STREET: 666 Fifth Avenue  
CITY: New York City  
STATE: New York  
COUNTRY: USA  
ZIP: 10103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/066,281B  
FILING DATE: April 24, 1998  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/845,528  
FILING DATE: April 25, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mary Anne Schofield  
REGISTRATION NUMBER: 36,669  
REFERENCE/DOCKET NUMBER: LUD-5455.2 US - JEL/MAS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 752-5958  
INFORMATION FOR SEQ ID NO: 19:  
LENGTH: 373  
TYPE: amino acid  
STRANDEDNESS: single-stranded  
TOPOLOGY: linear  
US-09-066-281B-19  
Query Match 7.1%; Score 7; DB 4; Length 373;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 25 LGGPEER 31  
Db 63 LGGPEER 69  
RESULT 13  
US-08-948-997-3  
Sequence 3, Application US/08948997  
Patent No. 6008020  
GENERAL INFORMATION:  
APPLICANT: HASTINGS, GREGG  
APPLICANT: COLEMAN, TIM  
APPLICANT: LAWRENCE, DANIEL  
TITLE OF INVENTION: BRAIN-ASSOCIATED INHIBITOR OF  
TITLE OF INVENTION: TISSUE-TYPE PLASMINOGEN ACTIVATOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/948,997  
FILING DATE: Oct-10-97  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: A. ANDERS BROOKES  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PP336  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 407 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-948-997-3  
Query Match 7.1%; Score 7; DB 3; Length 407;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 LLSLVL 17  
Db 6 LLSLVL 12  
RESULT 14  
US-09-348-817A-3  
Sequence 3, Application US/09348817A  
Patent No. 6191260  
GENERAL INFORMATION:  
APPLICANT: HASTINGS et al.  
TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen  
FILE REFERENCE: PP336D1  
CURRENT APPLICATION NUMBER: US/09/348,817A  
CURRENT FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: 08/948,997  
PRIOR FILING DATE: 1997-10-10  
PRIOR APPLICATION NUMBER: 60/026,117  
PRIOR FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 410  
TYPE: PRT  
ORGANISM: Gallus gallus  
US-09-348-817A-3  
Query Match 7.1%; Score 7; DB 3; Length 410;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 LLSLVL 17  
Db 6 LLSLVL 12  
RESULT 15  
US-09-722-292-3  
Sequence 3, Application US/09722292  
Patent No. 6541452  
GENERAL INFORMATION:  
APPLICANT: Hastings et al.  
TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen  
FILE REFERENCE: PP336D1  
CURRENT APPLICATION NUMBER: US/09/722,292  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 09/348,817

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; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: 60/028,117  
; PRIOR FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-722-292-3

Query Match 7.1%; Score 7; DB 4; Length 410;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LLSLVL 17  
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Db 6 LLSLVL 12

Search completed: November 28, 2003, 08:05:02  
Job time : 19 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 07:56:46 ; Search time 35 Seconds

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Title: US-10-059-395-142

Perfect score: 99

Sequence: 1 MKIPPLPAVLISLVHSA.....LNWAPFKLGRSATPPAQ 99

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Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Match Length | ID | Description                    |
|------------|-------|--------------|----|--------------------------------|
| 1          | 99    | 100.0        | 99 | 20 AAM67828 Human secreted pro |
| 2          | 99    | 100.0        | 99 | 21 AAY6681 Membrane-bound pro  |
| 3          | 99    | 100.0        | 99 | 22 AAB20117 Human immunostiml  |
| 4          | 99    | 100.0        | 99 | 22 AAB65204 Human PRO826 (UNG4 |
| 5          | 99    | 100.0        | 99 | 22 AAB50916 Human PRO826 prote |
| 6          | 99    | 100.0        | 99 | 22 AAB53094 Human angiogenesis |
| 7          | 99    | 100.0        | 99 | 23 AAB69586 Human polypeptide  |
| 8          | 99    | 100.0        | 99 | 23 AAB95488 Human angiogenesis |
| 9          | 99    | 100.0        | 99 | 23 AAB34040 Human Pro peptide  |

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|----|----|-------|------|--------------|
| 10 | 99 | 100.0 | 99   | 23 AAB84882  |
| 11 | 99 | 100.0 | 99   | 23 AAB93664  |
| 12 | 99 | 100.0 | 99   | 23 AAB81964  |
| 13 | 99 | 100.0 | 99   | 24 AAB59097  |
| 14 | 99 | 100.0 | 99   | 24 AAB59244  |
| 15 | 99 | 100.0 | 99   | 24 AAB59393  |
| 16 | 99 | 100.0 | 99   | 24 AAB60528  |
| 17 | 99 | 100.0 | 99   | 24 AAB58019  |
| 18 | 99 | 100.0 | 99   | 24 AAB58950  |
| 19 | 99 | 100.0 | 99   | 24 AAB13910  |
| 20 | 99 | 100.0 | 99   | 24 AAB10865  |
| 21 | 56 | 56.6  | 96   | 23 AAB69669  |
| 22 | 44 | 44.4  | 85   | 23 AAB69587  |
| 23 | 44 | 44.4  | 85   | 23 AAB14344  |
| 24 | 8  | 8.1   | 102  | 22 AAB48744  |
| 25 | 8  | 8.1   | 102  | 22 AAB28730  |
| 26 | 8  | 8.1   | 102  | 22 AAB33909  |
| 27 | 8  | 8.1   | 102  | 22 AAB19350  |
| 28 | 8  | 8.1   | 102  | 22 AAB54676  |
| 29 | 8  | 8.1   | 102  | 22 AAB67078  |
| 30 | 8  | 8.1   | 102  | 22 AAM14940  |
| 31 | 8  | 8.1   | 102  | 22 AAM27370  |
| 32 | 8  | 8.1   | 102  | 22 AAM02668  |
| 33 | 8  | 8.1   | 102  | 23 AAB36737  |
| 34 | 8  | 8.1   | 133  | 22 AABG05985 |
| 35 | 8  | 8.1   | 1163 | 22 AAB60191  |
| 36 | 7  | 7.1   | 55   | 20 AAY12863  |
| 37 | 7  | 7.1   | 55   | 21 AAG00453  |
| 38 | 7  | 7.1   | 72   | 20 AAM88618  |
| 39 | 7  | 7.1   | 72   | 22 ABB50385  |
| 40 | 7  | 7.1   | 80   | 19 AAM49763  |
| 41 | 7  | 7.1   | 81   | 23 AAB34111  |
| 42 | 7  | 7.1   | 96   | 11 AAR06605  |
| 43 | 7  | 7.1   | 96   | 11 AAB53651  |
| 44 | 7  | 7.1   | 102  | 21 AAB24999  |
| 45 | 7  | 7.1   | 108  | 21 AAB24998  |

#### ALIGNMENTS

RESULT 1  
ID AAM67828 standard: Protein; 99 AA.  
XX AAM67828;  
XX  
XX  
DT 25-MAR-1999 (first entry)  
XX  
DB Human secreted protein encoded by gene 22 clone HPERAF1.  
XX  
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;  
KW diagnosis; tissue; cancer; tumor; neurodegenerative disorder; leukemia;  
KW developmental abnormality; foetal deficiency; blood; allergy; renal;  
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
XX  
OS Homo sapiens.  
XX  
XX WO9842738-A1.  
XX  
XX 01-OCT-1998.  
XX  
XX 19-MAR-1998; 98WO-US05311.  
XX  
XX 30-MAY-1997; 97US-0050937.  
XX 21-MAR-1997; 97US-0041276.  
XX 21-MAR-1997; 97US-0041277.  
XX 21-MAR-1997; 97US-0041281.  
XX 21-MAR-1997; 97US-0042344.

Human PRO826 prote  
Human PRO protein,  
Human PRO826. Hom  
Novel human secret  
Human secreted/cra  
Novel human secret  
Human secreted/cra  
Human PRO polypept  
Human secreted/cr  
Human PRO826 polyp  
Human PRO polypept  
Human polypeptide  
Bovine pancreatic  
Human liver peptid  
Peptide #1381 enco  
Peptide #1415 enco  
Protein #1349 enco  
Human brain expres  
Human bone marrow  
Peptide #1374 enco  
Peptide #1407 enco  
Peptide #1350 enco  
Human peptide enco  
Novel human diagno  
Drosophila melanog  
Human 5' EST seque  
Human secreted pro  
Secreted protein e  
Human secreted pro  
Human D2-2 protein  
Human ORF2384 prot  
Calpastatin-like p  
Amino acid sequenc  
Plant SDF encoded  
Plant SDF encoded



PR 30-MAY-1997; 97US-0048069.  
PR 30-MAY-1997; 97US-0048094.  
PR 30-MAY-1997; 97US-0048095.  
PR 30-MAY-1997; 97US-0048096.  
PR 30-MAY-1997; 97US-0048099.  
PR 30-MAY-1997; 97US-0048131.  
PR 30-MAY-1997; 97US-0048135.  
PR 30-MAY-1997; 97US-0048154.  
PR 30-MAY-1997; 97US-0048160.  
PR 30-MAY-1997; 97US-0048186.  
PR 30-MAY-1997; 97US-0048188.  
PR 30-MAY-1997; 97US-0048350.  
PR 30-MAY-1997; 97US-0048351.  
PR 30-MAY-1997; 97US-0048352.  
PR 30-MAY-1997; 97US-0048355.  
PR 05-AUG-1997; 97US-0054804.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA,  
PI Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;  
PI Rosen CA, Ruben SM, Shi Y, Young P;  
XX WPI, 1999-070066/06.  
XX N-PSDB; AAX00632.  
DR  
XX New isolated human genes and the secreted polypeptides they encode -  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders  
XX  
XX Claim 11; Page 285; 385pp; English.  
XX  
XX This sequence represents a secreted human protein encoded by the gene  
CC clone detailed in the descriptor line. The gene can be used to generate  
CC fusion proteins by linking to the gene to a human immunoglobulin Fc  
CC portion (e.g. AAX00602) for increasing the stability of the fused  
CC protein as compared to the human protein only.  
CC The invention relates to 87 novel genes and their fragments (nucleic  
CC acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)  
CC which are useful for preventing, treating or ameliorating medical  
CC conditions e.g. by protein or gene therapy. Also, pathological  
CC conditions can be diagnosed by determining the amount of the new  
CC polypeptides in a sample or by determining the presence of mutations in  
CC the new polynucleotides. Specific uses are described for each of the 87  
CC polynucleotides, based on which tissues they are most highly expressed in  
CC (see AAX00611 for described uses).  
XX  
XX Sequence 99 AA;  
SQ

Query Match 100.0%; Score 99; DB 20; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.76-89;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 DEFLNMHALFESIKRKLPLINMDAPFKLKGLSATPDQAQ 99  
DB 61 DEFLNMHALFESIKRKLPLINMDAPFKLKGLSATPDQAQ 99

RESULT 2  
AAY66681  
ID AAY66681 standard; protein; 99 AA.  
XX  
XX AAY66681;  
AC  
XX  
XX 05-APR-2000 (first entry)  
DT  
XX  
XX Membrane-bound protein PRO826.  
DE  
XX

KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping.  
XX Homo sapiens.  
OS  
XX W09963088-A2.  
FN  
XX  
PD 09-DEC-1999.  
PF  
XX 02-JUN-1999;  
XX 99WO-US12252.  
XX  
XX 02-JUN-1998; 98US-0087607.  
XX 02-JUN-1998; 98US-0087609.  
XX 02-JUN-1998; 98US-0087759.  
XX 03-JUN-1998; 98US-0087827.  
XX 04-JUN-1998; 98US-0088021.  
XX 04-JUN-1998; 98US-0088025.  
XX 04-JUN-1998; 98US-0088028.  
XX 04-JUN-1998; 98US-0088029.  
XX 04-JUN-1998; 98US-0088030.  
XX 04-JUN-1998; 98US-0088033.  
XX 04-JUN-1998; 98US-0088326.  
XX 05-JUN-1998; 98US-0088157.  
XX 05-JUN-1998; 98US-0088202.  
XX 05-JUN-1998; 98US-0088212.  
XX 05-JUN-1998; 98US-0088217.  
XX 05-JUN-1998; 98US-0088255.  
XX 05-JUN-1998; 98US-0088732.  
XX 10-JUN-1998; 98US-0088730.  
XX 10-JUN-1998; 98US-0088734.  
XX 10-JUN-1998; 98US-0088738.  
XX 10-JUN-1998; 98US-0088740.  
XX 10-JUN-1998; 98US-0088741.  
XX 10-JUN-1998; 98US-0088742.  
XX 10-JUN-1998; 98US-0088810.  
XX 10-JUN-1998; 98US-0088811.  
XX 10-JUN-1998; 98US-0088824.  
XX 10-JUN-1998; 98US-0088825.  
XX 10-JUN-1998; 98US-0088826.  
XX 11-JUN-1998; 98US-0088858.  
XX 11-JUN-1998; 98US-0088861.  
XX 11-JUN-1998; 98US-0088863.  
XX 11-JUN-1998; 98US-0088876.  
XX 12-JUN-1998; 98US-0089090.  
XX 12-JUN-1998; 98US-0089105.  
XX 16-JUN-1998; 98US-0089440.  
XX 16-JUN-1998; 98US-0089512.  
XX 16-JUN-1998; 98US-0089514.  
XX 17-JUN-1998; 98US-0089532.  
XX 17-JUN-1998; 98US-0089538.  
XX 17-JUN-1998; 98US-0089598.  
XX 17-JUN-1998; 98US-0089599.  
XX 17-JUN-1998; 98US-0089600.  
XX 17-JUN-1998; 98US-0089653.  
XX 18-JUN-1998; 98US-0089801.  
XX 18-JUN-1998; 98US-0089907.  
XX 18-JUN-1998; 98US-0089908.  
XX 19-JUN-1998; 98US-0089947.  
XX 19-JUN-1998; 98US-0089948.  
XX 19-JUN-1998; 98US-0089952.  
XX 22-JUN-1998; 98US-0090246.  
XX 22-JUN-1998; 98US-0090254.  
XX 22-JUN-1998; 98US-0090255.  
XX 23-JUN-1998; 98US-0090349.  
XX 23-JUN-1998; 98US-0090355.  
XX 24-JUN-1998; 98US-0090429.  
XX 24-JUN-1998; 98US-0090431.  
XX 24-JUN-1998; 98US-0090435.  
XX 24-JUN-1998; 98US-0090444.  
XX 24-JUN-1998; 98US-0090445.  
XX 24-JUN-1998; 98US-0090461.  
XX 24-JUN-1998; 98US-0090472.  
XX 24-JUN-1998; 98US-0090535.

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PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 02-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 10-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 30-JUL-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095316.
PR 10-AUG-1998; 98US-0095829.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 24-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.

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PR 12-JAN-1999; 99US-0115565.
XX (GETH ) GENENTECH INC.
PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
XX Wood WJ, Yuan J;
PI
XX WPI: 2000-072883/06.
DR N-PsDB; AA265018.
XX
XX Membrane-bound proteins and related nucleotide sequences -
PT claim 12; Fig 129; 822pp; English.
XX
XX
PS
XX
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIR
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
SQ Sequence 99 AA;

```

```

Query Match 100.0%; Score 99; DB 21; Length 99;
Best Local Similarity 100.0%; Pred. No. 3,7e-89;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 1 MKIPPLPAVVLISLVLSAQAATGPEEESTIENYASREAFNTPLNIDKLSAFKA 60
DB 1 MKIPPLPAVVLISLVLSAQAATGPEEESTIENYASREAFNTPLNIDKLSAFKA 60
QY 61 DEFLNWHALFESIKRKLPFLNWDAPPKLGLRSATPDQ 99
DB 61 DEFLNWHALFESIKRKLPFLNWDAPPKLGLRSATPDQ 99

```

```

RESULT 3
AAB20117
ID AAB20117 standard; Protein; 99 AA.
XX
XX AAB20117;
XX
XX 30-APR-2001 (first entry)
DT
XX
XX Human immunostimulant PRO826.
DE
XX
XX PRO826; UNQ467; human; immune disease; autoimmune disease;
KW antirheumatic; antirheumatic; antinflammatory; antianemic;
KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;
KW hepatotropic; viticulate; dermatological; antipsoriatic;
KW antiaesthetic; antiallergic; immunostimulant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..22 /label= Signal_peptide
FT 23..99 /label= Mature_protein
FT /label= Mature_protein
FT Modified-site 22..28 "N-myristoylation site"
FT /note= "N-myristoylation site"
FT /note= "N-myristoylation site"
FT 16..48 /note= "homology to peroxidase"
FT Region

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XX  WO200105972-A1.
XX
XX  25-JAN-2001.
XX
XX  15-MAR-2000; 2000WO-US06884.
XX
XX  20-JUL-1999; 99US-0144758.
XX
XX  (GETH ) GENENTECH INC.
XX
XX  Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL,
XX  Hillan KJ, Mark MR, Marsters SA, Pittei RM, Tumas D, Watanabe CK;
XX  Wood WI;
XX  WPI; 2001-103149/11.
XX  N-PSDB; AAF30059.
XX
XX  New PRO polypeptides, nucleic acids and (ant)agonists, useful for
XX  diagnosing and treating immune-related disorders, such as multiple
XX  sclerosis, rheumatoid arthritis and diabetes -
XX
XX  Claim 20; Fig 20; 127pp; English.
XX
XX  The present sequence is that of novel human immunomodulator PRO826
XX  (UNQ467), as deduced from cDNA (see AAF30059) isolated from a
XX  database screening. PRO826 has a mol.wt. of 11 KDa and a pI of
XX  7.47. The invention provides polynucleotides (see AAF30050-62)
XX  encoding novel human PRO proteins (see AAB20108-20) including PRO826.
XX  Claimed compositions comprising these proteins or their agonists
XX  are useful for increasing infiltration of inflammatory cells into
XX  a tissue of a mammal, stimulating or enhancing an immune
XX  response, or increasing the proliferation of T-lymphocytes in a
XX  mammal in response to an antigen. Claimed compositions comprising
XX  a PRO polypeptide or its antagonist have the opposite effect. A
XX  claimed method for treating an immune related disorder, such as a T
XX  cell disorder, involves administering a PRO polypeptide, an agonist
XX  antibody or an antagonist antibody. The disorder is selected from
XX  systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX  juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,
XX  idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
XX  vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
XX  thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated
XX  renal disease, demyelinated diseases (such as multiple sclerosis),
XX  autoimmune chronic active hepatitis, primary biliary cirrhosis,
XX  granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel
XX  disease (ulcerative colitis and Crohn's disease), gluten-sensitive
XX  enteropathy, Whipple's disease, (auto)immune-mediated skin diseases
XX  (such as bullous skin disease, erythema multiforme and psoriasis),
XX  allergic diseases (such as asthma, allergic rhinitis, atopic
XX  dermatitis, food hypersensitivity and urticaria), immunologic
XX  diseases of the lung and transplantation associated diseases (such
XX  as graft rejection and graft-versus-host disease) (all claimed).
XX  Claimed methods of diagnosing these disorders comprises detecting
XX  the level of expression of the PRO gene. Also claimed are a method
XX  of identifying a compound capable of inhibiting the expression or
XX  activity of the PRO polypeptide, vectors, host cells, antibodies,
XX  and a method of stimulating the proliferation of T lymphocytes
XX  using PRO826.
XX
XX  Sequence 99 AA:
XX
XX  Query Match 100.0%; Score 99; DB 22; Length 99;
XX  Best Local Similarity 100.0%; Pred. No. 3,7e-89;
XX  Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

XX  1 MKIPVLPAVVLISLVLSAAGATLGGPEESTIENVASREAFVTPPLNTIDKRSARAKA 60
XX  1 MKIPVLPAVVLISLVLSAAGATLGGPEESTIENVASREAFVTPPLNTIDKRSARAKA 60
XX
XX  61 DEFLNHALFESIKRKLPLNWDAPFKJGIRSATPDAQ 99
XX  61 DEFLNHALFESIKRKLPLNWDAPFKJGIRSATPDAQ 99
XX
XX  RESULT 4
XX  ID AAB65204
XX  AAB65204 standard; Protein: 99 AA.
XX
XX  AAB65204;
XX
XX  02-APR-2001 (first entry)
XX
XX  Human PRO826 (UNQ467) protein sequence SEQ ID NO:201.
XX
XX  Human; secreted and transmembrane protein; PRO; cytosolic;
XX  cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
XX  diagnostic assay.
XX
XX  Homo sapiens.
XX
XX  WO200073454-A1.
XX
XX  07-DEC-2000.
XX
XX  30-MAR-2000; 2000WO-US08439.
XX
XX  02-JUN-1999; 99WO-US12252.
XX  23-JUN-1999; 99US-0141037.
XX  07-JUL-1999; 99US-0143048.
XX  20-JUL-1999; 99US-0144758.
XX  26-JUL-1999; 99US-0145698.
XX  28-JUL-1999; 99US-0146222.
XX  17-AUG-1999; 99US-0149386.
XX  15-SEP-1999; 99WO-US21090.
XX  15-SEP-1999; 99WO-US21547.
XX  08-OCT-1999; 99US-0158663.
XX  30-NOV-1999; 99WO-US28313.
XX  01-DEC-1999; 99WO-US28301.
XX  16-DEC-1999; 99WO-US30095.
XX  20-DEC-1999; 99WO-US30911.
XX  05-JAN-2000; 2000WO-US00219.
XX  06-JAN-2000; 2000WO-US00376.
XX  11-FEB-2000; 2000WO-US03565.
XX  18-FEB-2000; 2000WO-US04341.
XX  22-FEB-2000; 2000WO-US04414.
XX  24-FEB-2000; 2000WO-US04914.
XX  24-FEB-2000; 2000WO-US05004.
XX  15-MAR-2000; 2000WO-US05841.
XX  20-MAR-2000; 2000WO-US06884.
XX
XX  (GETH ) GENENTECH INC.
XX
XX  Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL,
XX  Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
XX  Grimaldi CJ, Gurney AL, Kljavin JF, Napier MA, Pan J, Paoni NF,
XX  Roy MA, Stewart TM, Tumas D, Watanabe CK, Williams PM, Wood WI,
XX  Zhang Z;
XX
XX  WPI; 2001-032160/04.
XX  N-PSDB; AAF44164.
XX
XX  PRO polynucleotides used to produce polypeptides used to target
XX  biocative molecules such as toxins, radiolabels or antibodies, to
XX  specific cells, to cause targeted cell death -
XX
XX  Claim 12; Fig 129; 935pp; English.
XX
XX  The present invention describes human secreted and transmembrane PRO
XX  proteins. The PRO proteins have cytosolic activity. The PRO proteins
XX  can be used for targeted delivery of bioactive molecules, such as
XX  toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
XX  sequences, and their fragments, can be used as hybridisation probes, in
XX  chromosomal and gene mapping, and in the generation of anti-sense RNA
XX  and DNA. They may also be used to produce transgenic animals which are

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CC used to develop and screen therapeutically useful reagents. The PRO  
 CC nucleotide and protein sequence can be used for tissue typing and in  
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX Sequence 99 AA;

Query Match 100.0%; Score 99; DB 22; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-89;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPPLPAVVLSTLVHSAQATLGGPEESTIENYASRPAFTPTPLNIDKLSAFKA 60  
 DB 1 MKIPPLPAVVLSTLVHSAQATLGGPEESTIENYASRPAFTPTPLNIDKLSAFKA 60  
 QY 61 DEFLNWHALFESIRKRLPFLNWDAPPKLKGLSATPPAQ 99  
 DB 61 DEFLNWHALFESIRKRLPFLNWDAPPKLKGLSATPPAQ 99

RESULT 5  
 AAB50916  
 ID AAB50916 standard; Protein; 99 AA.

XX AAB50916;

DT 21-MAR-2001 (first entry)

DE Human PRO826 protein.

XX Human; PRO; antiinflammatory; dermatological; antiarthritic;  
 KM antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;  
 KM antidiabetic; nocotropic; neuroprotective; hepatotropic; virucide;  
 KM antiallergic; antiaschmatic; immune related disorder;  
 KM hepatobiliary disease; autoimmune disease; allergy.

XX Homo sapiens.

PN WO200073452-A2.

PD 07-DEC-2000.

PE 02-JUN-2000; 2000MO-US15264.

XX 02-JUN-1999; 99MO-US12252.

PR 20-JUL-1999; 99US-0144732.

PR 28-JUL-1999; 99US-0144758.

PR 01-SEP-1999; 99MO-US20111.

PR 15-SEP-1999; 99MO-US21090.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99MO-US28313.

PR 01-DEC-1999; 99MO-US28313.

PR 20-DEC-1999; 99US-0170262.

PR 05-JAN-2000; 99MO-US30911.

PR 06-JAN-2000; 2000MO-US00219.

PR 11-FEB-2000; 2000MO-US03565.

PR 18-FEB-2000; 2000MO-US04341.

PR 22-FEB-2000; 2000MO-US04342.

PR 24-FEB-2000; 2000MO-US04914.

PR 15-MAR-2000; 2000MO-US06884.

PR 20-MAR-2000; 2000MO-US07377.

PR 21-MAR-2000; 2000MO-US07377.

PR 30-MAR-2000; 2000MO-US08439.

PR 17-MAY-2000; 2000MO-US13705.

PR 22-MAY-2000; 2000MO-US14042.

PA (GENTH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;

PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;

PI Wood WI;

XX WPI: 2001-02523/03.

DR N-PSDB; AAC91475.

PT Thirty three nucleic acids encoding PRO polypeptides which are useful

XX in the diagnosis and treatment of immune related disorders, e.g.

XX PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

XX chryoiditis and diabetes mellitus -

XX Claim 58, Fig 30; 218pp; English.

PS The present sequence is one of thirty three novel PRO polypeptides.

XX The PRO polypeptides, anti-PRO antibodies, agonists and

XX antagonists are useful for treating and diagnosing immune related

XX disorders such as systemic lupus erythematosus, rheumatoid arthritis,

XX osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,

XX systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's

XX syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

XX anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,

XX immune-mediated renal disease, demyelinating diseases of the central

XX and peripheral nervous systems (such as multiple sclerosis, idiopathic

XX demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic

XX inflammatory demyelinating polyneuropathy), hepatobiliary diseases

XX (such as infectious, autoimmune chronic active hepatitis, primary

XX biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),

XX inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's

XX disease, autoimmune or immune-mediated skin diseases (such as bullous

XX skin diseases, erythema multiforme, contact dermatitis, psoriasis),

XX allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,

XX food hypersensitivity and urticaria), immunological diseases of the

XX lung (such as eosinophilic pneumonia, idiopathic pulmonary fibrosis

XX and hypersensitivity pneumonitis), transplantation associated diseases

XX including graft rejection and graft-versus-host diseases.

XX Sequence 99 AA;

Query Match 100.0%; Score 99; DB 22; Length 99;

Best Local Similarity 100.0%; Pred. No. 3.7e-89;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPPLPAVVLSTLVHSAQATLGGPEESTIENYASRPAFTPTPLNIDKLSAFKA 60  
 DB 1 MKIPPLPAVVLSTLVHSAQATLGGPEESTIENYASRPAFTPTPLNIDKLSAFKA 60

QY 61 DEFLNWHALFESIRKRLPFLNWDAPPKLKGLSATPPAQ 99

DB 61 DEFLNWHALFESIRKRLPFLNWDAPPKLKGLSATPPAQ 99

RESULT 6

ID AAB53094 standard; Protein; 99 AA.

XX AAB53094;

DT 28-FEB-2001 (first entry)

XX Human angiogenesis-associated protein PRO826, SEQ ID NO:158.

DE Human; angiogenesis-associated protein; PRO; endothelial cell growth;

XX cardiac hypertrophy; cardiovascular disorder; endothelial disorder;

XX angiogenic disorder; atherosclerosis; osteoporosis; hypertension;

XX myocardial infarction; diabetic retinopathy; rheumatoid arthritis;

XX Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;

XX Alzheimer's disease; Huntington's disease; stroke; drug screening;

XX gene therapy; transgenic animal.

XX Homo sapiens.

XX WO200053753-A2.  
 XX 14-SEP-2000.  
 PF 05-JAN-2000; 2000WO-US00219.  
 XX 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 XX (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
 XX Godowski PJ, Gunney AP, Hillan KJ, Kuo SS, Mark MR, Masters SA;  
 PI Paoni NF, Pillel RM, Watanabe CK, Williams PM, Wood WJ;  
 XX WPI; 2001-090793/10.  
 DR N-PSDB; AAC97491.  
 XX New isolated nucleic acid for producing a PRO polypeptide, analyzing  
 PT genetic disorders and treating cardiovascular, endothelial or  
 PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
 XX  
 XX Claim 69; Fig 62; 293pp; English.  
 CC The invention relates to novel human angiogenesis-associated proteins  
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
 CC PRO proteins. The invention also relates to vectors and host cells  
 CC comprising a PRO nucleic acid, the recombinant production of a PRO  
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
 CC compounds which inhibit the expression of a PRO gene. The invention  
 CC additionally encompasses methods of identifying modulators of PRO  
 CC expression or activity; diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
 CC mutations in a PRO gene, or the expression level of a PRO gene within a  
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
 CC PRO nucleic acid, and methods of inhibiting or stimulating endothelial  
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
 CC administration of a PRO protein, or an agonist or antagonist thereof.  
 CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
 CC agonists and PRO antagonists may be used as therapeutic agents to treat  
 CC cardiovascular, endothelial or angiogenic disorders, such as  
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
 CC disease, or stroke. PRO nucleic acids are additionally useful in the  
 CC recombinant production of PRO proteins, as hybridization probes to  
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
 CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
 CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
 CC animals useful for the development and screening of potential  
 CC therapeutic agents. The present sequence represents a PRO protein of the  
 CC invention.  
 CC Sequence 99 AA;  
 XX

Query Match 100.0%; Score 99; DB 22; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 3, 7e-89;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKIPVPAVLLSLVTHSAGATLGGPEESTENTASRPAPNTFPLINDKRSAPKA 60  
 DB 1 MKIPVPAVLLSLVTHSAGATLGGPEESTENTASRPAPNTFPLINDKRSAPKA 60  
 QY 61 DEFNLWALFESIRKLPFLNMDAFPPLKGLRSATPDQ 99  
 DB 61 DEFNLWALFESIRKLPFLNMDAFPPLKGLRSATPDQ 99  
 RESULT 7  
 ID ABP69586 standard; Protein; 99 AA.  
 XX  
 AC ABP69586;  
 DT 20-JAN-2003 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 1633.  
 XX  
 KW Human; genome mapping; gene therapy; food supplement; virus; fungus;  
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;  
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;  
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
 KW arthritis; cytostatic; immunomodulator; noctropic; neuroprotective;  
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
 KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
 KW antithrptic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200270539-A2.  
 PD 12-SEP-2002.  
 XX  
 PF 05-MAR-2002; 2002WO-US05095.  
 XX  
 PR 05-MAR-2001; 2001US-0799451.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
 PI Wehrman T, Wang J, Wang D, Dzmanac RT;  
 XX WPI; 2002-759812/82.  
 DR N-PSDB; AB211803.  
 XX  
 PT New polynucleotides comprising sequences assembled from expressed  
 PT sequence tags (ESTs), useful for treating cell-proliferative,  
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or  
 PT platelet or coagulation disorders -  
 XX  
 XX Claim 9; SEQ ID NO 1633; 1012pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated polynucleotide (I) comprising a  
 CC nucleotide sequence selected from any of 948 sequences  
 CC (AB21113-AB212066) or their mature protein coding portion, active domain  
 CC coding protein or complementary sequences. The polynucleotides are useful  
 CC for identifying expressed genes or for physical mapping of human genome.  
 CC The encoded polypeptides (ABP68902-ABP69849) are useful as molecular  
 CC weight markers, as a food supplement, for generating antibodies, in  
 CC cell-proliferative disorders (cancer), neurodegenerative diseases  
 CC (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple  
 CC sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid  
 CC disorders, platelet or coagulation disorders, wound, burns, incision,  
 CC ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,  
 CC parasitic), arthritis, etc.  
 CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 99 AA;

Query Match 100.0%; Score 99; DB 23; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 3,7e-89;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPAVVLISLVLSAQAATGGPEESTIENVASRPFAFTPTPLNDKLSAFKA 60  
 DB 1 MKIPVLPAVVLISLVLSAQAATGGPEESTIENVASRPFAFTPTPLNDKLSAFKA 60

QY 61 DEFLNWHALFESIKRKLPELMDAPFKLGLRSATPDQ 99  
 DB 61 DEFLNWHALFESIKRKLPELMDAPFKLGLRSATPDQ 99

RESULT 8  
 ABB95488  
 ID ABB95488 standard; Protein; 99 AA.  
 XX  
 AC ABB95488;  
 XX  
 DT 19-JUL-2002 (first entry)  
 XX  
 DE Human angiogenesis related protein PRO826 SEQ ID NO: 132.  
 XX  
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiac; cystostatic; antiangiogenic; hypotensive; vulnery;  
 KW antiatherosclerotic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200208284-A2.  
 XX  
 PD 31-JAN-2002.  
 XX  
 PF 09-JUL-2001; 2001WO-US21735.  
 XX  
 XX 20-JUL-2000; 2000US-219556P.  
 XX 25-JUL-2000; 2000US-220624P.  
 XX 25-JUL-2000; 2000US-220664P.  
 XX 28-JUL-2000; 2000WO-US20710.  
 XX 02-AUG-2000; 2000US-222695P.  
 XX 17-AUG-2000; 2000US-0643657.  
 XX 23-AUG-2000; 2000WO-US23522.  
 XX 24-AUG-2000; 2000WO-US23328.  
 XX 07-SEP-2000; 2000US-230978P.  
 XX 15-SEP-2000; 2000US-000000P.  
 XX 18-SEP-2000; 2000US-064610.  
 XX 18-SEP-2000; 2000US-066350.  
 XX 24-OCT-2000; 2000US-242922P.  
 XX 08-NOV-2000; 2000US-0709238.  
 XX 08-NOV-2000; 2000WO-US30952.  
 XX 10-NOV-2000; 2000WO-US30873.  
 XX 01-DEC-2000; 2000WO-US32678.  
 XX 20-DEC-2000; 2000US-0747259.  
 XX 20-DEC-2000; 2000WO-US34956.  
 XX 22-JAN-2001; 2001US-0767609.  
 XX 28-FEB-2001; 2001US-0796498.  
 XX 28-FEB-2001; 2001WO-US06520.  
 XX 01-MAR-2001; 2001WO-US06666.  
 XX 09-MAR-2001; 2001US-0802706.  
 XX 14-MAR-2001; 2001US-0808689.  
 XX 22-MAR-2001; 2001US-0816744.  
 XX 05-APR-2001; 2001US-0828366.  
 XX 10-MAY-2001; 2001US-0854208.  
 XX 10-MAY-2001; 2001US-0854280.  
 XX 25-MAY-2001; 2001US-0866028.  
 XX 25-MAY-2001; 2001US-0866034.  
 XX 25-MAY-2001; 2001WO-US17092.

PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 28-JUN-2001; 2001WO-US00000.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA (BAKER) BAKER K P.  
 PA (FERR) FERRARA N.  
 PA (GERB) GERBER H.  
 PA (GERR) GERRITSEN M E.  
 PA (GODD) GODDARD A.  
 PA (GODO) GODOWSKI P J.  
 PA (GURN) GURNEY A L.  
 PA (HILL) HILLAN K J.  
 PA (MARS) MARSTERS S A.  
 PA (PANJ) PAN J.  
 PA (PAON) PAONI N F.  
 PA (STEP) STEPHAN J F.  
 PA (WATA) WATANABE C K.  
 PA (WILL) WILLIAMS P M.  
 PA (WOOD) WOOD W I.  
 XX  
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX WPI, 2002-171999/22.  
 DR N-PSDB; ABL95626.  
 XX  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX  
 XX Claim 11; Fig 132; 567pp; English.  
 PS  
 XX  
 CC The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a PRO protein of the invention.  
 XX  
 XX Sequence 99 AA;

Query Match 100.0%; Score 99; DB 23; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 3,7e-89;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPAVVLISLVLSAQAATGGPEESTIENVASRPFAFTPTPLNDKLSAFKA 60  
 DB 1 MKIPVLPAVVLISLVLSAQAATGGPEESTIENVASRPFAFTPTPLNDKLSAFKA 60

QY 61 DEFLNWHALFESIKRKLPELMDAPFKLGLRSATPDQ 99  
 DB 61 DEFLNWHALFESIKRKLPELMDAPFKLGLRSATPDQ 99

RESULT 9  
 ABB34040  
 ID ABB34040 standard; Protein; 99 AA.  
 XX  
 AC ABB34040;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Human Pro peptide #11.  
 XX  
 KW Human; PRO; secreted protein; transmembrane protein;  
 KW genetic disorder; tumour; cancer.  
 XX

OS Homo sapiens.  
XX WO200224888-A2.  
XX  
XX 28-MAR-2002.  
XX  
XX 29-AUG-2001; 2001WO-US27099.  
XX  
XX 01-SEP-2000; 2000US-229896P.  
XX 05-SEP-2000; 2000US-230621P.  
XX 22-SEP-2000; 2000US-235147P.  
XX 10-NOV-2000; 2000WO-US30873.  
XX 12-JAN-2001; 2001US-261878P.  
XX 16-JAN-2001; 2001US-261810P.  
XX 16-JAN-2001; 2001US-261939P.  
XX 16-JAN-2001; 2001US-262150P.  
XX 25-JAN-2001; 2001US-264395P.  
XX 02-FEB-2001; 2001US-266421P.  
XX 09-FEB-2001; 2001US-267623P.  
XX 28-FEB-2001; 2001WO-US06520.  
XX 09-MAR-2001; 2001US-274399P.  
XX 03-APR-2001; 2001US-280982P.  
XX 04-APR-2001; 2001US-282129P.  
XX 04-APR-2001; 2001US-282199P.  
XX 09-MAY-2001; 2001US-290589P.  
XX 25-MAY-2001; 2001WO-US17092.  
XX 01-JUN-2001; 2001WO-US17800.  
XX 20-JUN-2001; 2001WO-US19692.  
XX 29-JUN-2001; 2001WO-US21066.  
XX 09-JUL-2001; 2001WO-US21735.  
XX  
XX (GENTH ) GENENTECH INC.  
XX  
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,  
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
XX WPI: 2002-362426/39.  
XX N-PSDB; ABB69971.  
XX  
XX New PRO polypeptides and polynucleotides encoding the polypeptides,  
PT useful in gene therapy, chromosome identification, tissue typing, or  
PT for genetic analysis of individuals with genetic disorders -  
XX  
XX Claim 11; Figure 22; 21pp; English.  
XX  
XX This invention relates to the cDNA and protein sequences of novel  
CC secreted and transmembrane polypeptides PRO polypeptides. The  
CC invention also comprises a method for producing the proteins of the  
CC invention by recombinant means and antibodies specific for the protein  
CC of the invention. The antibody may be used for detecting the PRO  
CC proteins of the invention and may be used to modify their activity.  
CC polynucleotides may be used as hybridisation probes for a cDNA library  
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
CC construct hybridisation probes for mapping the gene which encodes that  
CC PRO and for genetic analysis of individuals with genetic disorders, in  
CC assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knock-out animals which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides are useful in gene therapy, and as molecular weight  
CC markers for protein electrophoresis purposes. The sequences may  
CC also be used to detect overexpression on PRO polypeptides in cancerous  
CC tumours and for screening for differentially expressed genes using  
CC microarray technology. The present sequence represents a human PRO  
CC protein of the invention.  
XX  
XX  
XX Sequence 99 AA:  
SQ  
Query Match 100.0%; Score 99; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred.No. 3.7e-89;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPAVVLISLVLVHSAQAGATLGGPEEBSTENTANTASPEAFNTPLNIDKLSAFKA 60  
DB 1 MKIPVLPAVVLISLVLVHSAQAGATLGGPEEBSTENTANTASPEAFNTPLNIDKLSAFKA 60  
QY 61 DEFLNWHALPESIRKRLPLINWDAFPPLKGLRSATPPAQ 99  
DB 61 DEFLNWHALPESIRKRLPLINWDAFPPLKGLRSATPPAQ 99  
RESULT 10  
ID ABB84882  
AC ABB84882; Protein: 99 AA.  
XX  
XX 16-MAY-2002 (first entry)  
XX  
XX Human PRO826 protein sequence SEQ ID NO:132.  
XX  
XX Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;  
XX vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
XX age-related macular degeneration; arterial revascularization; angina;  
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
XX wound healing; chromosome mapping; gene mapping.  
XX  
XX Homo sapiens.  
XX  
XX WO200200690-A2.  
XX  
XX 03-JAN-2002.  
XX  
XX 20-JUN-2001; 2001WO-US19692.  
XX  
XX 23-JUN-2000; 2000US-213637P.  
XX 20-JUL-2000; 2000US-219556P.  
XX 25-JUL-2000; 2000US-220624P.  
XX 25-JUL-2000; 2000US-220664P.  
XX 28-JUL-2000; 2000WO-US20710.  
XX 02-AUG-2000; 2000US-222695P.  
XX 17-AUG-2000; 2000US-0643657.  
XX 23-AUG-2000; 2000WO-US23522.  
XX 24-AUG-2000; 2000WO-US23328.  
XX 07-SEP-2000; 2000US-230978P.  
XX 18-SEP-2000; 2000US-0664610.  
XX 18-SEP-2000; 2000US-0665350.  
XX 24-OCT-2000; 2000US-242922P.  
XX 08-NOV-2000; 2000US-0709238.  
XX 08-NOV-2000; 2000WO-US30952.  
XX 10-NOV-2000; 2000WO-US30873.  
XX 01-DEC-2000; 2000WO-US32678.  
XX 20-DEC-2000; 2000US-0747259.  
XX 20-DEC-2000; 2000WO-US34956.  
XX 22-JAN-2001; 2001US-0767609.  
XX 28-FEB-2001; 2001US-0796498.  
XX 28-FEB-2001; 2001WO-US06520.  
XX 01-MAR-2001; 2001WO-US06666.  
XX 09-MAR-2001; 2001US-0802706.  
XX 14-MAR-2001; 2001US-0808689.  
XX 22-MAR-2001; 2001US-0816744.  
XX 05-APR-2001; 2001US-0828366.  
XX 10-MAY-2001; 2001US-0854208.  
XX 10-MAY-2001; 2001US-0854280.  
XX 25-MAY-2001; 2001US-0866028.  
XX 25-MAY-2001; 2001US-0866034.  
XX 25-MAY-2001; 2001WO-US17092.  
XX 30-MAY-2001; 2001US-0870574.  
XX 30-MAY-2001; 2001WO-US17443.  
XX 01-JUN-2001; 2001WO-US17800.  
XX  
XX (GENTH ) GENENTECH INC.

```

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Peoni NF,
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX WPI; 2002-090516/12.
DR N-PSDB; ABL88137.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 11; Fig 132; 565bp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cyostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC degeneration, atherosclerosis, hypertension, arterial restenosis,
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC carcinoma) and wound healing. The PRO polynucleotides have applications
CC in molecular biology, including use as hybridisation probes, and in
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC probes used in the exemplification of the present invention.
XX
SQ Sequence 99 AA;
XX
Query Match 100.0%; Score 99; DB 23; Length 99;
Best Local Similarity 100.0%; Pred. No. 3.7e-89;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MKIPVPAVVLSTLVLSAQAATLGGPEESTIENYASRPAFNTPLINIDKLSAFKA 60
DB 1 MKIPVPAVVLSTLVLSAQAATLGGPEESTIENYASRPAFNTPLINIDKLSAFKA 60
XX
QY 61 DEFLNMHALFESIKRKLPLINWDAPFKLGLRSATPDAQ 99
DB 61 DEFLNMHALFESIKRKLPLINWDAPFKLGLRSATPDAQ 99
XX
RESULT 11
ID ABL83664 standard; Protein; 99 AA.
XX
AC ABL83664;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human PRO protein, Seq ID No 146.
XX
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
XX breast cancer; prostate tumour; rectal tumour; liver tumour;
XX pericyte cell proliferation; chondrocyte cell proliferation;
XX tumour necrosis factor-alpha.
XX
OS Homo sapiens.
XX
XX WO200208288-A2.
XX
PN 31-JAN-2002.
XX
PD 29-JUN-2001; 2001WO-US21066.
XX
PF 20-JUL-2000; 2000US-219556P.
XX
XX 25-JUL-2000; 2000US-220585P.
XX
PR 25-JUL-2000; 2000US-220605P.
XX
PR 25-JUL-2000; 2000US-220607P.
XX
PR 25-JUL-2000; 2000US-220624P.
XX
PR 25-JUL-2000; 2000US-220638P.

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PR 25-JUL-2000; 2000US-220666P.
PR 25-JUL-2000; 2000US-220893P.
PR 26-JUL-2000; 2000US-220893P.
PR 28-JUL-2000; 2000WO-US20710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-00000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 26-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX
XX (GETH ) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-172001/22.
XX N-PSDB; ABR33608.
XX
DR 25-JUL-2000; 2000US-220666P.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour.
XX
PS Claim 11; Figure 146; 359bp; English.
XX
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. ABL83592-ABL83713 represent human PRO
CC protein sequences of the invention.
XX
SQ Sequence 99 AA;
XX
Query Match 100.0%; Score 99; DB 23; Length 99;
Best Local Similarity 100.0%; Pred. No. 3.7e-89;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MKIPVPAVVLSTLVLSAQAATLGGPEESTIENYASRPAFNTPLINIDKLSAFKA 60
DB 1 MKIPVPAVVLSTLVLSAQAATLGGPEESTIENYASRPAFNTPLINIDKLSAFKA 60
XX
QY 61 DEFLNMHALFESIKRKLPLINWDAPFKLGLRSATPDAQ 99
DB 61 DEFLNMHALFESIKRKLPLINWDAPFKLGLRSATPDAQ 99
XX
RESULT 12
ID ABL81964 standard; Protein; 99 AA.
XX
AC ABL81964;
XX
DT 09-APR-2002 (first entry)
XX
DE Human PRO826.
XX

```



Human, PRO; antiinflammatory; ophthalmological; vasotropic;  
 retinal cell injury; ocular disease; retinitis pigmentosa;  
 macular degeneration; retinal detachment; retinal tear; retinopathy;  
 retinal degenerative disease; macular hole; degenerative myopia;  
 acute retinal necrosis syndrome; traumatic chorioretinopathy;  
 Putzschner's retinopathy; oedema; ischaemic condition;  
 retinal vision occlusion; collagen vascular disease;  
 thrombocytopenic purpura; uveitis; retinal vasculitis; Sales disease;  
 systemic lupus erythematosus; environmental trauma.

Homo sapiens.

WO200109327-A2.

08-FEB-2001.

28-JUL-2000; 2000WO-US20710.

28-JUL-1999; 99US-146222P.  
 13-SEP-1999; 99WO-US20944.  
 15-SEP-1999; 99WO-US21090.  
 29-NOV-1999; 99WO-US28214.  
 30-NOV-1999; 99WO-US28313.  
 01-DEC-1999; 99WO-US28301.  
 05-JAN-2000; 2000WO-US00219.  
 06-JAN-2000; 2000WO-US00376.  
 11-FEB-2000; 2000WO-US03565.  
 18-FEB-2000; 2000WO-US04341.  
 22-FEB-2000; 2000WO-US04414.  
 24-FEB-2000; 2000WO-US05004.  
 02-MAR-2000; 2000WO-US05841.  
 15-MAR-2000; 2000WO-US06884.  
 30-MAR-2000; 2000WO-US08439.  
 17-MAY-2000; 2000WO-US13705.

(GERTH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;  
 Kljavin IJ, Lafleur M, Mark MR, Marsters SA, Pictl RM;  
 Matanabe CK, Wood WI;

WPI: 2002-130120/17.  
 N-PSDB; ABK28600.

Promoting survival of retinal cells, or delaying or preventing retinal  
 cell injury or death, by contacting retinal cells with PRO175, 220,  
 216, 243, 306, 346, 322, 536, 943, 840, 826, 1068 or PRO1132  
 polypeptide -

Claim 44; Fig 25; 152pp; English.

The invention relates to promoting the survival of retinal cells, or  
 delaying or preventing retinal cell injury or death, by contacting the  
 retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
 PRO243, PRO306, PRO346, PRO322, PRO336, PRO343, PRO840, PRO828, PRO826,  
 PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
 encoding the PRO proteins, a vector comprising the nucleic acid, a host  
 cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
 useful for promoting survival of retinal cells (retinal neurons such as  
 cells, displaced amacrine cells, displaced retinal ganglion cells, anacrine  
 rod photoreceptors, or supportive cells such as Muller cells or pigment  
 epithelial cells), or delaying or preventing retinal cell injury or  
 death caused by ocular disease (which is or is associated with  
 retinitis pigmentosa, macular degeneration, retinal detachment, retinal  
 tear, retinopathy, retinal degenerative disease, macular hole,  
 degenerative myopia, acute retinal necrosis syndrome, traumatic  
 chorioretinopathy or contusion, Putzschner's retinopathy, oedema, an  
 ischaemic condition, central or branch retinal vision occlusion,  
 collagen vascular disease, thrombocytopenic purpura, uveitis, retinal  
 vasculitis, occlusion associated with Sales disease or systemic lupus  
 erythematosus), retinal injury or environmental trauma. The retinal  
 cell injury or death is delayed or prevented by substantially not

CC causing angiogenesis or mitogenesis. The present sequence represents  
 CC a PRO protein.

XX  
 XX  
 SQ Sequence 99 AA;

Query Match 100.0%; Score 99; DB 23; Length 99;  
 Best local similarity 100.0%; Pred. No. 3.7e-89;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKIPVLPAVVLLSLVLSAOGATLGGPEBSESTENYASRPAPNTPFLNIDKRSAPKA 60  
 Db 1 MKIPVLPAVVLLSLVLSAOGATLGGPEBSESTENYASRPAPNTPFLNIDKRSAPKA 60

Qy 61 DEFPLNHALFESIRKRLPLNMDAFPKLGLRSATPDAQ 99  
 Db 61 DEFPLNHALFESIRKRLPLNMDAFPKLGLRSATPDAQ 99

RESULT 13  
 ABUS9097  
 ID ABUS9097 standard; Protein; 99 AA.  
 AC ABUS9097;  
 AC  
 AC  
 DT 28-APR-2003 (first entry)  
 DT  
 XX  
 DE Novel human secreted or transmembrane protein PRO826.  
 XX  
 KW Human, PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disorder;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis; herpetic keratitis; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis.

OS Homo sapiens.

XX  
 XX  
 FN US2002132252-A1.  
 XX  
 XX  
 PD 19-SEP-2002.  
 PD  
 PF 14-NOV-2001; 2001US-0990442.  
 PF  
 XX  
 XX  
 PR 05-NOV-1997; 97WO-US20069.  
 PR 16-SEP-1998; 98WO-US19350.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 06-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.

PR 30-MAR-2000; 2000WMO-US08439.  
 PR 15-MAY-2000; 2000WMO-US13358.  
 PR 17-MAY-2000; 2000WMO-US13705.  
 PR 22-MAY-2000; 2000WMO-US14042.  
 PR 30-MAY-2000; 2000WMO-US14941.  
 PR 02-JUN-2000; 2000WMO-US15264.  
 PR 28-JUL-2000; 2000WMO-US20710.  
 PR 11-AUG-2000; 2000WMO-US22031.  
 PR 23-AUG-2000; 2000WMO-US23522.  
 PR 24-AUG-2000; 2000WMO-US23328.  
 PR 08-NOV-2000; 2000WMO-US30952.  
 PR 01-DEC-2000; 2000WMO-US32678.  
 PR 28-FEB-2001; 2001WMO-US06520.  
 PR 01-JUN-2001; 2001WMO-US17800.  
 PR 20-JUN-2001; 2001WMO-US19692.  
 PR 29-JUN-2001; 2001WMO-US21066.  
 PR 09-JUL-2001; 2001WMO-US21735.  
 PR 16-JUN-1997; 97US-049787P.  
 PR 17-OCT-1997; 97US-062250P.  
 PR 12-NOV-1997; 97US-065311P.  
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 PR 25-FEB-1998; 98US-075945P.  
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 PR 28-MAY-1998; 98US-087106P.  
 PR 02-JUN-1998; 98US-087607P.  
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 PR 04-JUN-1998; 98US-088021P.  
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 PR 09-JUN-1998; 98US-088655P.  
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 PR 16-JUN-1998; 98US-089440P.  
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 PR 18-JUN-1998; 98US-089601P.  
 PR 18-JUN-1998; 98US-089607P.  
 PR 18-JUN-1998; 98US-089608P.  
 PR 28-AUG-2001; 2001US-094192.  
 PR XX  
 PR XX (GETH ) GENENTECH INC.  
 PR XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers I, Eaton DL,  
 PR PI Ferrera N, Fong S, Geber H, Gerritsen ME, Goddard A, Godowski PJ,  
 PR PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;  
 XX WPI; 2003-247083/24.  
 DR N-PSDB; ABX80254.  
 DR XX  
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT are therapeutically useful for enhancing immune response and in cancer  
 PT treatments  
 XX  
 PS Claim 12; Fig 129; 648pp; English.  
 PS XX

CC The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
 CC stimulate adrenal cortical capillary endothelial growth and PRO526,  
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
 CC useful for treating cancerous tumours. PRO812 inhibits vascular  
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 CC cells and is thus useful for inhibiting endothelial cell growth in  
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
 CC immune response. PRO828, PRO826, PRO1068 or PRO1312 enhance survival of  
 CC retinal neurons cells (PRO112 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or redifferentiation of chondrocytes in culture and  
 CC are thus useful for treating sports injuries, and arthritis. This  
 CC is the amino acid sequence of a novel human PRO protein.  
 CC XX

SQ Sequence 99 AA.

Query Match 100.0%; Score 99; DB 24; Length 99;  
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ID ABUS59244 standard; Protein; 99 AA.

AC ABUS59244;

DT 22-APR-2003 (first entry)

DE Human secreted/transmembrane protein, #78.

KW Human; PRO; secreted; transmembrane; pharmaceutical;

KW diagnostic; biosensor; bioreactor; tumour; therapeutic;

KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;

KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.

XX

OS Homo sapiens.  
XX US2003027162-A1.  
XX 06-FEB-2003.  
PD 15-NOV-2001; 2001US-0997428.  
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PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
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PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
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PR 01-JUN-2001; 2001WO-US17800.  
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PR 29-JUN-2001; 2001WO-US21066.  
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PR 23-JUN-1999; 99US-141037P.

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DB 61 DEFLMHALFESIKRKLPLINDAPPKLGLRSATPDQA 99

## RESULT 15

AEUS9393  
ID ABUS9393 standard; Protein; 99 AA.

XX ABUS9393;

DT 22-APR-2003 (first entry)

XX Novel human secreted or transmembrane protein PRO819.

XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;

KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.  
XX Homo sapiens.  
OS US2003027985-A1.  
XX 06-FEB-2003.  
XX 14-NOV-2001; 2001US-0990562.  
XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
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PR 30-MAY-2000; 2000WO-US14941.  
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PR 28-JUN-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
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PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
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PR 03-JUN-1998; 98US-087827P.  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 08:05:08 / Search time 2856 Seconds  
(without alignments)  
1418.086 Million cell updates/sec

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Searched: 2888711 segs, 2045481386 residues

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 510   | 100.0       | 414    | 6     | AX055438    |
| 2          | 510   | 100.0       | 415    | 6     | AR252517    |
| 3          | 510   | 100.0       | 415    | 6     | AX077031    |
| 4          | 510   | 100.0       | 415    | 6     | AX358892    |
| 5          | 510   | 100.0       | 415    | 6     | AX362385    |
| 6          | 510   | 100.0       | 415    | 6     | AX403313    |
| 7          | 510   | 100.0       | 415    | 6     | AX454546    |
| 8          | 510   | 100.0       | 415    | 6     | AX491024    |
| 9          | 510   | 100.0       | 415    | 6     | AX574494    |
| 10         | 510   | 100.0       | 456    | 6     | BD082389    |
| 11         | 510   | 100.0       | 490    | 6     | AX080817    |
| 12         | 503   | 98.6        | 529    | 6     | HS8A293408  |
| 13         | 497   | 97.5        | 435    | 6     | AX080816    |
| 14         | 481   | 94.3        | 432    | 6     | AX080815    |
| 15         | 481   | 94.3        | 432    | 6     | AX080818    |
| 16         | 322.5 | 63.2        | 449    | 10    | AB011028    |
| 17         | 308   | 60.4        | 288    | 6     | AX041085    |
| 18         | 267.5 | 52.5        | 278    | 6     | AR248775    |
| 19         | 140   | 27.5        | 44679  | 9     | CH19F21246  |
| 20         | 106   | 20.8        | 154673 | 2     | AC079472    |
| 21         | 84    | 16.5        | 223443 | 2     | AC112801    |
| 22         | 84    | 16.5        | 252427 | 2     | AC112801    |
| 23         | 82.5  | 16.2        | 590    | 6     | BD025234    |
| 24         | 82    | 16.1        | 104892 | 2     | AC093775    |
| 25         | 82    | 16.1        | 244944 | 2     | AC120613    |
| 26         | 82    | 16.1        | 263584 | 2     | AC099301    |
| 27         | 80    | 15.7        | 75415  | 10    | AL591425    |
| 28         | 80    | 15.7        | 181557 | 10    | AC069014    |
| 29         | 80    | 15.7        | 218866 | 2     | BX323890    |
| 30         | 79.5  | 15.6        | 240273 | 2     | AC109533    |
| 31         | 79    | 15.5        | 235178 | 2     | AC098921    |
| 32         | 78.5  | 15.4        | 700    | 6     | AX135555    |
| 33         | 78.5  | 15.4        | 1000   | 9     | BC011886    |
| 34         | 78.5  | 15.4        | 1579   | 9     | AK096215    |
| 35         | 78.5  | 15.4        | 1982   | 9     | BC035311    |
| 36         | 78.5  | 15.4        | 112626 | 9     | AC035144    |
| 37         | 78    | 15.3        | 11533  | 1     | AB009124    |
| 38         | 78    | 15.3        | 12074  | 1     | AB008089    |
| 39         | 78    | 15.3        | 156508 | 3     | AC007574    |
| 40         | 78    | 15.3        | 171151 | 3     | AC007574    |
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| 43         | 77.5  | 15.2        | 72887  | 2     | AC017882    |
| 44         | 77.5  | 15.2        | 160931 | 3     | AC093498    |
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RESULT 1

## ALIGNMENTS

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LOCUS AX055438 414 bp DNA linear PAT 13-JAN-2001  
DEFINITION Sequence 68 from Patent WO073452.  
ACCESSION AX055438  
VERSION AX055438.1 GI:12228711  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
1 Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L.,  
Tomas, D., Watanabe, C.K. and Wood, W.I.  
Compositions and methods for the treatment of immune related  
diseases  
Patent: WO 0073452-A 68 07-DEC-2000;  
JOURNAL  
Genentech, Inc. (US)  
FEATURES  
source location/Qualifiers  
1. 414  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
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Score: 510.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
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Query Match: 100.00% Indels: 0  
Gaps: 0  
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QY 21 GlnGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTYRAlaSerArg 40  
Db 73 CAGGAGGCCACCCCTGGTGGTCTCTGAAGAAGAACCATTTGAGATTACCGCAGCA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspIleuArgSerAlaPheIysAla 60  
Db 133 CCCGAGGCTTTAAACACCCCGTCTGAACATCGACAATTGCGATCGCTTTAAGCT 192  
QY 61 AspGluPheLeuAsnThrPheIleAlaLeuPheGluSerIleIleuArgIleuProPheLeu 80  
Db 193 GATGAGTTCCTGAACCTGGACGCGCTCTTGAAGTCTATCAAAAGAACTTCCTTCCTC 252  
QY 81 AsnTPAspAlaPheProIleuArgIleuArgSerAlaThrProAspAlaGln 99  
Db 253 AACTGGATGCTTCTTCTTAAGCTGAAGACCTGAAGAGCGCAACTCTGATGCCAG 309  
RESULT 2  
AR252517 415 bp DNA linear PAT 20-DEC-2002  
LOCUS AR252517  
DEFINITION Sequence 200 from patent US 6478825.  
ACCESSION AR252517  
VERSION AR252517.1 GI:27300425  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 415)  
Unclassified.  
AUTHORS Winterebottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.  
TITLE Implant, method of making same and use of the implant for the  
treatment of bone defects  
Patent: US 6478825-A 200 12-NOV-2002;  
JOURNAL  
Location/Qualifiers  
1. 415  
source

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BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN  
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Pred. No.: 3.73e-57 Length: 415  
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QY 21 GlnGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTYRAlaSerArg 40  
Db 73 CAGGAGGCCACCCCTGGTGGTCTCTGAAGAAGAACCATTTGAGATTACCGCAGCA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspIleuArgSerAlaPheIysAla 60  
Db 133 CCCGAGGCTTTAAACACCCCGTCTGAACATCGACAATTGCGATCGCTTTAAGCT 192  
QY 61 AspGluPheLeuAsnThrPheIleAlaLeuPheGluSerIleIleuArgIleuProPheLeu 80  
Db 193 GATGAGTTCCTGAACCTGGACGCGCTCTTGAAGTCTATCAAAAGAACTTCCTTCCTC 252  
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Db 253 AACTGGATGCTTCTTCTTAAGCTGAAGACCTGAAGAGCGCAACTCTGATGCCAG 309  
RESULT 3  
AX077031 415 bp DNA linear PAT 22-FEB-2001  
LOCUS AX077031  
DEFINITION Sequence 19 from Patent WO0105972.  
ACCESSION AX077031  
VERSION AX077031.1 GI:13121661  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
1 Ashkenazi, A.J., Baker, K.P., Fong, S., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Hillan, K.J., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
Tomas, D., Watanabe, C.K. and Wood, W.I.  
Compositions and methods for the treatment of immune related  
diseases  
Patent: WO 0105972-A 19 25-JAN-2001;  
JOURNAL  
Genentech, Inc. (US)  
FEATURES  
source location/Qualifiers  
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/db\_xref="taxon:9606"  
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Score: 510.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
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QY 21 GINGLYALATHTLEUGLYGTYPROGLUGLUGLUSERTHRIEGLUANTYRALASERARG 40

Db 73 CAGGGAGCCACCTGGTGTCTCTGAGGAGAAAGACATTGAGATTATGCGTCACCA 132

QY 41 PROGLUALAPHEANTHRPROPHLEUAANILEASPLYLEUARGSERIALAPHELYSALA 60

Db 133 CCGGAGGCTTTTACACCCCGTTCCTGAAACATGCAAAATTGGATCTCGTTTAAGGCT 192

QY 61 AEPGLUPHELEUAANTHRPHISALALEUPHEGLUSERILLYSARGLYSEUPROPHLEU 80

Db 193 GATGAGTCTCTGAACGCGACGCGCTCTTGAGTCTATCAAAAGAACTTCCTTCTC 252

QY 81 AANTTPAAPALAPHEPROLYSEULYSGLYLEUARGSERIALATHRPROAPALAGIN 99

Db 253 AACTGGAGTGCCTTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCAG 309

RESULT 4

AX358892

LOCUS AX358892 415 bp DNA linear PAT 13-FEB-2002

DEFINITION Sequence 145 from Patent WO0193983.

ACCESSION AX358892

VERSION AX358892.1 GI:18675347

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same Patent: WO 0193983-A 145 13-DEC-2001;

JOURNAL Genentech Inc. (US)

FEATURES

source 1..415

location/Qualifiers

BASE COUNT 99 a 126 c 92 g 98 t

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Alignment Scores:

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Score: 510.00 Matches: 99

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

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Db 13 ATGAAGATCCGGTCTTCTGCGGCTGCTCTCTCCCTCGTGTGCTCACTGTGCC 72

QY 21 GINGLYALATHTLEUGLYGTYPROGLUGLUGLUSERTHRIEGLUANTYRALASERARG 40

Db 73 CAGGGAGCCACCTGGTGTCTCTGAGGAGAAAGACATTGAGATTATGCGTCACCA 132

QY 41 PROGLUALAPHEANTHRPROPHLEUAANILEASPLYLEUARGSERIALAPHELYSALA 60

Db 133 CCGGAGGCTTTTACACCCCGTTCCTGAAACATGCAAAATTGGATCTCGTTTAAGGCT 192

QY 61 AEPGLUPHELEUAANTHRPHISALALEUPHEGLUSERILLYSARGLYSEUPROPHLEU 80

Db 193 GATGAGTCTCTGAACGCGACGCGCTCTTGAGTCTATCAAAAGAACTTCCTTCTC 252

QY 81 AANTTPAAPALAPHEPROLYSEULYSGLYLEUARGSERIALATHRPROAPALAGIN 99

Db 253 AACTGGAGTGCCTTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCAG 309

RESULT 5

AX362385

LOCUS AX362385 415 bp DNA linear PAT 15-FEB-2002

DEFINITION Sequence 145 from Patent WO0208288.

ACCESSION AX362385

VERSION AX362385.1 GI:18694650

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same Patent: WO 0208288-A 145 31-JUN-2002;

JOURNAL Genentech, Inc. (US)

FEATURES

source 1..415

location/Qualifiers

BASE COUNT 99 a 126 c 92 g 98 t

ORIGIN

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Pred. No.: 3.73e-57 Length: 415

Score: 510.00 Matches: 99

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

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QY 21 GINGLYALATHTLEUGLYGTYPROGLUGLUGLUSERTHRIEGLUANTYRALASERARG 40

Db 73 CAGGGAGCCACCTGGTGTCTCTGAGGAGAAAGACATTGAGATTATGCGTCACCA 132

QY 41 PROGLUALAPHEANTHRPROPHLEUAANILEASPLYLEUARGSERIALAPHELYSALA 60

Db 133 CCGGAGGCTTTTACACCCCGTTCCTGAAACATGCAAAATTGGATCTCGTTTAAGGCT 192

QY 61 AEPGLUPHELEUAANTHRPHISALALEUPHEGLUSERILLYSARGLYSEUPROPHLEU 80

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AX403313

LOCUS AX403313 415 bp DNA linear PAT 14-JUN-2002

DEFINITION Sequence 200 from Patent WO0073454.

ACCESSION AX403313

VERSION AX403313.1 GI:21436871

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Batton, D., Ferrar, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,





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Qy 1 MetlyslleProValleuProAlaValleuLeuSerleuLeuValleuHissEra1a 20
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Db 73 CAGGAGGACCACTGGGTGTGTCTGAGGAGAGAGACCACTGAGATTAATGCGTCACGA 132
Qy 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLeuLeuArgSerAlaPheLeuYala 60
Db 133 CCGGAGGCTTTAAACCCCGCTTCTGGAACATCGAACAATGGATCTGCTTAAAGCT 192
Qy 61 AAspGluPheLeuAsnTyrIleAlaLeuPheGluSerIleLeuArgIleuLeuProPheLeu 80
Db 193 GATGAGTCTCTGAACCTGACGCGCTTGTGATCATCAAAAGAACTTCTCTTCCCTC 252
Qy 81 AAsnTPAspAlaPheProlyleuGlyLeuArgSerAlaThrProAspAlaGln 99
Db 253 AACTGGAGTCTCTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTTATGCCCGCAG 309

RESULT 9
LOCUS AX574494 415 bp DNA linear PAT 07-JAN-2003
DEFINITION Sequence 21 from Patent WO0224888.
ACCESSION AX574494
VERSION AX574494.1 GI:27551800
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Baker, K.P., Batton, D.L., Pilvaroff, E., Goddard, A., Grimaldi, J.C.,
Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., Wood, W.I.,
Zhang, Z. and Fong, S.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0224888-A 21 28-MAR-2002;
GENENTECH, INC. (US)
FEATURES
source 1..415
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BASE COUNT 99 a 126 c 92 g 98 t
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Score: 510.00 Matches: 99
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Db 73 CAGGAGGACCACTGGGTGTGTCTGAGGAGAGAGACCACTGAGATTAATGCGTCACGA 132
Qy 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLeuLeuArgSerAlaPheLeuYala 60
Db 133 CCGGAGGCTTTAAACCCCGCTTCTGGAACATCGAACAATGGATCTGCTTAAAGCT 192
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Qy 81 AAsnTPAspAlaPheProlyleuGlyLeuArgSerAlaThrProAspAlaGln 99
Db 253 AACTGGAGTCTCTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTTATGCCCGCAG 309

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LOCUS BD082389 456 bp DNA linear PAT 27-AUG-2002
DEFINITION 87 human secreted proteins.
ACCESSION BD082389
VERSION BD082389.1 GI:22627999
KEYWORDS JP 2001522239-A/31.
SOURCE
ORGANISM Maestadenovirus
Maestadenovirus
Viruses; dsDNA viruses, no RNA stage; Adenoviridae.
REFERENCE
1 (bases 1 to 456)
Young, P., Greene, J.M., Ferrie, A.M., Ruben, S.M., Rosen, C.A.,
Duan, R.D., Hu, J.S., Florence, K.A., Olsen, H.S., Ebner, R.,
Brewer, L.A., Moore, P.A., Shi, Y., Lafleur, D.W. and Ni, J.
87 human secreted proteins
Patent: JP 2001522239-A 31 13-NOV-2001;
HUMAN GENOME SCIENCES INC SECRETARY OF THE DEPARTMENT OF HEALTH
HUMAN SERVICES
PN JP 2001522239-A/31
PD 13-NOV-2001
PF 19-MAR-1998 JP 1998542119
PR 21-MAR-1997 US 60/041281, 21-MAR-1997 US 60/041276 PR
21-MAR-1997 US 60/042344, 21-MAR-1997 US 60/041277 PR
30-MAY-1997 US 60/048355, 30-MAY-1997 US 60/048096 PR
30-MAY-1997 US 60/048351, 30-MAY-1997 US 60/048154 PR
30-MAY-1997 US 60/048160, 30-MAY-1997 US 60/048069 PR
30-MAY-1997 US 60/048131, 30-MAY-1997 US 60/048186 PR
30-MAY-1997 US 60/048095, 30-MAY-1997 US 60/048187 PR
30-MAY-1997 US 60/048092, 30-MAY-1997 US 60/050937 PR
30-MAY-1997 US 60/048352, 30-MAY-1997 US 60/048135 PR
30-MAY-1997 US 60/048188, 30-MAY-1997 US 60/048094 PR
30-MAY-1997 US 60/048350, 05-AUG-1997 US 60/054804 PR
19-AUG-1997 US 60/056370, 02-OCT-1997 US 60/060862 PI
YOUNG, JOHN M GREENE, ANN M FERRIE, STEVEN M RUBEN, CRAIG A PI
ROSEN,
PI ROXANNE D DUAN, JING SHAN HU, KIMBERLY A FLORENCE, HENRIK S
OLSEN,
PI REINHARD EBNER, LAURIE A BREWER, PAUL A MOORE, YANGU SHI, DAVID W
PI LAFLAUR,
PI JIAN NI
PC C07K14/00
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
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Pred. No.: 4.16e-57 Length: 456
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6
US-10-059-395-142 (1-99) x BD082389 (1-456)
Qy 1 MetlyslleProValleuProAlaValleuLeuSerleuLeuValleuHissEra1a 20
Db 21 ATGAAGATCCCGGCTCTTCTGCGGCGGCTCTCTCTCTGTCCTCCACCTGCGC 80
Qy 21 GlnGlyAlaThrleuGlyGlyProGluGluGluSerThrIleGluAsnTyrAlaSerArg 40

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|                |     |  |     |
|----------------|-----|--|-----|
| D <sub>b</sub> | 81  | CAGGAGGCCACCTCGGTGCTCTGAGAGAAAGCACCATTTGAAATTTATCCGTCACGA  | 140 |
| Q <sub>y</sub> | 41  | ProGlu <sup>1</sup> Ala <sup>2</sup> ProAsn <sup>3</sup> Thr <sup>4</sup> ProPhe <sup>5</sup> Leu <sup>6</sup> Asn <sup>7</sup> Ile <sup>8</sup> Asp <sup>9</sup> Leu <sup>10</sup> Arg <sup>11</sup> Ser <sup>12</sup> Ala <sup>13</sup> Phe <sup>14</sup> Leu <sup>15</sup> Ala <sup>16</sup>  | 60  |
| D <sub>b</sub> | 141 | CCCGAGGCGCTTTAACACCCCGTCTCTGAAATCGACAAATTCGATCTCGCTTTAAGGCT  | 200 |
| Q <sub>y</sub> | 61  | AepGlu <sup>1</sup> Phe <sup>2</sup> Leu <sup>3</sup> Asn <sup>4</sup> Trp <sup>5</sup> Ile <sup>6</sup> Ala <sup>7</sup> Leu <sup>8</sup> Phe <sup>9</sup> Glu <sup>10</sup> Ser <sup>11</sup> Ile <sup>12</sup> Val <sup>13</sup> Arg <sup>14</sup> Leu <sup>15</sup> Pro <sup>16</sup> Phe <sup>17</sup> Leu <sup>18</sup>                | 80  |
| D <sub>b</sub> | 201 | GATGAGTTCCCTGGAATCGGCACGCCCTCTTTGAGTCTATATAAAGAGAACTTCTCTTCCCTC  | 260 |
| Q <sub>y</sub> | 81  | Asn <sup>1</sup> Trp <sup>2</sup> Asp <sup>3</sup> Ala <sup>4</sup> Phe <sup>5</sup> Pro <sup>6</sup> Leu <sup>7</sup> Leu <sup>8</sup> Arg <sup>9</sup> Gly <sup>10</sup> Leu <sup>11</sup> Arg <sup>12</sup> Ser <sup>13</sup> Ala <sup>14</sup> Thr <sup>15</sup> Pro <sup>16</sup> Asp <sup>17</sup> Ala <sup>18</sup> Gln <sup>19</sup> | 99  |
| D <sub>b</sub> | 261 | AACAGGATGCCCTTTCTTAAGCTGAAAGACCTGAGAGGCGCACCTCTGATGCCAGC   | 317 |

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|------------|------------------------------------|-------------|----------|--------|-----|--------|-----------------|
| DEFINITION | Sequence 63 from Patent WO0109327. | ACCESSION   | AX080817 |        |     |        |                 |
| VERSION    | AX080817.1                         | GI:13169786 |          |        |     |        |                 |
| KEYWORDS   |                                    |             |          |        |     |        |                 |
| SOURCE     | synthetic construct                |             |          |        |     |        |                 |
| ORGANISM   | synthetic construct                |             |          |        |     |        |                 |
|            | artificial sequences.              |             |          |        |     |        |                 |

**AUTHORS**  
ASHKAEV, I. A., BAKER, K. P., GODDARD, A., GODOWSKI, P. J., GURNEY, A. L.,  
KILAVNH, I. J., LAFLEUR, M., MARK, M. R., MARSTERS, S. A., PITCH, R. M.,  
MARANABE, C. K. and WOOD, W. I.

**TITLE**  
Method of preventing the injury or death of retinal cells and  
treating ocular diseases

**JOURNAL**  
Patent; WO 0109377-A 63 08-FEB-2001;  
Genentech, Inc. (US)

| FEATURES   | source | Location/Qualifiers   |
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|            |        | /mol_type="genomic DNA"   |
|            |        | /db_xref="taxon:32630"  |
|            |        | /note="Virtual DNA fragment used in the isolation of DNAs7694." |
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| ORIGIN     | 149 c  | 107 t   |

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| Pred. No.:             | 4.53e-57 |
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US-10-059-395-142 (1-99) X AX080817 (1-490)

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| Oy | MetVslleProValleuProValValleuLeuSerIleuValleuHisSerAla         | 20  |
| Db | ATGAGAGTCCCGGCTCTCTCGCCGGTGGTCTCTCTCCCTGGTGTCTCACTCTGCC        | 139 |
| Oy | GlnGlyValAthrLeuGlyGlyProGlnGlnGlnSerThrIleGluAsnTyrAlaSerArg  | 40  |
| Db | 140 CAGGAGACCACCCCTGGGTGGTCTCTGAGAAAGAAAGACCATGAGAAATTATGCTCAG | 199 |
| Oy | ProGlnValAphaAanthrProPheLeuAsnIleAspValGluArgSerAlaPheValVala | 60  |
| Db | 200 CCGAGGCGCTTTAACCCCGCTCTCGAACATGACAAATTCGAGTCCGCTTAAAGCT    | 258 |
| Oy | AspGlnPheLeuAsnTrpHisAlaLeuPheGlnSerIleTyrArgValLeuProPheLeu   | 80  |
| Db | 260 GATGAGTTCCTGAACAGGACGCGCTCTTGTAGTCAATCAAAAGAACTCTCTTTCCTC  | 319 |
| Oy | AsnTrpAsnAlaPheProValGlyLeuValGlyLeuArgSerAlaThrProAsnAlaGln   | 99  |
| Db | 320 AACGGGATGCTTTCTCTAAGCTGAAGAAGACCTGAGAGGCAACTCTCGAATGCCAG   | 376 |

|            |   |
|------------|---|
| RESULT 12  |   |
| HSA293408  | 529 bp mRNA linear PRI 06-JAN-2003  |
| LOCUS      |   |
| DEFINITION | Homo sapiens mRNA differentially expressed in malignant melanoma,<br>Clone NN 15. |
| ACCESSION  | AJ293408  |
| VERSION    | AJ293408.1 GI:27526545  |
| KEYWORDS   | differential expression; malignant; melanoma.                                     |
| SOURCE     | Homo sapiens (human)  |
| ORGANISM   | Homo sapiens  |

| REFERENCE  |
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| AUTHORS<br>TITLE<br>JOURNAL<br>REFERENCE   |
| 1<br>Deichmann, M., Thome, M., Wacker, J. and Naeher, H.<br>Genes differentially expressed in malignant melanoma<br>Unpublished<br>2 (bases 1 to 529)                      |
| AUTHORS<br>TITLE<br>JOURNAL<br>REFERENCE   |
| Direct Submission<br>Submitted (28-JUN-2000) Deichmann M., Dermatology, University of<br>Heidelberg, Voestrasse 2, 69115 Heidelberg, GERMANY<br>Location/Qualifiers<br>E70 |
| FEATURES   |

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NN 15"
1. .529
mRNA

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| /note="differentially expressed in malignant melanoma" |       |       |       |
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| BASE COUNT   | 133 a | 157 c | 126 g |
| ORIGIN   |       |       | 113 t |

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| Gaps:                  | 0        |

US-10-059-395-142 (1-99) X HSA293408 (1-529)

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| Oy | 1   | MetysllePvovLleuProAlaValIleuIeuSerIeuValIeuHiserAla        | 20  |
| Db | 51  | ATGAGAGATCCCGGTCCTTCCTGGCGGGTGTCTCTCTCCCTCGGGTCACTGCTCC     | 110 |
| Oy | 21  | GInglYAlaThrIleuGlYglYProgluGlIuIuSerThrIleGluaNtYAlaserArg | 40  |
| Db | 111 | CAGGAGGCGACCCCTGGGTGTCTCGAGGAGAGAAAGCACCATTTAGAAATTAGCGGTCA | 170 |
| Oy | 41  | ProgluAlaPheAsnThrProPheIuAsnIleAspYsIeuArgSerAlaPheYsAla   | 60  |
| Db | 171 | CCCCAGGCGCTTAAACACCCCGTCTCTGAACTGCACAAATTGCATTCGCGTTAAAGCT  | 230 |
| Oy | 61  | AspGIuPheIuAsnTPH:IaAlaIeuPheGIuSerIleYsArgYsIeuProPheIu    | 80  |
| Db | 231 | GATGATGTTCTTGAACCTGCACGCGCTCTTTAGTGTATCAAGGAACTTCCTTCCCTC   | 290 |
| Oy | 81  | AsnTPAspAlaPheProYsIeuYsGIuArgSerAlaThrProAspAlaGln         | 99  |
| Db | 291 | AACGTGGATGCTTCTTCTTAAGCTGAAGGAGCTGAGAGAGCGCAACTCTGATGCCAG   | 347 |

RESULT 13  
 LOCUS AX080816  
 DEFINITION Sequence 62 from Patent WO0109327.  
 ACCESSION AX080816  
 VERSION AX080816.1 GI:13169785  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 1 synthetic construct  
 synthetic construct  
 artificial sequences.

**AUTHORS** Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L., Kljavin, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M., Watanabe, C.K. and Wood, W.I.  
**TITLE** Method of preventing the injury or death of retinal cells and treating ocular diseases  
**JOURNAL** Patent: WO 0109327-A 62 08-FEB-2001;  
 Genentech, Inc. (US)  
**FEATURES** Location/Qualifiers  
 source 1..435  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="Virtual DNA fragment used in the isolation fo DNA57694."

**BASE COUNT** 108 a 130 c 96 g 101 t

**ORIGIN**

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| Alignment Scores:                           | Pred. No.: | Score: | Percent Similarity: | Best Local Similarity: | Query Match: | Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
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**DB** 15 ATGAAGATCCCGGTCCTTCTGCGGTCCTCTCCCTCGTGTCCACCTGCGC 74

**QY** 21 GINGIYATHTLEUGLYGLYPROGIUGIUGUSERTHIIEGUAANTYRLASERARG 40

**DB** 75 CAGGAGCCACCCCTGGGTGCTCTGAGAGAAAGACCATGAGAAATTATGCGTCACCA 134

**QY** 41 -Progliala pheasantProphel euansileaplysleuargserialathProaspalagin 60

**DB** 135 CCCCAGGCGCTTTAAACCCCGTCTCTGAACATGCAATTCGCGATCGCGTTTAAAGC 194

**QY** 60 aapggclupheleuAentTTPHialaleuphegluserIlelyeAryglyleuProphelu 80

**DB** 195 TATATGATTCCTGAACTGACAGCCCTCTTGAAGTCTATCAAAAGAACTTCTTCT 254

**QY** 80 uAentTpaapalaphProlysleuulgyleuargserialathProaspalagin 99

**DB** 255 CAACCTGGATGCTTTCTTAAGCTGAAGACTGAAGACCGCACTCTGATGCCAG 312

**RESULT 14**

**LOCUS** AX080815 432 bp DNA linear PAT 27-FEB-2001

**DEFINITION** Sequence 61 from Patent WO0109327.

**ACCESSION** AX080815

**VERSION** AX080815.1 GI:13169784

**KEYWORDS** synthetic construct  
 synthetic construct  
 artificial sequences.

**ORGANISM** Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L., Kljavin, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M., Watanabe, C.K. and Wood, W.I.  
 Method of preventing the injury or death of retinal cells and treating ocular diseases  
 Patent: WO 0109327-A 61 08-FEB-2001;  
 Genentech, Inc. (US)  
**FEATURES** Location/Qualifiers  
 source 1..432  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="Virtual DNA fragment used in the isolation of DNA57694."

**BASE COUNT** 106 a 127 c 94 g 102 t 3 others

**ORIGIN**

**Alignment Scores:**

| Alignment Scores:                           | Pred. No.: | Score: | Percent Similarity: | Best Local Similarity: | Query Match: | Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
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**DB** 13 ATGAAGATCCCGGTCCTTCTGCGGTCCTCTCCCTCGTGTCCACCTGCGC 72

**QY** 21 GINGIYATHTLEUGLYGLYPROGIUGIUGUSERTHIIEGUAANTYRLASERARG 40

**DB** 73 CAGGAGCCACCCCTGGGTGCT-CTTGAAGAAAGACCATGAGAAATTATGCGTCACCA 131

**QY** 41 Progliala pheasantProphel euansileaplysleuargserialathProaspalagin 60

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**QY** 61 AapgiupheleuAentTTPHialaleuphegluserIlelyeAryglyleuProphelu 80

**DB** 192 GATGAGTCTCTGAACTGACAGCCCTCTTGAAGTCTATCAAAAGAACTTCTTCTC 251

**QY** 81 AentTpaapalaphProlysleuulgyleuargserialathProaspalagin 99

**DB** 252 AACTGGATGCTTTCTTAAGCTGAAGACTGAAGACCGCAACTCTGATGCCCA 308

**RESULT 15**

**LOCUS** AX080818 432 bp DNA linear PAT 27-FEB-2001

**DEFINITION** Sequence 64 from Patent WO0109327.

**ACCESSION** AX080818

**VERSION** AX080818.1 GI:13169787

**KEYWORDS** Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

**ORGANISM** Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L., Kljavin, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M., Watanabe, C.K. and Wood, W.I.  
 Method of preventing the injury or death of retinal cells and treating ocular diseases  
 Patent: WO 0109327-A 64 08-FEB-2001;  
 Genentech, Inc. (US)  
**FEATURES** Location/Qualifiers  
 source 1..432  
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**BASE COUNT** 106 a 127 c 94 g 102 t 3 others

**ORIGIN**

**Alignment Scores:**

| Alignment Scores:                           | Pred. No.: | Score: | Percent Similarity: | Best Local Similarity: | Query Match: | Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
|---|------------|--------|---------------------|------------------------|--------------|---------|----------|---------------|-------------|---------|-------|
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**DB** 13 ATGAAGATCCCGGTCCTTCTGCGGTCCTCTCCCTCGTGTCCACCTGCGC 72

**QY** 1 MetlysileProvalleuProalavalValleuSerleuValleuHisserala 20

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Db 73 CAGGAGGCCACCCCTGGGTGT-CCTGAGGAGAGAAAGCACCATTTGAGAAATTATGCCGCACGA 131
Oy 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60
Db 132 CCCGAGGCGCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCCGTTAAGGCT 191
Oy 61 AspGluPheLeuAsnThrPheAlaLeuPheGlnUserIleLysArgLysLeuProPheLeu 80
Db 192 GATGAGTTCCTGAACTGGCACGCCCTCTTGAGTCTATCAAAAGGAACTTCCTTCCTC 251
Oy 81 AsnTpaAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99
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Job time : 2865 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

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(without alignments)  
794.490 Million cell updates/sec

Title: US-10-059-395-142

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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|------------|-------|-------------------|----------------------------|--------------------|
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| 2          | 267.5 | 52.5              | 288 4 US-09-313-294A-4134  | Sequence 4134, Ap  |
| 3          | 78.5  | 15.4              | 686 3 US-09-328-111-364    | Sequence 364, App  |
| 4          | 67.5  | 13.2              | 1830121 4 US-09-557-884-1  | Sequence 1, Appli  |
| 5          | 67.5  | 13.2              | 1830121 4 US-09-643-990A-1 | Sequence 1, Appli  |
| 6          | 66.5  | 13.0              | 1230025 4 US-09-198-452A-1 | Sequence 1, Appli  |
| 7          | 65.5  | 12.8              | 234 4 US-09-107-532A-2008  | Sequence 2008, Ap  |
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| 9          | 65    | 12.7              | 1830121 4 US-09-643-990A-1 | Sequence 1, Appli  |
| 10         | 63    | 12.4              | 11461 3 US-08-669-161A-29  | Sequence 29, Appl  |
| 11         | 62.5  | 12.3              | 2523 4 US-09-620-312D-2990 | Sequence 290, Appl |
| 12         | 62.5  | 12.3              | 4084 3 US-08-866-340-1     | Sequence 1, Appli  |

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| 14   | 62.5 | 12.3 | 7216 2 US-08-750-703-3     | Sequence 3, Appli  |
| 15   | 62   | 12.2 | 936 4 US-09-252-991A-1763  | Sequence 1763, Ap  |
| 16   | 62   | 12.2 | 1845 4 US-09-328-352-1350  | Sequence 1350, Ap  |
| c 17 | 62   | 12.2 | 71989 4 US-09-443-501A-2   | Sequence 2, Appli  |
| c 18 | 62   | 12.2 | 162450 4 US-09-345-882-1   | Sequence 1, Appli  |
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| c 23 | 61   | 12.0 | 771 4 US-09-252-991A-13016 | Sequence 13016, A  |
| c 24 | 60.5 | 11.9 | 655 4 US-09-288-143-20     | Sequence 20, Appl  |
| 25   | 60.5 | 11.9 | 1893 4 US-09-252-991A-1131 | Sequence 3131, Ap  |
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| c 29 | 59.5 | 11.7 | 537 4 US-09-397-787-48     | Sequence 48, Appl  |
| c 30 | 59.5 | 11.7 | 621 4 US-09-221-017B-375   | Sequence 375, App  |
| c 31 | 59.5 | 11.7 | 702 4 US-09-328-352-1933   | Sequence 1933, Ap  |
| 32   | 59.5 | 11.7 | 869 3 US-08-998-416-518    | Sequence 518, App  |
| 33   | 59.5 | 11.7 | 2253 4 US-09-107-532A-2214 | Sequence 2214, Ap  |
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| c 37 | 59   | 11.6 | 3520 4 US-09-220-132-84    | Sequence 84, Appl  |
| c 38 | 59   | 11.6 | 3684 4 US-09-252-991A-65   | Sequence 65, Appl  |
| c 39 | 59   | 11.6 | 7527 4 US-09-252-991A-71   | Sequence 71, Appl  |
| c 40 | 59   | 11.6 | 40123 4 US-08-311-731A-137 | Sequence 137, Appl |
| 41   | 59   | 11.6 | 4403765 3 US-09-103-840A-2 | Sequence 2, Appli  |
| 42   | 58.5 | 11.5 | 1095 3 US-08-882-501-31    | Sequence 31, Appl  |
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#### ALIGNMENTS

RESULT 1  
US-09-996-243-200  
Sequence 200, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanpeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paul, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P.C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16







Percent Similarity: 39.19% Conservative: 6  
 Best Local Similarity: 31.08% Mismatches: 20  
 Query Match: 15.39% Indels: 25  
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US-10-059-395-142 (1-99) x US-09-328-111-364 (1-686)

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 DB 209 TTTGACACTTCTGAGAGATTATTAATCCAGCTGGTTTCATCACTGGATGCCATA 268  
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 QY 71 GUSerlleySArgLySleuProPheLeuAsnTrpAspAla 84  
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RESULT 4  
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 ; Sequence 1, Application US/09557884  
 ; Patent No. 6506581  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fleischmann et al.  
 ; TITLE OF INVENTION: The Nucleotide sequence of  
 ; the Haemophilus influenzae Rd Genome, Fragments  
 ; thereof, and Uses Thereof  
 ;  
 ; NUMBER OF SEQUENCES: 1  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Human Genome Sciences, Inc.  
 ; STREET: 9410 Key West Avenue  
 ; CITY: Rockville  
 ; STATE: MD  
 ; COUNTRY: USA  
 ; ZIP: 20850  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3 1/2 inch diskette  
 ; COMPUTER: Dell Pentium  
 ; OPERATING SYSTEM: MS DOS v6.22  
 ; SOFTWARE: ASCII Text  
 ;  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/557,884  
 ; FILING DATE: 25-Apr-2000  
 ; CLASSIFICATION: <Unknown>  
 ;  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/476,102  
 ; FILING DATE: JUN-5-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Michelle S. Marks  
 ; REGISTRATION NUMBER: 41,971  
 ; REFERENCE/DOCKET NUMBER: PB186P3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 301-309-8504  
 ; TELEFAX: 301-309-8439  
 ;  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1830121 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ;  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-557-884-1

Alignment Scores:  
 Pred. No.: 2,27e+05 Length: 1830121  
 Score: 67.50 Matches: 7  
 Best Local Similarity: 66.67% Mismatches: 13  
 Query Match: 43.33% Indels: 9  
 DB: 9 Gaps: 9

Query Match: 13.24% Indels: 1  
 DB: 4 Gaps: 1

US-10-059-395-142 (1-99) x US-09-557-884-1 (1-1830121)

QY 54 LeuAIGSerAlaPheLySaLaSpGluPheLeuAsnTrpHisAlaLeuPheGluSerIle 73  
 |||||:::|||||  
 DB 1299803 CTCAAAAGTGGCGTAAGAAAAAGAAACGTTTATGATGGCATTCATCATAAAAAATAG 1299862  
 QY 74 Lys---ArgLySleuProPheLeuAsnTrp 82  
 |||||:::|||||  
 DB 1299863 AAAGAGAGAAATATAATCCCAATTGG 1299892

RESULT 5  
 US-09-643-990A-1  
 ; Sequence 1, Application US/09643990A  
 ; Patent No. 6528289  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robert D. Fleischmann  
 ; Mark D. Adams  
 ; Owen White  
 ; Hamilton O. Smith  
 ; J. Craig Venter  
 ;  
 ; TITLE OF INVENTION: The Nucleotide sequence of  
 ; the Haemophilus influenzae Rd Genome, Fragments  
 ; thereof, and Uses Thereof  
 ;  
 ; NUMBER OF SEQUENCES: 1  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Human Genome Sciences, Inc.  
 ; STREET: 9410 Key West Avenue  
 ; CITY: Rockville,  
 ; STATE: MD  
 ; COUNTRY: USA  
 ; ZIP: 20850  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3 1/2 inch diskette  
 ; COMPUTER: Dell Pentium  
 ; OPERATING SYSTEM: MS DOS v6.22  
 ; SOFTWARE: ASCII Text  
 ;  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/643,990A  
 ; FILING DATE: 23-Aug-2000  
 ; CLASSIFICATION: <Unknown>  
 ;  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/487,429  
 ; FILING DATE: 1995-06-07  
 ; APPLICATION NUMBER: 08/426,787  
 ; FILING DATE: 1995-04-21  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kenley K. Hoover  
 ; REGISTRATION NUMBER: 40,302  
 ; REFERENCE/DOCKET NUMBER: PB186P1C1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 301-610-5790  
 ; TELEFAX: 310-309-8439  
 ;  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1830121 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ;  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-643-990A-1

Alignment Scores:  
 Pred. No.: 2,27e+05 Length: 1830121  
 Score: 67.50 Matches: 13  
 Best Local Similarity: 66.67% Conservative: 7  
 Query Match: 43.33% Mismatches: 9  
 DB: 4 Gaps: 1

US-10-059-395-142 (1-99) x US-09-643-990A-1 (1-1830121)

Qy 54 leuArgSerAlaPheIysAlaAspGluPheLeuAsnTrpHisAlaLeuPheGluSerIle 73  
Db 1299803 CTCGAAAGTCGCGTAAAGAAAAAGAACGTTTTCGATTGGCATTCATCAATAAAAAATTAG 1299862  
Qy 74 Lys--ArgIysLeuProPheLeuAsnTrp 82  
Db 1299863 AAAGAGAGGAAATATAAATCCCAATTGG 1299892

RESULT 6  
US-09-198-452A-1  
Sequence 1, Application US/09198452A  
Patent No. 6559294  
GENERAL INFORMATION:  
APPLICANT: Griffiths, R.  
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
FILE REFERENCE: 9710-003-999  
CURRENT APPLICATION NUMBER: US/09/198,452A  
CURRENT FILING DATE: 1998-11-24  
NUMBER OF SEQ ID NOS: 6849  
SEQ ID NO 1  
LENGTH: 1230025  
TYPE: DNA  
ORGANISM: Chlamydia pneumoniae  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(15000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (15001)..(30000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (30001)..(45000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (45001)..(60000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (60001)..(75000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (75001)..(90000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (90001)..(105000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (105001)..(120000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (120001)..(135000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (135001)..(150000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (150001)..(165000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (165001)..(180000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (180001)..(195000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (195001)..(210000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (210001)..(225000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature

LOCATION: (225001)..(240000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (240001)..(255000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (255001)..(270000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (270001)..(285000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (285001)..(300000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (300001)..(315000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (315001)..(330000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (330001)..(345000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (345001)..(360000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (360001)..(375000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (375001)..(390000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (390001)..(405000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (405001)..(420000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (420001)..(435000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (435001)..(450000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (450001)..(465000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (465001)..(480000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (480001)..(495000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (495001)..(510000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (510001)..(525000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (525001)..(540000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (540001)..(555000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (555001)..(570000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (570001)..(585000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (585001)..(600000)

OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (600001)..(615000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (615001)..(630000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (630001)..(645000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (645001)..(660000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (660001)..(675000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (675001)..(690000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (690001)..(705000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (705001)..(720000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (720001)..(735000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (735001)..(750000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (750001)..(765000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (765001)..(780000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (780001)..(795000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (795001)..(810000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (810001)..(825000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (825001)..(840000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (840001)..(855000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (855001)..(870000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (870001)..(885000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (885001)..(900000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature  
LOCATION: (900001)..(915000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc\_feature

Alignment Scores:  
Pred. No.: 1.78e+05 Length: 1230025  
Score: 66.50 Matches: 19  
Percent Similarity: 46.15% Conservative: 11  
Best Local Similarity: 29.23% Mismatches: 28  
Query Match: 13.04% Indels: 7  
Gaps: 4  
Ds: 1

US-10-059-395-142 (1-99) x US-09-198-452A-1 (1-1230025)  
Qy 11 LeuLeuSerLeuLeuValLeuHisSerAlaGlnGlyAlaThrLeuGlyProGluGlu 30  
Db 1034560 TTAATATATCTTGCGCTATGACTACATAATATGTTCTCGATGATATCTTAAT 1034619  
Qy 31 GluSerThrIleGluAsnTyraSerAlaPheGlyProGluAlaPheAsnThrProPheLeuAsn 50  
Db 1034620 GAAATTACTGTGGAGATACAAAAACGTTTGAAGCCATGCTGGAGATATTATGAA 1034679  
Qy 51 IleAspTyrLeuArgSerAlaPheLeuAlaAspGluPheLeuAsnTrpHisAlaLeuPhe 70  
Db 1034680 ATTGAT-----GGGATATGATTTTACCATATTCAGAGACATTC 1034718  
Qy 71 GluSerIleLeuArg 75  
Db 1034719 TCGAGCATCAACCG 1034733

RESULT 7  
US-09-107-532A-2008  
Sequence 2008, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 2008:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 234 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (B) LOCATION 1...234  
SEQUENCE DESCRIPTION: SEQ ID NO: 2008:  
US-09-107-532A-2008  
Alignment Scores:



STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1  
US-09-643-990A-1

Alignment Scores:  
Pred. No.: 4.62e+05 Length: 1830121  
Score: 65.00 Matches: 22  
Percent Similarity: 45.33% Conservative: 12  
Best Local Similarity: 29.33% Mismatches: 35  
Query Match: 12.75% Indels: 6  
DB: 4 Gaps: 2

US-10-059-395-142 (1-99) x US-09-643-990A-1 (1-1830121)

QY 26 GlyylProgluGlulSerThrIleGlulSerAlaSerArgProgluAlaPheAsn 45  
DB 1767958 GGGGAGACGACCGCGTTCTTATTAATGTTGCTAATGCTCTTGCTAAACAGGATATGAT 1767899

QY 46 ThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsn 65  
DB 1767898 GTTCTTTTATTAAGATTGGCGGTAAACAAGCCTTTTCCAAAGTTGATGAAAAATTAT 1767839

QY 66 TrpHisAlaLeuPheGluSerIleLysArgLysLeuProPhe--LeuAsnTrpAspAla 84  
DB 1767838 ATTACGCAATG-----AATAAATGCCCTATTCAATGAAAAAGATTAT 1767794

QY 85 PheProLysLeuLysGlyLeuLysSerAlaThrProAspAlaGln 99  
DB 1767793 TTTTCTATCATTAAATAAATTAAAGAAATTGTTAAAGAAATTACAG 1767749

RESULT 10  
US-08-669-161A-29/c  
Sequence 29, Application US/08669161A  
Patent No. 6013481  
GENERAL INFORMATION:  
APPLICANT: Debacker, Olivier, Van den Eynde,  
APPLICANT: Benoit, Boon-Falleur, Thierry  
TITLE OF INVENTION: Isolated, truncated Nucleic Acid  
TITLE OF INVENTION: Molecules Which Code For GAGS Tumor Rejection Antigen,  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felte & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,161A  
FILING DATE: 24-June-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/531,662  
FILING DATE: 21-September-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/370,648  
FILING DATE: 10-January-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/250,162  
FILING DATE: 27-May-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/096,039  
FILING DATE: 22-July-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6013481man D.  
REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5443  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11461 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-669-161A-29

Alignment Scores:  
Pred. No.: 496 Length: 11461  
Score: 63.00 Matches: 29  
Percent Similarity: 38.05% Conservative: 14  
Best Local Similarity: 25.66% Mismatches: 26  
Query Match: 12.35% Indels: 44  
DB: 3 Gaps: 6

US-10-059-395-142 (1-99) x US-08-669-161A-29 (1-11461)

QY 2 LysIleProValLeuProAlaValAlaLeuLysSerLeuValLeuHis-----Ser 19  
DB 7347 CAATCCCGCTCTCACAGACACTTACACTCTGCGCTTACATGCGATGAGT 7288

QY 20 AlaGlnGlyAlaThrLeuGlyGlyProgluGlulSerThrIleGlulSerAlaSer 39  
DB 7287 AGCCACCAATTAACGCTG-----AGTGAAGAAACTCTTTAAATATCATGAAA 7240

QY 40 ArgProgluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLys 59  
DB 7239 AAGCCC-----AAACTACAGAAATATTCTGCAA 7213

QY 60 AlaAspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLys-----74  
DB 7212 ACC-----AACTGCTTATCTCTCCAAATATGCGTATGCGATGACAG 7165

QY 75 -----ArgLysLeuPro-----78  
DB 7164 AAAAATTAAAGAAACATTACAGTTAAAGAAATTAAACACCTGAAAGACATGCAA 7105

QY 79 -----PheLeuAsnTrpAspAlaPheProLysLeuLys 89  
DB 7104 GGTGTGATTCTCACTGACTGTGATCAGAAAAAGAAA 7066

RESULT 11  
US-09-620-312D-290  
Sequence 290, Application US/09620312D  
Patent No. 6569662  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhang, Jie  
APPLICANT: Ren, Feiyan  
APPLICANT: Chen, Rui-hong  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wehrman, Tom  
APPLICANT: Xue, Aidong J.  
APPLICANT: Yang, Yonghong  
APPLICANT: Wang, Jlan-Rui  
APPLICANT: Zhou, Ping  
APPLICANT: Ma, Yungding  
APPLICANT: Wang, Dunrui  
APPLICANT: Wang, Zhiwei  
APPLICANT: John Tillinghast  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 784CIP2B  
CURRENT APPLICATION NUMBER: US/09/620,312D  
CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 1105  
SOFTWARE: pc\_Fl\_genes Version 1.0  
SEQ ID NO 290  
LENGTH: 2523  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (81)..(2138)  
US-09-620-312D-290

Alignment Scores:  
Pred. No.: 58  
Score: 62.50  
Percent Similarity: 34.78%  
Best Local Similarity: 26.96%  
Query Match: 12.25%  
Length: 2523  
Matches: 31  
Conservative: 9  
Mismatch: 38  
Indels: 37  
Gaps: 5

US-10-059-395-142 (1-99) x US-09-620-312D-290 (1-2523)

QY 11 LeuLeuSerLeuLeuValLeuHisSerAlaGlnGlyAlaThrLeuGlyProGluGlu 30  
1086 TTAATCTGCTATTCTTTAGTCTGTTCTGACACTGTGTACTTGAACCAAGAA 1145

QY 31 GluSerThrIleGluLeuSerArgProGluAlaPheAsnThrProPheLeuAsn 50  
1146 AGAAGAGTGTAGAAATTTATTTAGTGAACCAAGACTACTGCGACAGAAATTTGTAAT 1205

QY 51 -----IleAspIleLeuArg----- 55  
1206 CCTGTGAGATATATGATGTGTGTGTCACAAATAATTATGAACCTGAGAAATACTT 1265

QY 56 -----SerAlaPheLeuSala-----AspGluPheLeu 64  
1266 GAAAGGTGAGGCTGATCAGATTACTCTGAGAGAAAGATCCTGAGAAATCTTG 1325

QY 65 AsnTrpHisAlaLeuPheGluSerIleLeuArgIleLeuProPheLeuAsnTrpAspAla 84  
1326 AAT-----ATTCTGTTTCATCATATTTTAAGGTGAACCTTGCTTAATA----- 1370

QY 85 PheProIleLeuLeuGlyLeuArgSerAlaThrProAspAlaGln 99  
1371 -----ATTAAGATCAGCAGTCAAAAGGTACAA 1397

RESULT 12  
US-08-866-340-1/c  
Sequence 1, Application US/08866340  
Patent No. 6020318  
GENERAL INFORMATION:  
APPLICANT: Sytef, Moshe  
APPLICANT: Bigey, Pascal  
APPLICANT: Ramchandani, Shyam  
TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE AND DORR LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: United States of America  
ZIP: 02109  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/866,340  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Keown, Wayne A.  
REGISTRATION NUMBER: 33,923  
REFERENCE/DOCKET NUMBER: 106,101,187  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4084 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-866-340-1

Alignment Scores:  
Pred. No.: 121  
Score: 62.50  
Percent Similarity: 56.60%  
Best Local Similarity: 33.96%  
Query Match: 12.25%  
Length: 4084  
Matches: 18  
Conservative: 12  
Mismatch: 11  
Indels: 3  
Gaps: 3

US-10-059-395-142 (1-99) x US-08-866-340-1 (1-4084)

QY 44 PheAsnThrProPheLeuAsnIleAspIleLeuArgSerAlaPheLeuAlaAspGluPhe 63  
2745 TTTGAAACTCCATGG-----GAAAAAATGCAAAATCCATTAAAGAAAAACAATT 2695

QY 64 LeuAsnTrp-----HisAlaLeuPheGluSer-----IleLeuArg 75  
2694 CTTTATTGAGCCACAAAGTGTGTCAGTCAATTGTTGTAATAAGAAAAATTTAAGAGG 2635

QY 76 LysLeuProPheLeuAsnTrpAspAlaPheProIleLeu 88  
2634 AGATTACCTTTCTGTGTTAAGCTGCTCTTCCAAATCTT 2596

RESULT 13  
US-09-103-875-4/c  
Sequence 4, Application US/09103875A  
Patent No. 6221849  
GENERAL INFORMATION:  
APPLICANT: Sytef, Moshe  
APPLICANT: Bigey, Pascal  
APPLICANT: Ramchandani, Shyam  
TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC SEQUENCES AND ANTISENSE  
FILE REFERENCE: 106101,194  
CURRENT APPLICATION NUMBER: US/09/103,875A  
CURRENT FILING DATE: 1998-06-24  
EARLIER APPLICATION NUMBER: 60/069,865  
EARLIER FILING DATE: 1997-12-17  
EARLIER APPLICATION NUMBER: 08/866,340  
EARLIER FILING DATE: 1997-05-30  
NUMBER OF SEQ ID NOS: 138  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 4  
LENGTH: 4460  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-103-875-4

Alignment Scores:  
Pred. No.: 139  
Score: 62.50  
Percent Similarity: 56.60%  
Best Local Similarity: 33.96%  
Length: 4460  
Matches: 18  
Conservative: 12  
Mismatch: 12

Query Match: 12.25% Indels: 11  
DB: 3 Gaps: 3  
US-10-059-395-142 (1-99) x US-09-103-875-4 (1-4460)  
QY 44 PheantrhProPheLeuAniLeaApLySeLaArgSerAlaPheLyAlaAapLuphe 63  
DB 2743 TTTGAACTCCATGG-----GAAAAATGCAAAATCCATTAAAGAAAAACAATTT 2693  
QY 64 LeuAnTrp--HialaleuPhegluser-----lleyaArg 75  
DB 2692 CTTTATGAGCCACAAAGTGTGTCAGTCAGATTGTAATAGAAAAATTTAAGAGG 2633  
QY 76 LysLeuProPheLeuAnTrpAapAlaPheProLySeLau 88  
DB 2632 AGATTACCTTTCTGTGTAAGCTGTCTCTTCCAAATCTT 2594  
RESULT 14  
US-08-750-703-3  
; Sequence 3, Application US/08750703  
; Patent No. 5891633  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Frank J.; Idle, Jeffrey R.  
; TITLE OF INVENTION: DEFECTS IN DRUG  
; TITLE OF INVENTION: METABOLISM  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morgan & Plimegan  
; STREET: 345 Park Ave.  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10154-0053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/750,703  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/07605  
; FILING DATE: 16-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dorothy R. Auth  
; REGISTRATION NUMBER: 36,434  
; REFERENCE/DOCKET NUMBER: 2026-4196PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-4800  
; TELEFAX: (212) 751-6849  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7216 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA  
; FEATURE:  
; NAME/KEY: CYP2A6v2  
; LOCATION:  
; OTHER INFORMATION:  
US-08-750-703-3  
Alignment Scores:  
Pred. No.: 290 Length: 7216  
Score: 62.50 Matches: 30  
Percent Similarity: 37.07% Conservative: 13  
Best Local Similarity: 25.86% Mismatches: 32  
Query Match: 12.25% Indels: 41  
DB: 2 Gaps: 5

US-10-059-395-142 (1-99) x US-08-750-703-3 (1-7216)  
QY 5 ValLeuProAlaValValLeuSerLeuLeuValLeuHisSerAlaGlnGlyAlaThr 24  
DB 2974 ATGCTCCCTACCCAGGCTCTTGAATATTTTAACACCCGGAACCCCTGGGTAAACC 3033  
QY 25 -----LeuGlyGlyProGlnGlnGlnSerThr1leglu 35  
DB 3034 TTCCTGTAAACTTAGAGATTAGTTCTTATCCGCCCCCTCTGAA-----ATACCT 3084  
QY 36 AsnTyAlaSerArgProGlnAlaPheAnThr----- 46  
DB 3085 AACACAC---CGAGACACAGATGCTTTAACTCACTTCCTCTTCTATGAAACAAATCC 3141  
QY 47 -----ProPheLeuAniLeaApLySeLauArg 55  
DB 3142 CATTCACATCAGCTTCGCCCCGTGACAGCTGTCTTCCTCCATCTCTCTCTGCA 3201  
QY 56 SerAlaPheLyAlaAapGluPheLeuAnTrpHisAlaLeuPhegluser1leyaArg 75  
DB 3202 CCCAGCTC-----TATGAGATGTTCTCTTGATGATGAA 3237  
QY 76 LysLeuProPheLeuAnTrpAapAlaPheProLySeLauGlyLeu 91  
DB 3238 CACCTGCCAGGACCGCAGCAAGGCTTTCAGTTGCTGCAAGGCTG 3285  
RESULT 15  
US-09-252-991A-1763  
; Sequence 1763, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCES: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 1763  
; LENGTH: 936  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-1763  
Alignment Scores:  
Pred. No.: 15.1 Length: 936  
Score: 62.00 Matches: 25  
Percent Similarity: 51.14% Conservative: 20  
Best Local Similarity: 28.41% Mismatches: 23  
Query Match: 12.16% Indels: 20  
DB: 4 Gaps: 5  
US-10-059-395-142 (1-99) x US-09-252-991A-1763 (1-936)  
QY 18 HisSerAlaGlnGlyAlaThrLeuGlyGlyProGlnGlnGlnSerThr1legluAnTrp 37  
DB 652 AACGCTGCGTGGCGGCGGCTTCTTCCGCGCGGCGGAGCTTCACCTGAGACCTG 711  
QY 38 AlaSerArgProGlnAlaPheAnThrProPheLeuAniLeaApLySeLaArgSerAla 57  
DB 712 GCCAGCCG-----TTTTCG-----GTCAACCTGTGAAGCTCCAGACGCG 753  
QY 58 PheLyAlaAapGlu-----PheLeuAnTrpHisAla 68  
DB 754 CCGCAGAACGCGAGGAGATCGCAGGCGCTGCGCAGCGGCGGATCAAGTGCACATAC 813  
QY 69 LeuPhegluser1leya-----ArgLySeLauProPheLeu--AsnTrpAap 83  
DB 814 ATCGAAGATCTCTGCGCACTACCAACCAAGCGCTTCCTCTGTCGAACAGAT 873

Qy 84 AlapheProlystleuylsGlyLeu 91  
|||  
Db 874 GCGAGCCGATCTATCGATGCGCTG 897  
:::|||||

Search completed: November 28, 2003, 09:42:29  
Job time : 958 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 07:55:16 ; Search time 26 seconds

(without alignment)  
366.181 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 510  
Sequence: 1 MKIPVPAVVLISLVLSA.....LNWDAFPKUKRSAPPAQ 99

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 76    | 14.9        | 234    | 2     | D81342      |
| 2          | 74    | 14.5        | 807    | 2     | S29242      |
| 3          | 73    | 14.3        | 390    | 2     | G97561      |
| 4          | 72.5  | 14.2        | 741    | 2     | G84888      |
| 5          | 70    | 13.7        | 500    | 2     | T36090      |
| 6          | 69    | 13.5        | 521    | 2     | S55318      |
| 7          | 69    | 13.5        | 521    | 2     | S34184      |
| 8          | 69    | 13.5        | 522    | 2     | A28789      |
| 9          | 68.5  | 13.4        | 871    | 2     | E97035      |
| 10         | 68    | 13.3        | 292    | 2     | AB3564      |
| 11         | 68    | 13.3        | 522    | 2     | S51557      |
| 12         | 68    | 13.3        | 1225   | 1     | B64234      |
| 13         | 67.5  | 13.2        | 459    | 2     | A75097      |
| 14         | 67    | 13.1        | 208    | 2     | AF0278      |
| 15         | 67    | 13.1        | 263    | 1     | S23009      |
| 16         | 66.5  | 13.0        | 366    | 2     | S46727      |
| 17         | 66.5  | 13.0        | 376    | 2     | AB3905      |
| 18         | 66    | 12.9        | 360    | 2     | AB3534      |
| 19         | 66    | 12.9        | 443    | 2     | AF1901      |
| 20         | 66    | 12.9        | 1044   | 2     | T43800      |
| 21         | 66    | 12.9        | 1298   | 2     | T47523      |
| 22         | 65.5  | 12.8        | 321    | 2     | C89823      |
| 23         | 65.5  | 12.8        | 506    | 2     | C83181      |
| 24         | 65.5  | 12.8        | 518    | 2     | B87754      |
| 25         | 65.5  | 12.8        | 2434   | 2     | S44661      |
| 26         | 65    | 12.7        | 301    | 2     | H95308      |
| 27         | 65    | 12.7        | 353    | 2     | F64175      |
| 28         | 65    | 12.7        | 368    | 2     | A71727      |
| 29         | 65    | 12.7        | 670    | 2     | S77463      |

|    |      |      |      |   |        |                    |
|----|------|------|------|---|--------|--------------------|
| 30 | 65   | 12.7 | 735  | 2 | D86465 | probable integral  |
| 31 | 65   | 12.7 | 736  | 2 | D90574 | hypothetical prote |
| 32 | 64.5 | 12.6 | 519  | 2 | S54300 | transketolase (EC  |
| 33 | 64.5 | 12.6 | 583  | 2 | JT0395 | DNA-binding protei |
| 34 | 64.5 | 12.6 | 1350 | 2 | T13254 | nitric-oxide synth |
| 35 | 64.5 | 12.6 | 1400 | 2 | T31555 | hypothetical prote |
| 36 | 64   | 12.5 | 253  | 1 | PMRTM  | hypothetical prote |
| 37 | 64   | 12.5 | 480  | 2 | T18905 | phosphoglycerate m |
| 38 | 64   | 12.5 | 569  | 2 | B99587 | hypothetical prote |
| 39 | 64   | 12.5 | 732  | 2 | T40861 | hypothetical zinc  |
| 40 | 63.5 | 12.5 | 129  | 2 | A98038 | hypothetical prote |
| 41 | 63.5 | 12.5 | 397  | 2 | AD0040 | hypothetical prote |
| 42 | 63.5 | 12.5 | 663  | 2 | A97066 | aromatic-amino-aci |
| 43 | 63.5 | 12.5 | 1777 | 2 | AC2088 | transketolase, TKT |
| 44 | 63   | 12.4 | 659  | 2 | B81082 | serine/threonine k |
| 45 | 63   | 12.4 | 856  | 2 | AD0042 | transketolase NMB1 |

## ALIGNMENTS

RESULT 1  
D81342  
tRNA (guanine-N1)-methyltransferase (EC 2.1.1.31) Cj0713 [imported] - Campylobacter jej  
C/Species: Campylobacter jejuni  
C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
C/Accession: D81342  
R/Parthill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chillin  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel  
Nature 403, 665-668, 2000  
A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp  
A/Reference number: A81250; MUID:20150912; PMID:1068204  
A/Accession: D81342  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-234 <PAR>  
A/Cross-references: GB:AL139076; GB:AL111168; NID:G65968128; PIDN:CA872987.1; PID:G6596817  
A/Experimental source: serotype O2, strain NCTC 11168  
C/Genetics:  
A/Gene: trmD; Cj0713  
A/Superfamily: tRNA (guanine-N1) methyltransferase  
C/Keywords: methyltransferase; S-adenosylmethionine

Query Match 14.9%; Score 76; DB 2; Length 234;  
Best Local Similarity 33.0%; Pred. No. 1;  
Matches 29; Conservative 10; Mismatches 39; Indels 10; Gaps 5;

QY 6 LPVVLSLVLSHQAQATIGPE--ESTTENTASREAPFPTPLNIDKRSAPKADRF 63  
DB 142 LPALVWCD-ALIRNVNG-VLGWMSLEBSFENNILBAPAFSKPTFEKDKKFTTPSEF 199  
QY 64 LNW-HALFESIKR-----KLPLNWDAP 85  
DB 200 LKGNHARIASLKTILASCKTKFRPDLF 227

RESULT 2  
S29242  
sucrose synthase (EC 2.4.1.13) Ssl - barley  
N/Acronym names: sucrose-UDP glucosyltransferase; UDPglucose-fructose glucosyltransfer  
C/Species: Hordeum vulgare (barley)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 18-Jun-1999  
C/Accession: S29242; S21494  
R/de la Hoz, P.S.; Vicente-Carballo, J.; Mena, M.; Carbonero, P.  
FEBS Lett. 310, 46-50, 1992  
A/Title: Homologous sucrose synthase genes in barley (Hordeum vulgare) are located in ch  
A/Reference number: S29242; MUID:92405741; PMID:1388123  
A/Accession: S29242  
A/Molecule type: mRNA  
A/Residues: 1-807 <HOZ>  
A/Cross-references: EMBL:X65871; NID:g19105; PIDN:CAA46701.1; PID:g19106  
C/Genetics:  
A/Map position: 7H

|                          |       |                |            |             |
|--------------------------|-------|----------------|------------|-------------|
| Query Match              | 13.5% | Score 69;      | DB 2;      | Length 521; |
| Best Local Similarity    | 27.0% | Pred. NO. 16;  |            |             |
| Matches 27; Conservative | 17;   | Mismatches 32; | Indels 24; | Gaps 5;     |

```

Qy 1 MKIPVLPAVVLISLVLSA---QGATLGGPEESTIENYASRPAPNTPFLINDKLSA 57
Db 81 IQIGRPVVVLSGSTVQALIKG-----DFAGRPDLYSFRFLIN-DGKSLA 127

Qy 58 FKADEFNLWHLFESIKRKLPLNWDAPPKLGLRSATPD 97
Db 128 FSTDQAGWRA-----RRKLAYSALRSFATLEG---TTPPE 159

RESULT 7
334184
cytochrome P450 1A1 - plaice
C:Species: Pleuronectes platessa (plaice)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-Jul-2000
C:Accession: S34184
R:Leaver, M.J.; Piritt, L.; George, S.G.
submitted to the EMBL Data Library, June 1993
A:Reference number: S34184
A:Accession: S34184
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-521 <LEA>
A:Cross-references: EMBL:X73631; NID:g313316; PIDN:CA52010.1; PID:g313317
A:Gene: CYP1A1
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: chromoprotein; heme; iron; metalloprotein
F:319-485/Domain: cytochrome P450 homology <P45>
F:463/Binding site: heme iron (Cys) (axial ligand) #status predicted.

Query Match
Best Local Similarity 13.5%; Score 69; DB 2; Length 521;
Matches 27; Conservative 16; Mismatches 33; Indels 24; Gaps 5;

Qy 1 MKIPVLPAVVLISLVLSA---QGATLGGPEESTIENYASRPAPNTPFLINDKLSA 57
Db 81 IQIGRPVVVLSGSTVQALIKG-----DFAGRPDLYSFRFLIN-DGKSLA 127

Qy 58 FKADEFNLWHLFESIKRKLPLNWDAPPKLGLRSATPD 97
Db 128 FSTDQAGWRA-----RRKLAYSALRSFATLEG---TTPPE 159

RESULT 8
A28789
cytochrome P450 1A1, hepatic - rainbow trout
N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 28-Jul-2000
R:Heilmann, L.D.; Sheen, Y.Y.; Bigelow, S.W.; Nebert, D.W.
DNA 7, 379-387, 1988
A:Title: Trout P4501A1: cDNA and deduced protein sequence, expression in liver, and evol
A:Reference number: A28789; MUID:89978171; PMID:3203599
A:Accession: A28789
A:Molecule type: mRNA
A:Residues: 1-522 <HEA>
A:Cross-references: GB:M21310; NID:g213779; PIDN:AAA49550.1; PID:g213780
A:Note: the authors translated the codon TCC for residue 241 as Phe
C:Genetics:
A:Gene: CYP1A1
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: chromoprotein; electron transfer; heme; iron; liver; metalloprotein; monooxy
F:319-485/Domain: cytochrome P450 homology <P45>
F:463/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match
Best Local Similarity 13.5%; Score 69; DB 2; Length 522;
Matches 28; Conservative 15; Mismatches 33; Indels 24; Gaps 5;

Qy 1 MKIPVLPAVVLISLVLSA---QGATLGGPEESTIENYASRPAPNTPFLINDKLSA 57

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```

Db 81 IQIGRPVVVLSGSTVQALIKG-----DFAGRPDLYSFRFLIN-DGKSLA 127

Qy 58 FKADEFNLWHLFESIKRKLPLNWDAPPKLGLRSATPD 97
Db 128 FSTDQAGWRA-----RRKLAYSALRSFATLEG---TTPPE 159

RESULT 9
E97035
DNA polymerase I, polA [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: E97035
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E97035
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-871 <KUR>
A:Cross-references: GB:A8001437; PIDN:AAK79072.1; PID:g15024015; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1098
C:Superfamily: DNA-directed DNA polymerase I

Query Match
Best Local Similarity 13.4%; Score 68.5; DB 2; Length 871;
Matches 31; Conservative 15; Mismatches 36; Indels 29; Gaps 5;

Qy 16 VLHSAQATLGGPEESTIENYASRP-----AFNTPF-LNIDKLSAFKDEFILNW 66
Db 213 VLDMNQ--NIGKKIKENLVYAEQAVSKKLATIMTVPEIDIEIRSKESFVEGAR 270

Qy 67 HAL-----FESIKRKLPLNWDAPPKLGLRSATPD 99
Db 271 HLRLRLOPKSIIEKIPSLNVAEKSDFVEYNLIDEPKFEHLPSAIKOTE 321

RESULT 10
AB3564
D-ribose-binding periplasmic protein precursor BMEI10435 [imported] - Brucella melitensis
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C:Accession: AB3564
R:DelVecchio, V.G.; Kaparat, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, I.
Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Leese
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis.
A:Reference number: AD3252; PMID:11756688
A:Accession: AB3564
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-292 <KUR>
A:Cross-references: GB:A8008918; PIDN:AAL53677.1; PID:g17984597; GSPDB:GN00191
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI10435
A:Map position: II
C:Superfamily: D-galactose-binding protein

Query Match
Best Local Similarity 13.3%; Score 68; DB 2; Length 292;
Matches 25; Conservative 12; Mismatches 35; Indels 22; Gaps 3;

Qy 15 LVHSAQATLGGPEESTIENYASRPAPNTPFLINDKLSAFKADFLNWLHFLFESIK 74
Db 104 LVSNNAQAAALGAATQWVSDGKGYVELFGAPSDNNAATRSNG-----YETVL 152

Qy 75 RKLPL-----NMD-----AFPLKGLRSATPD 97

```



A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-263 <SNR>  
 A:Cross-references: EMBL:X54979; NID:g435; PIDN:CAA38723.1; PID:g436  
 A/Note: the authors translated the codon TGG for residue 30 as Cys  
 C/Superfamily: insulin-like growth factor binding protein 1; thyroglobulin type I repeat  
 F:180-255/Domain: thyroglobulin type I repeat homology <THYI>

Query Match 13.1%; Score 67; DB 1; Length 263;  
 Best Local Similarity 29.6%; Pred. No. 11;  
 Matches 24; Conservative 12; Mismatches 35; Indels 10; Gaps 4;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 14  | LVVHSAQGATLGGPEESTIENVASRPFAFNTPFINIDKLSAFKADPEL-NWHALFES | 72  |
| Db | 96  | LHALTRGGQACMTSPCDEAIDTKDTTSPF-----NVSPESEITQEQULDNFHLMAES | 148 |
| Qy | 73  | IKRKLPFLNWDAPPKLKGLRS                                     | 93  |
| Db | 149 | -SEDLPII-MNAISNYESLRA                                     | 167 |

Search completed: November 28, 2003, 07:57:40  
 Job time : 31 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: November 28, 2003, 07:33:16 ; Search time 17 Seconds

(without alignments)  
273.861 Million cell updates/sec

Title: US-10-059-395-142

Sequence: 1 MKRPLVPLAVYLISLVLRHSA.....LNMDFPKKLGKRSATPDQAQ 99

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 76    | 14.9        | 234    | 1     | TRMD_CAMJE  |
| 2          | 74    | 14.5        | 807    | 1     | SUS1_HORVU  |
| 3          | 71    | 13.9        | 521    | 1     | CP11_PLAFL  |
| 4          | 69    | 13.5        | 521    | 1     | CP11_PLAFL  |
| 5          | 69    | 13.5        | 521    | 1     | CP11_PLAFL  |
| 6          | 68.5  | 13.4        | 413    | 1     | ACDS_PIG    |
| 7          | 68    | 13.3        | 522    | 1     | CP11_ONCMY  |
| 8          | 68    | 13.3        | 1225   | 1     | Y309_MYCGE  |
| 9          | 67    | 13.1        | 263    | 1     | IBP1_BOVIN  |
| 10         | 67    | 13.1        | 521    | 1     | CP11_LIMLI  |
| 11         | 67    | 13.1        | 521    | 1     | CP11_LIMLI  |
| 12         | 66.5  | 13.0        | 366    | 1     | YHP7_YEAST  |
| 13         | 66    | 12.9        | 1044   | 1     | BUB1_SCHPO  |
| 14         | 65.5  | 12.8        | 506    | 1     | YNM3_YEAST  |
| 15         | 65.5  | 12.8        | 1053   | 1     | TP2M_CARBL  |
| 16         | 65    | 12.7        | 353    | 1     | YG98_HABIN  |
| 17         | 65    | 12.7        | 358    | 1     | Y165_RICPR  |
| 18         | 64.5  | 12.6        | 519    | 1     | TKTC_CRAFL  |
| 19         | 64.5  | 12.6        | 568    | 1     | GAGJ_DROME  |
| 20         | 64.5  | 12.6        | 1349   | 1     | NOS_DROME   |
| 21         | 64    | 12.5        | 252    | 1     | PMG2_MOUSE  |
| 22         | 64    | 12.5        | 252    | 1     | PMG2_MOUSE  |
| 23         | 63    | 12.4        | 1709   | 1     | CHD1_HUMAN  |
| 24         | 62.5  | 12.3        | 520    | 1     | CP11_DICLA  |
| 25         | 62    | 12.2        | 339    | 1     | OYE1_YEAST  |
| 26         | 62    | 12.2        | 437    | 1     | EP1G_HUMAN  |
| 27         | 62    | 12.2        | 437    | 1     | EP1G_HUMAN  |
| 28         | 62    | 12.2        | 437    | 1     | EP1G_MOUSE  |
| 29         | 62    | 12.2        | 525    | 1     | Y107_METUA  |
| 30         | 61.5  | 12.1        | 1711   | 1     | CHD1_MOUSE  |
| 31         | 61.5  | 12.1        | 339    | 1     | IC11_TRIHA  |
| 32         | 61.5  | 12.1        | 433    | 1     | UROK_MOUSE  |
| 33         | 61.5  | 12.1        | 872    | 1     | IP3L_RAT    |

|    |      |      |      |   |            |
|----|------|------|------|---|------------|
| 34 | 61.5 | 12.1 | 1233 | 1 | HCVA_OCTDO |
| 35 | 61.5 | 12.1 | 1247 | 1 | NOS_ANOST  |
| 36 | 61.5 | 12.1 | 2896 | 1 | HCYV_OCTDO |
| 37 | 61   | 12.0 | 521  | 1 | CP11_LIZAU |
| 38 | 61   | 12.0 | 521  | 1 | CP11_LIZAU |
| 39 | 61   | 12.0 | 669  | 1 | CYR2_YEAST |
| 40 | 61   | 12.0 | 3061 | 1 | FOUG_PYTBU |
| 41 | 60.5 | 11.9 | 248  | 1 | GPWA_METAC |
| 42 | 60.5 | 11.9 | 384  | 1 | TMFB_TREPH |
| 43 | 60.5 | 11.9 | 563  | 1 | YAS8_SCHPO |
| 44 | 60.5 | 11.9 | 1216 | 1 | PIB1_BOVIN |
| 45 | 60.5 | 11.9 | 1216 | 1 | PIB1_HUMAN |

## ALIGNMENTS

RESULT 1  
TRMD\_CAMJE ID TRMD\_CAMJE STANDARD, PRT, 234 AA.

AC Q9PJ4;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-  
DE methyltransferase) (CRNA [GM37] methyltransferase).  
GN TRMD OR CJO713.  
OS Campylobacter jejuni.  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
OC Campylobacteraceae; Campylobacter.  
OX NCBI\_TaxID=197;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NCTC 11168;  
RX MEDLINE=20150912; PubMed=10688204;  
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,  
RA Basham D., Chillingworth T., Davies R.M., Feltham T., Holtroyd S.,  
RA Jags K., Kariyasev A.V., Moule S., Pallen M.J., Penn C.W.,  
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,  
RA Whitehead S., Barrett B.G.;  
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni  
RT reveals hypervariable sequences.";  
RL Nature 403:665-668(2000).  
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs  
CC (By similarity).  
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-  
CC homocysteine + tRNA containing N(1)-methylguanine.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.

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DR EMBL: AL139076; CAB72987.1; -  
DR PIR: D81342; D81342.  
DR HAMAP: MF\_00605; -; 1.  
DR InterPro: IPR002649; tRNA\_mIG\_MT.  
DR Pfam: PF01746; tRNA\_mIG\_MT; 1.  
DR ProDom: PD004978; tRNA\_mIG\_MT; 1.  
DR TIGRFAMs: TIGR00088; tmd; 1.  
KW Transferase; Methyltransferase; tRNA processing; Complete proteome.  
SQ  
SEQUENCE 234 AA; 27110 MW; 6A69B63BDC8E6C CR64;

Query Match 14.9%; Score 76; DB 1; Length 234;

Best Local Similarity 33.0%; Pred. No. 0.51;  
Matches 29; Conservative 10; Mismatches 39; Indels 10; Gaps 5;

QY 6 LRAVYVLSLVHSAQAGATLQPE--ESTIENYASRPAPFPTPNIDKASAPRADDF 63

Db 142 LPAIWMCD-AIRNNG-VLGNNESEESFENNILLADAPAFKPFIFKXKKFTYPSHF 199  
 Qy 64 LNW-HALFESIRK-----XLPFLNMDAF 85  
 Db 200 LKGNHARISLKTTLASCKTKFRPDLF 227

RESULT 2  
 SUSTI\_HORVU STANDARD; PRT; 807 AA.  
 ID SUSTI\_HORVU P31922;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Sucrose synthase 1 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 1).  
 GN SSI.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Hordeum.  
 OC NCBI\_TaxID=4513;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Abyssinian 2231; TISSUE=Endosperm;  
 RX MEDLINE=92405741; PubMed=138123;  
 RA Sanchez de la Hoz P., Vicente-Carabajosa J., Mena M., Carbonero P.;  
 RT "Homologous sucrose synthase genes in barley (*Hordeum vulgare*) are  
 RT located in chromosomes 7H (syn. 1) and 2H. Evidence for a gene  
 RT translocation?";  
 RL FEBS Lett. 310:46-50(1992).  
 RN [2]  
 RM SEQUENCE OF 223-807 FROM N.A.  
 RC STRAIN=cv. Pallas;  
 RA Brandt J., Thordal-Christensen H., Collinge D.B.;  
 RT Submitted (JUN-1992) to the EMBL/GenBank/DBJ database.  
 CC -1- FUNCTION: SUCROSE-CLEAVING ENZYME THAT PROVIDES UDP-GLUCOSE AND  
 CC FRUCTOSE FOR VARIOUS METABOLIC PATHWAYS.  
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN DEVELOPING ENDOSPERM AND  
 CC IN ROOTS AND, AT LOWER LEVELS, IN COLEOPTILES AND ALERHORE.  
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1. PLANT  
 CC SUCROSE SYNTHASE SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; X65871; CAA46701.1; -  
 CC EMBL; X66728; CAA47264.1; -  
 CC PIR; S29242; S29242.  
 DR InterPro; IPR001296; Glyco\_transf\_1.  
 DR InterPro; IPR000368; Sucrose\_synth.  
 DR Pfam; PF00534; Glyco\_transf\_1; 1.  
 DR Pfam; PF00862; Sucrose synth; 1.  
 KW Transferrase; Glycosyltransferase; Multigene family.  
 FT CONFLICT 370 370 I -> Y (IN REF. 2).  
 FT CONFLICT 374 374 I -> Y (IN REF. 2).  
 FT CONFLICT 392 392 NE -> KO (IN REF. 2).  
 SQ SEQUENCE 807 AA; 92211 MW; A863A8C876A060C8 CRC64;

Query Match 14.5%; Score 74; DB 1; Length 807;  
 Best Local Similarity 27.7%; Pred. No. 3.2; Indels 24; Gaps 3;  
 Matches 26; Conservative 12; Mismatches 32;

Qy 30 EESTENASRP-----EAFNTPPLNIDKLSAFKADFLNWR--ALFESIRKLPF 79  
 Db 116 KQALVDEHRSKRFVLELDFEPNNAFPSPMSKSYGKGIVFLNRHLSLTFQDKESLVPL 175

Qy 80 LNW-----DAFPLKGLRSATPDAQ 99  
 Db 176 INFLKAHNYKGTMIINDRIQSLRGLOSLARKAE 209

RESULT 3  
 CP11\_PLAUF STANDARD; PRT; 521 AA.  
 ID CP11\_PLAUF Q9YH64;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).  
 GN CYP1A1 OR CYP1A.  
 OS *Platichtys flesus* (European flounder).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciformes; Pleuronectiformes;  
 OC Pleuronectoidae; Pleuronectidae; *Platichtys*.  
 OC NCBI\_TaxID=8260;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=North Sea population; TISSUE=Liver;  
 RX MEDLINE=21353730; PubMed=11460673;  
 RA Williams T.D., Lee J.S., Shearer D.L., Chipman J.K.;  
 RT "The cytochrome P450 1A gene (CYP1A) from European flounder  
 RT (*Platichtys flesus*), analysis of regulatory regions and development  
 RT of a dual luciferase reporter gene system.";  
 RL Mar. Environ. Res. 50:1-6(2000).  
 CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOALATE  
 CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED  
 CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.  
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
 CC oxidized flavoprotein + H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.  
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.  
 CC -----  
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 CC -----  
 CC EMBL; AJ123353; CAA10645.1; -  
 CC HSSP; P00179; 10T6.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR Pfam; PF00067; P450; 1.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME P450; 1.  
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
 KW Microsome; Endoplasmic reticulum.  
 FT METAL 463 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
 SQ SEQUENCE 521 AA; 59009 MW; 58BA7DC313C9091 CRC64;

Query Match 13.9%; Score 71; DB 1; Length 521;  
 Best Local Similarity 27.0%; Pred. No. 4.3;  
 Matches 27; Conservative 17; Mismatches 32; Indels 24; Gaps 5;

Qy 1 MKIPLPAVVLISLVHSA---OGATLGGFEESTENYASREAFNTPPLNIDKLSA 57  
 Db 81 IQIGRPVVLVSGSEYRQALIKG-----DDFAGRPDLVSFRFINNG-SLA 127

Qy 58 FKADEFNLWHLFESIRKLPFLNMDAPPKLGLSATPD 97  
 Db 128 FSTQAGWRA-----RKLAYSALRSFSNDEG---TTPE 159

RESULT 4  
 CP11\_PLEPL STANDARD; PRT; 521 AA.  
 ID CP11\_PLEPL Q92100;

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DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).
GN CYP1A1.
OS Pleuronectes platessa (Plaice).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectidae; Pleuronectidae; Pleuronectes.
OK NCBI_TaxID=8262;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94251288; PubMed=8193668;
RA Leaver M.J., Spirit L., George S.G.;
RT "Cytochrome P450 1A1 cDNA from plaice (Pleuronectes platessa) and
RT induction of P450 1A1 mRNA in various tissues by 3-methylcholanthrene
RT and isoactrole."
RL Mol. Biol. Biotechnol. 2:338-345(1993).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- INDUCTION: BY 3-METHYLCHOLANTHRENE (3MC) AND ISOSAFROLE (ISF).
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
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CC -----
DR EMBL: X73631; CAAS2010.1; -.
DR PIR: S34184; S34184.
DR HSSP: P00179; 1DT6.
DR InterPro: IPR001128; Cytochrome_P450.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
KW METAL
SQ SEQUENCE 521 AA; 59061 MW; AA7A97CB4578F9B6 CRC64;

Query Match 13.5%; Score 69; DB 1; Length 521;
Best Local Similarity 27.0%; Pred. No. 7;
Matches 27; Conservative 16; Mismatches 33; Indels 24; Gaps 5;

QY 1 MKIPVLPAVVLISLVLSHA--QGATLGGPEESTIENYASRPAPNTPIINIDKLKSA 57
DB 81 IQIGKRPVVVLSGSETRQALIKQ-----DFAAGRPDLYSRFINAGK-SLA 127
QY 58 FRADEFINMHAFESIKRKLPIFINDAPFKLGLRSATPD 97
DB 128 FSTDQAGWRA-----RRKLAYSALRSFSTLEG---TTPB 159

RESULT 5
CPI1_SPAU STANDARD; PRT; 521 AA.
AC 042457; 042458;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).
GN CYP1A1.
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OK NCBI_TaxID=8175;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cousinou M., Lopez-Barea J., Dorado G.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE OF 175-521 FROM N.A.
RC TISSUE=Liver;
RX Tom M.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
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CC -----
DR EMBL: AF011223; AAB64297.1; -.
DR EMBL: AF005719; AAB62867.1; -.
DR HSSP: P00179; 1DT6.
DR InterPro: IPR001128; Cytochrome_P450.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
KW METAL
SQ SEQUENCE 521 AA; 59122 MW; 8FE00D86460B3B CRC64;

Query Match 13.5%; Score 69; DB 1; Length 521;
Best Local Similarity 27.0%; Pred. No. 7;
Matches 27; Conservative 17; Mismatches 32; Indels 24; Gaps 5;

QY 1 MKIPVLPAVVLISLVLSHA--QGATLGGPEESTIENYASRPAPNTPIINIDKLKSA 57
DB 81 IQIGKRPVVVLSGSETRQALIKQ-----DFAAGRPDLYSRFIN-DGSLA 127
QY 58 FRADEFINMHAFESIKRKLPIFINDAPFKLGLRSATPD 97
DB 128 FSTDQAGWRA-----RRKLAYSALRSFSTLEG---TTPB 159

RESULT 6
ACDS_PIG STANDARD; PRT; 413 AA.
AC P79273;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acyl-CoA dehydrogenase, short-chain specific, mitochondrial precursor
DE (EC 1.3.99.2) (SCAD) (Butyryl-CoA dehydrogenase).
GN ACADS.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OK NCBI_TaxID=9823;
RN (1)

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RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Suzuki H., Itch T., Kimura M., Murakami Y., Hamajima N., Yasue H.;  
 RT "Isolation of the pig short-chain acyl-CoA dehydrogenase gene and  
 assignment to chromosome 14q16.2-q23.2."  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Butanoyl-CoA + Etf = 2-butanoyl-CoA + reduced  
 Etf.  
 CC -1- COFACTOR: FAD.  
 CC -1- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first  
 step.  
 CC -1- SUBUNIT: Homotetramer.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -1- MISCELLANEOUS: A NUMBER OF STRAIGHT-CHAIN ACYL-CoA DEHYDROGENASES  
 OF DIFFERENT SUBSTRATE SPECIFICITIES ARE PRESENT IN MAMMALIAN  
 TISSUES.  
 CC -1- SIMILARITY: BELONGS TO THE ACYL-CoA DEHYDROGENASE FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; D89477; BAAL3964.1; -  
 CC HSSP; 006319; 1BUC.  
 DR InterPro; IPR006089; Acyl-CoA dh.  
 DR InterPro; IPR006090; Acyl-CoA dh.  
 DR InterPro; IPR006091; Acyl-CoA dh.  
 DR InterPro; IPR006092; Acyl-CoA dh.  
 DR Pfam; PF00441; Acyl-CoA dh; 1.  
 DR Pfam; PF02770; Acyl-CoA dh; 1.  
 DR Pfam; PF02771; Acyl-CoA dh; 1.  
 DR PROSITE; PS00072; ACYL\_COA\_DH\_1; 1.  
 DR PROSITE; PS00073; ACYL\_COA\_DH\_2; 1.  
 DR Oxidoreductase; Flavoprotein; FAD; Fatty acid metabolism;  
 KM Mitochondrion; Transit peptide.  
 FT TRANSIT 1 24  
 FT CHAIN 25 413  
 FT ACT\_SITE 393 393 SPECIFIC BASE (BY SIMILARITY)  
 FT SEQUENCE 413 AA; 44850 MW; B8C480ADEDF7E98 CRC64;  
 SQ  
 Query Match 13.4%; Score 68.5; DB 1; Length 413;  
 Best Local Similarity 26.9%; Pred. No. 6.2; Mismatches 7; Gaps 1;  
 Matches 18; Conservative 8; Indels 34;  
 QY 36 NYASREAFNTPLNIDKLR-----SAFKADEFLNWEALFESIRKLPFLNWDAPPYL 88  
 DB 292 NYAENRRAGVPLTKGIQFKLADWALLESARLLTWBAAMKDKKPFIEKPEAMATL 351  
 QY 89 KGIKRSAT 95  
 DB 352 AASEAAT 358  
 RESULT 7  
 CP11\_ONCMY STANDARD; PRT; 522 AA.  
 ID CP11\_ONCMY  
 AC Q92110; O42195; P10609; P79630;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYPIA1) (CYPIA2).  
 GN CYP1A1.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Procatopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA MEDLINE=94213487; PubMed=8161204;  
 RA Berntson A.K., Chen T.T.;  
 RT "Two unique Cyp1 genes are expressed in response to 3-  
 methylcholanthrene treatment in rainbow trout";  
 RL Arch. Biochem. Biophys. 310:187-195(1994).  
 CC [2]  
 RP SEQUENCE FROM N.A.  
 RA Bailey G., You L., Harttig U.;  
 RT "Cloning, sequencing and functional expression of two trout CYP1A  
 cDNAs in yeast."  
 RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 CC [3]  
 RP SEQUENCE FROM N.A.  
 RA Bailey G., You L., Harttig U.;  
 RT "Cloning, sequencing and functional expression of two trout CYP1A  
 cDNAs in yeast."  
 RT Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 CC [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89078171; PubMed=3203599;  
 RA Hellmann L.J., Sheen Y.-Y., Bigelow S.W., Nebert D.W.;  
 RT "Trout P4501A1: cDNA and deduced protein sequence, expression in  
 liver, and evolutionary significance."  
 RL DNA 7:379-387(1988).  
 CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE  
 MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED  
 COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.  
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
 oxidized flavoprotein + H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.  
 CC -1- TISSUE SPECIFICITY: Liver.  
 CC -1- INDUCTION: By 3-methylcholanthrene (3MC).  
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.  
 CC -1- CAUTION: THE SEQUENCE FROM REF.4 WAS A CHIMERA: ITS N-TERMINAL  
 PART HAS BEEN SHOWN TO BE DERIVED FROM WHAT IS NOW KNOWN AS THE  
 CYP1A3. CYP1A1 HAS ALSO BEEN CALLED CYP1A2.  
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 CC -----  
 CC EMBL; S69278; AADI4036.1; -  
 CC EMBL; U62797; AAB40627.1; -  
 CC EMBL; AF015660; AAB69383.1; -  
 CC EMBL; M21310; AAA49550.1; ALT\_SEQ.  
 DR PIR; A28789; A28789.  
 DR PIR; S51557; S51557.  
 DR HSSP; P00179; 1DT6.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR Pfam; PF00067; P450; 1.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
 KM Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
 KW Microsome; Endoplasmic reticulum.  
 FT METAL 463 463  
 FT ACT\_SITE 51 51 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
 FT CONFLICT 97 97 L -> P (IN REF. 3).  
 FT CONFLICT 97 97 V -> D (IN REF. 3).  
 FT CONFLICT 124 124 K -> N (IN REF. 3).  
 FT CONFLICT 306 306 Q -> H (IN REF. 3).  
 FT CONFLICT 380 380 T -> G (IN REF. 3).  
 FT CONFLICT 390 390 D -> G (IN REF. 2).  
 FT CONFLICT 459 459 Y -> H (IN REF. 3).  
 FT CONFLICT 470 470 R -> F (IN REF. 1).  
 FT CONFLICT 474 474 Y -> K (IN REF. 2).  
 FT CONFLICT 483 483  
 SQ SEQUENCE 522 AA; 59344 MW; 9D063B5891102CE9 CRC64;

Query Match 13.3%; Score 68; DB 1; Length 522;  
 Best Local Similarity 28.0%; Pred. No. 9.1;  
 Matches 28; Conservative 15; Mismatches 33; Indels 24; Gaps 5;

QY 1 MKIPVLPVAVLISLVLSHA-----OGATLGGPEBESTIENYASRPEAFNPLINIDKLRSA 57  
 DB 81 IQIGRPVVLSSGNETVRQALIKQ-----EDFAGPDLISYKFTIN-DOKSLA 127  
 QY 58 FADDEFIMNHALPESIKRKLPLFMDNPFKLGKLSATPD 97  
 DB 128 FSTDRAGVRA-----RRKLMSALRSFATLEG---TTPE 159

RESULT 8  
 Y309\_MYCGE STANDARD; PRT; 1225 AA.  
 ID Y309\_MYCGE  
 AC P47551; Q49317;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical lipoprotein MG309 precursor.  
 GN MG309.  
 OS Mycoplasma genitalium.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OX NCBI\_TaxID=2097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 33530 / G-37;  
 RX MEDLINE=96026346; PubMed=7569993;  
 RA Frazer C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,  
 RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,  
 RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,  
 RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,  
 RA Tomb J.-F., Dougherty B.A., Bort K.F., Hu P.-C., Lincel T.S.,  
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;  
 RA "The minimal gene complement of Mycoplasma genitalium.",  
 RL Science 270:397-403(1995).  
 RN [2]  
 RP SEQUENCE OF 1138-1224 FROM N.A.  
 RC STRAIN=ATCC 33530 / G-37;  
 RX MEDLINE=94075230; PubMed=8253680;  
 RA Peterson S.N., Hu P.-C., Bort K.F., Hutchison C.A. III,  
 RA "A survey of the Mycoplasma genitalium genome by using random  
 RT sequencing.",  
 RT J. Bacteriol. 175:7918-7930(1993).  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
 (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE MG307 / MG309 / MG338 FAMILY.  
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 CC EMBL; U39711; AAC71531.1; -  
 CC EMBL; U02200; AAD12488.1; -  
 CC PIR; B64234; B64234.  
 CC TIGR; MG309; -  
 CC PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
 CC DR Hypothetical protein; Lipoprotein; Membrane; Signal;  
 CC KM Complete proteome.  
 CC FT SIGNAL 1 27 POTENTIAL.  
 CC FT CHAIN 28 1225 HYPOTHETICAL LIPOPROTEIN MG309.  
 CC FT LIPID 28 28 N-ACYL DIGLYCERIDE (POTENTIAL).  
 CC FT CONFLICT 1185 1185 L -> V (IN REF. 2).  
 CC FT SEQUENCE 1225 AA; 138375 MW; C3E4F5B4319B6E8 CRC64;

Query Match 13.3%; Score 68; DB 1; Length 1225;  
 Best Local Similarity 24.3%; Pred. No. 23;  
 Matches 25; Conservative 19; Mismatches 23; Indels 36; Gaps 6;

QY 1 MKIPVLPVAVLISLVLSHA-----SLVLHSAOGATLGGPEBESTI-ENYASRPEAF 44  
 DB 681 LKVSIVPSPQSVQILVDTKLSDDPRNTSLALNLAIVLSDEDLQNTIRRDY----- 733  
 QY 45 NMPFLINIDKLRSAFADE--FLNMHALPESIKRKLPLINWDNF 85  
 DB 734 --FVNDQPFKQALDLDKLTFFKNMSLNNE-----NMNIF 765

RESULT 9  
 IBP1\_BOVIN STANDARD; PRT; 263 AA.  
 ID IBP1\_BOVIN  
 AC P24591;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Insulin-like growth factor binding protein 1 precursor (IGFBP-1)  
 DE (IGFBP-1) (IGF-binding protein 1).  
 GN IGFBP1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Holstein-Friesian; TISSUE=Liver;  
 RX MEDLINE=92119331; PubMed=1722724;  
 RA Sneyers M., Kettmann R., Massart S., Renaville R., Burny A.,  
 RA Portetalle D.,  
 RT Cloning and characterization of a cDNA encoding the bovine  
 RT insulin-like growth factor binding protein 1 (IGFBP-1).  
 RL DNA Seq. 1:407-408(1991).  
 CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs  
 CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH  
 CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE  
 CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- MISCELLANEOUS: BINDS EQUALLY WELL IGF-I AND IGF-II.  
 CC -1- SIMILARITY: Contains 1 IGFBP domain.  
 CC -1- SIMILARITY: Contains 1 thyroglobulin type-I domain.  
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 CC EMBL; X54979; CAA38723.1; -  
 CC PIR; S23009; S23009.  
 CC HSSP; P24593; IBOE.  
 CC InterPro; IPR000867; Inel\_gro\_fac\_pr.  
 CC DR InterPro; IPR00716; Thyroglobulin\_1.  
 CC Pfam; PF00219; IGFBP\_1.  
 CC DR Pfam; PF00086; thyroglobulin\_1; 1.  
 CC DR SMART; SM00121; IB; 1.  
 CC DR SMART; SM00211; TY; 1.  
 CC DR PROSITE; PS00222; IGF\_BINDING; 1.  
 CC DR PROSITE; PS00484; THYROGLOBULIN\_1; 1.  
 CC KW Growth factor binding; Signal.  
 CC FT SIGNAL 1 25  
 CC FT CHAIN 26 263 INSULIN-LIKE GROWTH FACTOR BINDING  
 CC FT DOMAIN 206 255 THYROGLOBULIN TYPE 1.  
 CC FT SITE 250 252 CELL ATTACHMENT SITE.  
 CC FT DISULFID 73 86 BY SIMILARITY.  
 CC FT DISULFID 80 106 BY SIMILARITY.  
 CC FT DISULFID 180 210 BY SIMILARITY.  
 CC FT SEQUENCE 263 AA; 28796 MW; 0403B642DDDC45B6 CRC64;

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Query Match      13.1%; Score 67; DB 1; Length 263;
Best Local Similarity 29.6%; Pred. No. 5.5;
Matches 24; Conservative 12; Mismatches 35; Indels 10; Gaps 4;

QY 14 LVVHSAQATLGGPEESTIENYASRPAFNTPLINDKLSAPKAEPL-NWHALES 72
DB 96 LHALTRGGACWTSFCDDEATDTKDTTSPS-----NVSPESSEITQEQLLDNPHLMES 148
QY 73 IRRKLPFLNWDAPFKLGRS 93
DB 149 -SEDLPL-LWNAISNYSIRA 167

RESULT 10
CP11_LIML1 STANDARD; PRT; 521 AA.
AC 042430;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYPIA1).
GN CYP1A1.
OS Limanda limanda (Dab).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectidae; Pleuronectidae; Limanda.
OX NCBI_Taxid=277711;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=2115568; PubMed=11423384;
RA Craft J.A., Robertson F.E., McPhail M.E., Brown E., Seagg R.M.,
"Measurement of cytochrome P4501A induction in dab (Limanda limanda)
and other teleosts with species-specific cDNA probes: isolation and
characterisation of dab cDNA and its use in expression studies with
beta-naphthoflavone-treated fish.";
RT Biochem. Physiol. 129C:115-127(2001).
RL Comp. FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
-----
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CC EMBL; AJ001724; CA04953.1; -.
DR HSSP; P00179; 1DT6.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT METAL 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 521 AA; 59063 MW; 11DB326C8A7FDBF9 CRC64;

Query Match      13.1%; Score 67; DB 1; Length 521;
Best Local Similarity 27.0%; Pred. No. 12;
Matches 27; Conservative 17; Mismatches 32; Indels 24; Gaps 5;

QY 1 MKIPVLPVAVLLSLVLSA---QGATLGGPEESTIENYASRPAFNTPLINDKLSA 57
DB 81 IQIGRPVVVLSGSETVRQALIKG-----DFAGRPDLVSFRFTNGK-SLA 127

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QY 58 FKADFLNWHALFSSIRKLPFLNWDAPFKLGRSATPD 97
DB 128 FSTDAGIWRP-----RKILAYSALRSFATLEG--TTPE 159

RESULT 11
CP11_STECH STANDARD; PRT; 521 AA.
AC 092116;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).
GN CYP1A1.
OS Stenotomus chrysops (Scup).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Stenotomus.
OX NCBI_Taxid=35579;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95275266; PubMed=7755595;
RA Morrison H.G., Oleksiak M.F., Corneli N.W., Sogin M.L., Stegeman J.J.,
"Identification of cytochrome P-450 1A (CYP1A) genes from two teleost
fish, coadfish (Opsanus tau) and scup (Stenotomus chrysops), and
phylogenetic analysis of CYP1A genes.";
RT Biochem. J. 308:97-104(1995).
RL Comp. FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
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CC EMBL; U14162; AAA74969.1; -.
DR HSSP; P00179; 1DT6.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT METAL 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 521 AA; 59019 MW; 8BDC4312074025D4 CRC64;

Query Match      13.1%; Score 67; DB 1; Length 521;
Best Local Similarity 27.0%; Pred. No. 12;
Matches 27; Conservative 16; Mismatches 33; Indels 24; Gaps 5;

QY 1 MKIPVLPVAVLLSLVLSA---QGATLGGPEESTIENYASRPAFNTPLINDKLSA 57
DB 81 IQIGRPVVVLSGSETVRQALIKG-----DXFAGRPLVLSFRFTN-DGKSLA 127
QY 58 FKADFLNWHALFSSIRKLPFLNWDAPFKLGRSATPD 97
DB 128 FSTDAGIWRP-----RKILAYSALRSFATLEG--TTPE 159

RESULT 12
YHP7_YEAST STANDARD; PRT; 366 AA.
AC P38809;

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DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Hypothetical 40.7 kDa protein in HXT5-NRK1 intergenic region.
GN YHR097C.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetiales; Saccharomycetaceae; Saccharomyces.
OC NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Faville A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kueba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,
RA Nhan M., Rifkin L., Riles L., St Peter H., Trevisan E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VII."
RT Science 265:2077-2082(1994).
CC -1 SIMILARITY: TO S. POMBE SPBC6B1.03C.
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CC -----
CC EMBL: U00600; AAC8935.1; -.
CC DR PIR: S46727; S46727.
CC DR SGD: S000139; YHR097C.
CC DR Hypothetical protein.
CC SEQUENCE 366 AA; 40663 MW; AD04D034CDB6764D CRC64;
SQ
Query Match 13.0%; Score 66.5; DB 1; Length 366;
Best Local Similarity 25.4%; Pred. No. 8.9;
Matches 18; Conservative 10; Mismatches 22; Indels 21; Gaps 2;
QY 22 GATGGGPE-----ESTENYASRPAFNPFPINIDLRSAFADETLNMH 67
DB 5 GATGGGQGVNTVINPFRVSSSEDRVSSRDETPNYNNPFLMEDTRAHNS----- 57
QY 68 ALFESIKRLP 78
DB 58 SVSNRQERLP 68
RESULT 13
BUB1 SCHPO STANDARD; PRT; 1044 AA.
AC 094751.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Checkpoint serine/threonine-protein kinase bub1 (EC 2.7.1.-).
GN BUB1 OR SPOC1322.12C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OC NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
RX STRAIN=SP011;
RX MEDLINE=9085059; PubMed=9864354;
RX Bernard P., Hardwick K.G., Javerz J.-P.;
RT "Fission yeast Bub1 is a mitotic centromere protein essential for the
RT spindle checkpoint and the preservation of correct ploidy through

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RT mitosis."
RT J. Cell Biol. 143:1775-1787(1998).
RN [2]
RN RP SEQUENCE FROM N.A.
RX STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Frazer A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald J., McLean J.,
RA Moorey P., Moyle S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Shenv S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tiley A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymoprez B.,
RA Meljens I., Vanatrelis E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motlier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakowski G.V., Ussery D., Barrett B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RT Nature 415:871-880(2002).
CC -1 FUNCTION: INVOLVED IN CELL CYCLE CHECKPOINT ENFORCEMENT. ACTS TO
CC STABILIZE THE SPINDLE DURING MITOSIS. CATALYZES THE
CC PHOSPHORYLATION OF BUB3.
CC -1 SUBCELLULAR LOCATION: Nuclear.
CC -1 PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC BUB1 SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF064796; AAC98348.1; -.
CC DR EMBL: AL035259; CA22865.1; -.
CC DR PIR: T43800; T43800.
CC DR GeneDB: SPOmbe; SPOC1322.12C; -.
CC DR InterPro: IPR000719; Prot kinase.
CC DR Pfam: PF000069; Pkinase; 1.
CC DR ProDom: PD000001; Prot kinase; 1.
CC DR PROSITE: PS50011; PROTEIN KINASE, DOM; 1.
CC KW Transferase; Serine/threonine-protein kinase; ATP-binding;
CC Cell cycle; Mitosis; Phosphorylation; Nuclear protein.
CC FT DOMAIN 718 1044
CC FT NP BIND 724 732 ATP (BY SIMILARITY).
CC FT BINDING 762 762 ATP (BY SIMILARITY).
CC FT ACT SITE 861 861 BY SIMILARITY.
CC SEQUENCE 1044 AA; 118351 MW; 32CE71E71BC1BF6 CRC64;
SQ
Query Match 12.9%; Score 66; DB 1; Length 1044;
Best Local Similarity 32.4%; Pred. No. 32;
Matches 23; Conservative 12; Mismatches 22; Indels 14; Gaps 4;
QY 19 SAQAT-IGPPEESTIT-----NYASRPAFNPFPINIDLRSAFADETLNMH 68
DB 432 SNSGATSLTGSQEHDLFIPSLTPSKYV---PSKIVPNKLLDPSHTASKAETKYSNNE 488
QY 69 LFESIKRLP 79

```

DB 489 L-ENKREOPF 498

RESULT 14

YNM3\_YEAST STANDARD; PRT; 506 AA.

ID YNM3\_YEAST

AC P53867

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Hypothetical 56.6 kDa protein in URE2-S5072 intergenic region.

GN YN123W OR N1274.

OS Saccharomyces cerevisiae (Baker's Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.

OX NCBI\_TaxID=4932;

RN [1]

RN SEQUENCE FROM N.A.

RX MEDLINE=97051596; PubMed=8896273;

RT Pandolfo D., de Antoni A., Lantiranchi G., Valle G.;

RT "The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open

RT reading frames including a novel gene encoding a globin-like

RT domain".

RL Yeast 12:1071-1076 (1996).

RN [2]

RN SEQUENCE FROM N.A.

RA Dueterhoeft A., Floeth M., Filtz C., Heuss-Netzel D., Hilbert H.,

RA Moestl D.;

RL Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.

RN [3]

RN SEQUENCE OF 13-506 FROM N.A.

RA Sun Z., Hampsey M.;

RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.

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CC -----

CC EMBL; 269381; CAA93375.1; -

DR EMBL; 271499; CAA96126.1; -

DR EMBL; U20390; AAA86498.1; -

DR PIR; S63181; S63181.

DR MEROPS; C54.001; -

DR SGD; S0005167; AUT2.

DR GO; GO:0005875; C:microtubule associated complex; IPI.

DR GO; GO:0008017; F:microtubule binding activity; IPI.

DR GO; GO:0006914; P:autophagy; IMP.

DR GO; GO:0006623; P:protein-vacuolar targeting; IMP.

DR InterPro; IPR005078; Peptidase\_C54.

DR Pfam; PF03416; Peptidase\_C54; 2.

KW Hypothetical protein.

SO SEQUENCE 506 AA; 56553 MW; 95EB599D6CDBB6F9 CRC64;

Query Match 12.8%; Score 65.5; DB 1; Length 506;

Best Local Similarity 25.8%; Pred. No. 16; Indels 33; Gaps 3;

Matches 25; Conservative 13; Mismatches 26; Indels 33; Gaps 3;

QY 2 KIPVLPAVVLISLVLSHNOGATLGPEBEETIENYASPEAFNTPF----- 48

DB 119 RAPDPSPLSLNLV-----RTNPISITIEDYIANPDGFNDIGMCMIRTGSQL 168

QY 49 ---LNIIDGRSAFKADEFLNMLAFESIRKPLPLNW 82

DB 169 GNAQLIHLGRDFRVNG-----NESLRESKFVNW 198

RESULT 15

TP2M\_CAEBL

ID TP2M\_CAEBL STANDARD; PRT; 1053 AA.

AC P34534;

DT 01-FEB-1994 (Rel. 28, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Putative DNA topoisomerase II, mitochondrial precursor (EC 5.99.1.3).

GN R05D3.1.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI\_TaxID=6239;

RN [1]

RN SEQUENCE FROM N.A.

RX STRAIN=Bristol N2;

RL MEDLINE=94150718; PubMed=7906398;

RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,

RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,

RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,

RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,

RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Riffen L., Roopra A., Saunders D., Showken R.,

RA Sims M., Smaison N., Smith A., Smith M., Sonhammer E., Staden R.,

RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,

RA Waterston R., Watson A., Weinstock L., Wilkerson-Sprat J.,

RA Wohldman P.;

RL "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RL elegans".

RL Nature 368:32-38(1994).

RN [2]

RN REVISIONS.

RA Waterston R.;

RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.

CC -----

CC -1- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT

CC BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II

CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining

CC of double-stranded DNA.

CC -1- SUBUNIT: Homodimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).

CC -1- SIMILARITY: Belongs to the type II topoisomerase family.

CC -----

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CC -----

CC EMBL; L07144; AAM54162.1; -

DR HSSP; P06786; IBCW.

DR WormPep; R05D3.1; CE31047.

DR InterPro; IPR003594; ATPbind\_ATPase.

DR InterPro; IPR001241; DNA\_topoisolt.

DR InterPro; IPR002205; DNA\_topoisolt.

DR Pfam; PF00204; DNA\_gyraseB; 1.

DR Pfam; PF00521; DNA\_topoisolt; 1.

DR Pfam; PF02518; HATPase\_c; 1.

DR PRINTS; PR01158; TOPISMRASEII.

DR PRINTS; PR00418; TP12FAMILY.

DR PRODom; PD000742; DNA\_topoisolt; 1.

DR SMART; SM00433; TOP2c; 1.

DR SMART; SM00434; TOP4c; 1.

DR PROSITE; PS00177; TOPOISOMERASE II; 1.

KW Hypothetical protein; Isomerase; Topoisomerase; DNA-binding;

KW ATP-binding; Mitochondrion; Transit peptide.

FT TRANSIT 1 ? 1053 MITOCHONDRION (POTENTIAL).

FT NP BIND 60 65 ATP (POTENTIAL).

FT ACT SITE 697 697 DNA CLEAVAGE (BY SIMILARITY).

SO SEQUENCE 1053 AA; 120285 MW; BB167F2B01BF8A45 CRC64;

|                       |       |   |  |             |
|-----------------------|-------|---|--|-------------|
| Query Match           | 12.8% | Score 65.5  | DB 1                                     | Length 1055 |
| Best Local Similarity | 31.6% | Pred. No 37                                       |  |             |
| Matches               | 18    | Conservative 10                                   | Mismatches 18                            | Indels 11   |
|                       |       |   |  | Gaps 2      |
| Qy                    | 42    | BAFMTPLNT---                                      | DKTAAFKODEFLMHALFESTKTLPLPLNDAPFKLGLASAT | 95          |
|                       |       |   |  |             |
|                       |       |   |  |             |
|                       |       |   |  |             |
|                       |       |   |  |             |
| Db                    | 474   | QSFTPLKAKGKQKVRGFSFMSNRKKADVDGGKKIKI-----YGLGLGSI |  | 522         |

Search completed: November 28, 2003, 07:55:35  
Job time : 21 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 07:43:56 ; Search time 54 Seconds

(without alignments)  
473.096 Million cell updates/sec

Title: US-10-059-395-142

Sequence: 1 MKIPPLPAVLLSLVLSA.....LNWDAFKLGRSATPPAQ 99

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvivirus:\*
- 16: sp\_bacteriophage:\*
- 17: sp\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description            |
|------------|-------|-------------|--------|-------|------------------------|
| 1          | 77.5  | 15.2        | 1544   | 5     | Q9VU57 drosophila      |
| 2          | 75    | 14.7        | 254    | 5     | Q9SW96 helioidactyl    |
| 3          | 74.5  | 14.6        | 407    | 11    | Q8C4L6 mus musculus    |
| 4          | 73.5  | 14.4        | 1251   | 2     | Q9ZBD1 mus musculus    |
| 5          | 73    | 14.3        | 390    | 16    | Q8UES9 Oribacterium    |
| 6          | 72.5  | 14.2        | 634    | 10    | Q22143 Arabidopsis     |
| 7          | 71.5  | 14.0        | 743    | 10    | Q9FPB6 Oryza sativa    |
| 8          | 71    | 13.9        | 439    | 13    | Q98SG4 Acrophthalma    |
| 9          | 71    | 13.9        | 439    | 13    | Q98SG7 Platyhelminthes |
| 10         | 70.5  | 13.8        | 251    | 16    | Q935B8 salmonella      |
| 11         | 70    | 13.7        | 500    | 16    | Q9X863 streptococcus   |
| 12         | 70    | 13.7        | 521    | 13    | Q90WD4 lithognathu     |
| 13         | 70    | 13.7        | 521    | 13    | Q90XPI salmo salar     |
| 14         | 70    | 13.7        | 522    | 13    | Q8QGP2 salmo salar     |
| 15         | 70    | 13.7        | 522    | 13    | Q9PRH3 oncorhynchus    |
| 16         | 69    | 13.5        | 186    | 10    | Q9SF44 Arabidopsis     |

|    |      |      |      |    |        |              |
|----|------|------|------|----|--------|--------------|
| 17 | 69   | 13.5 | 674  | 16 | Q8D5M6 | Oribacterium |
| 18 | 68.5 | 13.4 | 203  | 4  | Q9B8YC | Oribacterium |
| 19 | 68.5 | 13.4 | 439  | 13 | Q9B8YC | Oribacterium |
| 20 | 68.5 | 13.4 | 871  | 16 | Q97K23 | Oribacterium |
| 21 | 68.5 | 13.4 | 899  | 5  | Q9VIC5 | Oribacterium |
| 22 | 68.5 | 13.4 | 952  | 11 | Q8CG80 | Oribacterium |
| 23 | 68   | 13.3 | 292  | 16 | Q8YCU3 | Oribacterium |
| 24 | 68   | 13.3 | 315  | 16 | Q8FV13 | Oribacterium |
| 25 | 68   | 13.3 | 349  | 2  | Q8VQL5 | Oribacterium |
| 26 | 68   | 13.3 | 727  | 5  | Q81S64 | Oribacterium |
| 27 | 67.5 | 13.2 | 173  | 16 | Q8K6N5 | Oribacterium |
| 28 | 67.5 | 13.2 | 459  | 17 | Q9UZH9 | Oribacterium |
| 29 | 67.5 | 13.2 | 519  | 13 | Q9PTV6 | Oribacterium |
| 30 | 67.5 | 13.2 | 519  | 13 | Q9PTV7 | Oribacterium |
| 31 | 67.5 | 13.2 | 519  | 13 | Q8UW07 | Oribacterium |
| 32 | 67.5 | 13.2 | 519  | 13 | Q8QGS5 | Oribacterium |
| 33 | 67.5 | 13.2 | 521  | 13 | Q8QJ18 | Oribacterium |
| 34 | 67   | 13.1 | 208  | 16 | Q8ZB97 | Oribacterium |
| 35 | 67   | 13.1 | 439  | 16 | Q8XZ88 | Oribacterium |
| 36 | 67   | 13.1 | 912  | 5  | Q8T034 | Oribacterium |
| 37 | 66.5 | 13.0 | 376  | 16 | Q9K387 | Oribacterium |
| 38 | 66.5 | 13.0 | 531  | 5  | Q9VH11 | Oribacterium |
| 39 | 66.5 | 13.0 | 620  | 10 | Q941A8 | Oribacterium |
| 40 | 66.5 | 13.0 | 887  | 5  | Q8T617 | Oribacterium |
| 41 | 66.5 | 13.0 | 1288 | 16 | Q8EWY0 | Oribacterium |
| 42 | 66   | 12.9 | 346  | 8  | Q8HUB9 | Oribacterium |
| 43 | 66   | 12.9 | 360  | 16 | Q8YD10 | Oribacterium |
| 44 | 66   | 12.9 | 443  | 16 | Q8YVY6 | Oribacterium |
| 45 | 66   | 12.9 | 519  | 13 | Q9PT96 | Oribacterium |

## ALIGNMENTS

| ID     | Query Match | Length | DB ID | Description            |
|--------|-------------|--------|-------|------------------------|
| Q9VU57 | 15.2        | 1544   | 5     | Q9VU57 drosophila      |
| Q9VU57 | 14.7        | 254    | 5     | Q9SW96 helioidactyl    |
| Q9VU57 | 14.6        | 407    | 11    | Q8C4L6 mus musculus    |
| Q9VU57 | 14.4        | 1251   | 2     | Q9ZBD1 mus musculus    |
| Q9VU57 | 14.3        | 390    | 16    | Q8UES9 Oribacterium    |
| Q9VU57 | 14.2        | 634    | 10    | Q22143 Arabidopsis     |
| Q9VU57 | 14.0        | 743    | 10    | Q9FPB6 Oryza sativa    |
| Q9VU57 | 13.9        | 439    | 13    | Q98SG4 Acrophthalma    |
| Q9VU57 | 13.9        | 439    | 13    | Q98SG7 Platyhelminthes |
| Q9VU57 | 13.8        | 251    | 16    | Q935B8 salmonella      |
| Q9VU57 | 13.7        | 500    | 16    | Q9X863 streptococcus   |
| Q9VU57 | 13.7        | 521    | 13    | Q90WD4 lithognathu     |
| Q9VU57 | 13.7        | 521    | 13    | Q90XPI salmo salar     |
| Q9VU57 | 13.7        | 522    | 13    | Q8QGP2 salmo salar     |
| Q9VU57 | 13.7        | 522    | 13    | Q9PRH3 oncorhynchus    |
| Q9VU57 | 13.5        | 186    | 10    | Q9SF44 Arabidopsis     |

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkley G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spletter E., Spredling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-P., Zaveri U.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Zibds R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RA "The genome sequence of *Drosophila melanogaster*."  
 RT Science 287:2185-2195 (2000).  
 DR EMBL: AE003538; AAF49833.1;  
 DR Flybase: FBgn0036348; CG17687.  
 SQ SEQUENCE 1544 AA; 179386 MW; 98087CADFB966E63 CRC64;

Query Match 15.2%; Score 77.5; DB 5; Length 1544;  
 Best Local Similarity 32.6%; Pred. No. 13;  
 Matches 30; Conservative 9; Mismatches 26; Indels 25; Gaps 4;

QY 2 KLPVPAVLLSLVLSAQAATLGGPEESTIENVASRPEAFNTPF-LNIDKLSAFKA 60  
 DB 1168 KRPKPGKVFNSVLICMEASNKLSGKP-----SHRPFPLPDVL----- 1207

QY 61 DEFILMHAFESIKRKLPLF---NMDAPFKK 89  
 DB 1208 -EPLNHLAEFDQKCPFVNDPKSWDAFYKLR 1238

RESULT 2

ID 095W96 PRELIMINARY; PRT; 254 AA.

AC 095W96; 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Primary mesenchyme-specific protein PM27.  
 GN PM27.  
 OS Helicoidaris erythrogramma (Sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinomericidae;  
 OC Helicoidaris.  
 OC NCBI\_TaxID=7634;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Stander M.C., Raft R.A.;  
 RT "Gene expression and skeleton formation in the sea urchin *Helicoidaris*  
 RT erythrogramma."  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF59343; JAL27536.1;  
 DR InterPro: IPR001304; Lectin\_C.  
 DR Pfam: PF00059; Lectin\_C; 1.  
 DR SMART: SM00034; LECTIN\_1.  
 DR PROSITE: PS50041; C TYPE LECTIN 2; 1.  
 SQ SEQUENCE 254 AA; 27430 MW; 48246B97966EB554 CRC64;

Query Match 14.7%; Score 75; DB 5; Length 254;  
 Best Local Similarity 24.4%; Pred. No. 2.8;  
 Matches 21; Conservative 19; Mismatches 26; Indels 20; Gaps 3;

QY 4 PVLPAVLLSLVLSAQAATLGGPEESTIENVASRPEAFNTPF-LNIDKLS 56  
 DB 96 PVLAGM-----TIADQTSNAVNLKSLSTQALDIPFTGLANNILTA 142

QY 57 AFKADEFILMHAFESIKRKLPLF 82  
 DB 143 ILERIEGWMKPSGMSSTQOALPFVNW 168

RESULT 3  
 ID 08C4L6 PRELIMINARY; PRT; 407 AA.

AC 08C4L6; 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Inferred: RIKEN CDNA 1110014F24.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=C57BL/6J; TIGR=Head;  
 RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,  
 RA "The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RT Nature 420:563-573 (2002).  
 DR EMBL: AK081753; BAC38319.1;  
 SQ SEQUENCE 407 AA; 42735 MW; 9D243DA7077983F6 CRC64;

Query Match 14.6%; Score 74.5; DB 11; Length 407;  
 Best Local Similarity 25.9%; Pred. No. 5.6;  
 Matches 22; Conservative 10; Mismatches 32; Indels 21; Gaps 3;

QY 18 HSAGATATGGPEESTIENVASRPEAFNTPF-LNIDKLSAFKA-DEFILMHAF 68  
 DB 241 YQHGSGNGNTQKAVNGMLTNSDASTLPF-NIDFWENIKSKTRFIMDAINKGAPS 299

QY 69 -----LFSIKRKLPLF 82  
 DB 300 PSTRALYFRKLWENFKSTPFVNW 324

RESULT 4

ID 09ZBD1 PRELIMINARY; PRT; 1251 AA.

AC 09ZBD1; 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Beta-galactosidase.  
 OS Saccharopolyspora rectivirgula.  
 OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;  
 OC Pseudomonadiales; Pseudomonadaceae; Saccharopolyspora.  
 OC NCBI\_TaxID=28042;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98449763; PubMed=9774708;  
 RA Inohara-Ochiai M., Nakayama T., Nakao M., Fujita T., Ueda T.,  
 RA Ashikari T., Nishino T., Shibano Y.;  
 RT "Unique primary structure of a thermostable multimeric beta-  
 RT galactosidase from *Saccharopolyspora rectivirgula*."  
 RL Biochim. Biophys. Acta 1388:77-83 (1998).  
 DR EMBL: D86429; BAA34817.1;  
 DR HSBP: P00722; IBGL

DR InterPro: IPR006101; Glyco\_hydro\_2.  
 DR InterPro: IPR006102; Glyco\_hydro\_2ig.  
 DR InterPro: IPR006104; Glyco\_hydro\_2SB.  
 DR InterPro: IPR006103; Glyco\_hydro\_2TM.  
 DR InterPro: IPR004200; Glyco\_hydro\_42C.  
 DR InterPro: IPR004199; Glyco\_hydro\_42N.  
 DR InterPro: IPR006558; Iamg\_like.  
 DR Pfam: PF02930; Bgal\_small1\_C; 1.  
 DR Pfam: PF02929; Bgal\_small1\_N; 1.  
 DR Pfam: PF02929; Bgal\_small1\_N; 1.  
 DR Pfam: PF02929; Glyco\_hydro\_2; 1.  
 DR Pfam: PF02836; Glyco\_hydro\_2\_C; 1.  
 DR Pfam: PF02837; Glyco\_hydro\_2\_N; 1.  
 DR PRINTS: PR00132; GLHYDRLASE2.



```

DR SMART; SMO0560; LamGL; 1.
SQ SEQUENCE 1251 AA; 139978 MW; 825C3B825AFED6AF CRC64;
Query Match 14.4%; Score 73.5; DB 2; Length 1251;
Best Local Similarity 29.2%; Pred. No. 28;
Matches 33; Conservative 15; Mismatches 30; Indels 35; Gaps 7;

QY 7 PAVLLSL-----LVVHSAQAGATLGGPEESTENYASRPE-----AFNPEPLNI 51
DB 7 PAVLLSLVAVTGLGLPAAHAQVDPGSPDAIESLYEDPQRTGSGQPPHAFARPYADA 66
QY 52 DK-LRSAPK-----ADE-----FLN--WHALESIKRKLPE-----FLNWDA 84
DB 67 EQALRSARBDLFAPADEPPTWTLSTNGRNGQYADHYRDLPAQWQSGSEMDA 119

RESULT 5
Q8UES9 PRELIMINARY; PRT; 390 AA.
AC Q8UES9;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Para-aminobenzoate synthase component I.
GN PAB1 OR ATU1676 OR AGR C 3082.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_Taxid=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Seubald J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kuyavirin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA "Nester E.W.";
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Gurillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houniel K., Gordon J., Vaudin M., Iartchouk O., Bpp A., Liu F.,
RA Wolman C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328 (2001).
RN [3]
RP EMBL; AEO09124; AAL42676.1; ALT INIT.
DR EMBL; AEO08089; AAK87448.1; -.
DR InterPro; IPR005801; Anth synth chor.
DR Pfam; PF00425; chorismate bind; 1.
DR PRINTS; PR00095; ANTSMTNASEI.
DR ProDom; PD000779; Anth_synth_chor; 1.
KM Complete proteome.
SQ SEQUENCE 390 AA; 43232 MW; 65EB9B0D09E7FF16 CRC64;

Query Match 14.3%; Score 73; DB 16; Length 390;
Best Local Similarity 33.7%; Pred. No. 7.8;
Matches 30; Conservative 11; Mismatches 34; Indels 14; Gaps 5;

QY 22 GATLGGPEESTIENYASRPAFNTPLNIDKLSAPK-ADEFILNWA--LFE-----71
DB 20 GTVTAETPEPEIT--VADEPEAFPTALQRMELRBAQKVLGYGYEAGPLFEPKLAPFA 77

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QY 72 SIKRLPLFLNMDAF--PKLKGRLSATPDA 98
DB 78 AEPNVPEPLNFGVFSQPQDEGRFARPDA 106

RESULT 6
Q22143 PRELIMINARY; PRT; 634 AA.
ID Q22143
AC Q22143; Q932H6;
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Putative transketolase (At2g45290/F4L23.20).
GN AT2G45290.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucots II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
RA Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R.,
RA Venter J.C.;
RL Submitted (Aug-1997) to the EMBL/genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koeseema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Natusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriguni M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (SEP-2001) to the EMBL/genbank/DBJ databases.
RN [5]
RP EMBL; AC002387; AAB82634.2; -.
DR EMBL; AY057528; AAL09768.1; -.
DR HSSP; P23254; 1TRK.
DR InterPro; IPR005478; BactTransketolase.
DR InterPro; IPR005475; Transketolase_C.
DR InterPro; IPR005474; Transketolase_N.
DR Pfam; PF00456; transketolase; 1.
DR Pfam; PF02780; transketolase_C; 1.
DR Pfam; PF02779; transket pyr; 1.
DR TIGRPFAM; TIGR00232; Cklase bact; 1.
DR PROSITE; PS00802; TRANSKETOLASE 2; 1.
SQ SEQUENCE 634 AA; 68851 MW; 42A8D1657C260113 CRC64;

Query Match 14.2%; Score 72.5; DB 10; Length 634;
Best Local Similarity 25.7%; Pred. No. 16;
Matches 27; Conservative 15; Mismatches 26; Indels 37; Gaps 5;

QY 18 HSAQAGTGGPEESTIENYASRPAFNTPLNIDKLS-----AFRADERLWNG 67
DB 230 YSVHGAALGKEKEVEATRNRLGMPYEPFHP-----EDVSKHMSRRHTPEGAALRAD--WN 281
QY 68 ALFESIKRKLPE-----LWWDAPPKLKGRLSATPDA 98

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RESULT 10
OQ35B8
ID OQ35B8 PRELIMINARY; PRT; 251 AA.
AC OQ35B8;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Hypoetical protein HCM2.0044c.
GN HCM2.0044c.
OS Salmonella typhi.
OG Plasmid pHCN2.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
NCBI_TaxID=601;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Churchill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahinia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagers K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.,
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
EMBL: AL513384; CAD09911.1;
KM Hypoetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 251 AA; 29282 MW; DA64A8B147B4AA3 CRC64;

Query Match 13.7%; Score 70.5; DB 16; Length 251;
Best Local Similarity 25.3%; Pred. No. 8;
Matches 22; Conservative 14; Mismatches 20; Indels 31; Gaps 4;

OQ 25 LGPPEESTTEN-----YASRPEANTP-----LNDKLSAKAD----- 61
Db 6 VGNADDDKYLEYDAFVENGTTIASRPLDFNDPAELKVILDFPADPDVVKKRYADNPEK 65
OQ 62 ---EFLNWHALFESIKRKLPLNWDAP 85
Db 66 TEEEFPLAWYSSFRERAK-----SWIAY 87

RESULT 11
OQX863
ID OQX863 PRELIMINARY; PRT; 500 AA.
AC OQX863;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Putative integral membrane efflux protein.
GN SCO3507 OR SCE134.08.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomyces; Streptomyces.
NCBI_TaxID=1902;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=2196410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleeer H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrett B.G., Parkhill J.,
RA Hopwood D.A.;

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RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)."
RL Nature 417:141-147(2002).
DR EMBL: AL539116; CAB41206.1;
DR InterPro; IPR007114; MFS.
DR PROSITE; PS00850; MFS; 1.
KM Complete proteome.
SQ SEQUENCE 500 AA; 52492 MW; F990D89D310E5C4D CRC64;

Query Match 13.7%; Score 70; DB 16; Length 500;
Best Local Similarity 24.8%; Pred. No. 23;
Matches 30; Conservative 16; Mismatches 45; Indels 30; Gaps 3;

OQ 6 LPAVVLISLVHSAQATLGGPEESTIENTVASRPEA-----FNTPLINIKRS 56
Db 257 LACMLMRSRELDHAAVRAERAGKQLREGRLVYAGRPDLVMPVLVGFPGTALNFPVHS 316
OQ 57 AFKADEF---LNMWALF-----ESIKRKLPLNWDAPPKLGRSAT 95
Db 317 AFADVFDAGAGATSLFNTLVAGSLTGALLAARHATRRRLPFLAALFQVLQAVAAVA 376
OQ 96 P 96
Db 377 P 377

RESULT 12
OQ90WD4
ID OQ90WD4 PRELIMINARY; PRT; 521 AA.
AC OQ90WD4;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Cytochrome P450A.
OS Lithogastus morumyrus (Striped seabream).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Lithogastus.
NCBI_TaxID=50591;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Tom M.,
RT "A cytochrome P450 (CYP1A) cDNA from the liver of the sparid fish
RT lithogastus morumyrus."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL: AF264037; AAK69390.1;
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KM Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 521 AA; 59409 MW; 48B25B37DBDD78B6 CRC64;

Query Match 13.7%; Score 70; DB 13; Length 521;
Best Local Similarity 28.0%; Pred. No. 24;
Matches 28; Conservative 15; Mismatches 33; Indels 24; Gaps 5;

OQ 1 MKIPVLNVLISLVLSA---QGATLGGPEESTIENTVASRPEANTPPLINIKLSA 57
Db 81 IQIGRPVVLVSGNETVROALIKG-----EEFARPDVLSFRFTN-DKSLIA 127
OQ 58 FKADEFNWHALFESIKRKLPLNWDAPPKLGLRSATPD 97
Db 128 FSTDQAGWRA-----RRRLVASLRSPATLGG---TTP 159

RESULT 13
OQ90XP1
ID OQ90XP1 PRELIMINARY; PRT; 521 AA.
AC OQ90XP1;

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DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Cytochrome P450 1A.  
 OS Salmo salar (Atlantic salmon).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
 NCBI\_TaxID=8030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Arukwe A.;  
 RT "Molecular cloning, sequence analysis and expression of the cytochrome  
 P4501A gene in Atlantic salmon (Salmo salar).";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR EMBL; AF364076; AAK52513.2; -.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR Pfam; PF00067; P450; 1.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
 KW Heme; Monooxygenase; Oxidoreductase.  
 SQ SEQUENCE 521 AA; 58574 MW; C1859561E453F5CC CRC64;

Query Match 13.7%; Score 70; DB 13; Length 521;  
 Best Local Similarity 28.0%; Pred. No. 24;  
 Matches 28; Conservative 16; Mismatches 32; Indels 24; Gaps 5;

Qy 1 MKIPVLPAVVLISLVHSA---OGATLGPBESTIENTYASRPENPTPLNTDKLSA 57  
 Db 81 IQIGRPVPLVLSGSETVRQALIKG-----EDFAGRPDLVSFKFIN-DGKSLA 127  
 Qy 58 FKADFLNWHALFESIRKRLPFLNWDAPFKLGIRSATPD 97  
 Db 128 FSTDKAGWMRA-----RRKLMSALRSFATLEG---STPE 159

RESULT 14  
 08QGP2 PRELIMINARY; PRT; 522 AA.  
 AC 08QGP2;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Cytochrome P450 1A.  
 GN CYPLA.  
 OS Salmo salar (Atlantic salmon).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
 NCBI\_TaxID=8030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Rees C.B., Li W.;  
 RT "Cloning and induction of Atlantic salmon CYPLA."  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR EMBL; AF361643; AAM00254.1; -.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR Pfam; PF00067; P450; 1.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
 KW Heme; Monooxygenase; Oxidoreductase.  
 SQ SEQUENCE 522 AA; 59192 MW; 560C4E10F704A568 CRC64;

Query Match 13.7%; Score 70; DB 13; Length 522;  
 Best Local Similarity 28.0%; Pred. No. 24;  
 Matches 28; Conservative 16; Mismatches 32; Indels 24; Gaps 5;

Qy 1 MKIPVLPAVVLISLVHSA---OGATLGPBESTIENTYASRPENPTPLNTDKLSA 57  
 Db 81 IQIGRPVPLVLSGSETVRQALIKG-----EDFAGRPDLVSFKFIN-DGKSLA 127  
 Qy 58 FKADFLNWHALFESIRKRLPFLNWDAPFKLGIRSATPD 97

Db 128 FSTDKAGWMRA-----RRKLMSALRSFATLEG---STPE 159

## RESULT 15

Q9PRH3 PRELIMINARY; PRT; 522 AA.  
 ID Q9PRH3;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Cytochrome P450 1A3.  
 GN CYPLA3.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Liver;  
 RA Carvan M.J. III, Ponomareva L.V., Solis W.A., Matlib R.S., Puga A.,  
 Nebert D.W.;  
 RT "Trout CYPLA3 Gene: Recognition of Fish DNA Motifs by Mouse Regulatory  
 Proteins.";  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR EMBL; AF059711; AAD45967.1; -.  
 DR EMBL; AF059710; AAD45966.1; -.  
 DR HSP; P00179; IPT6.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR Pfam; PF00067; P450; 1.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
 KW Heme; Monooxygenase; Oxidoreductase.  
 SQ SEQUENCE 522 AA; 59086 MW; AF36786EB19D73DA CRC64;

Query Match 13.7%; Score 70; DB 13; Length 522;  
 Best Local Similarity 28.0%; Pred. No. 24;  
 Matches 28; Conservative 16; Mismatches 32; Indels 24; Gaps 5;

Qy 1 MKIPVLPAVVLISLVHSA---OGATLGPBESTIENTYASRPENPTPLNTDKLSA 57  
 Db 81 IQIGRPVPLVLSGSETVRQALIKG-----EDFAGRPDLVSFKFIN-DGKSLA 127  
 Qy 58 FKADFLNWHALFESIRKRLPFLNWDAPFKLGIRSATPD 97  
 Db 128 FSTDKAGWMRA-----RRKLMSALRSFATLEG---STPE 159

Search completed: November 28, 2003, 07:56:39  
 Job time : 61 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 08:05:39 (Search time 1715 Seconds)

(without alignments)  
1402.999 Million cell updates/sec

## SUMMARIES

29: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Title: US-10-059-395-142  
Perfect score: 510  
Sequence: 1 MKRIPVLPAYVLTSLVTLHSA.....LNMDFPKLKGARSATPDQA 99

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

-MODE=frame+ p2n.model -DEV=x1h  
-Q=/cgr2\_1/USPRO.spool/US10059395/rnatc.25112003.140713.7115/app.query.fasta\_1.263  
-DB=EST -OPMT=faetap -SUFFIX=ext -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTPMT=pro -NORM=ext -HEA8SIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USMR=US10059395.QCGN\_1.1.2810.@rnatc.25112003.140713.7115 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database:

EST:\*

1: em\_estba:\*

2: em\_estnum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gse\_hum:\*

18: em\_gse\_inv:\*

19: em\_gse\_pln:\*

20: em\_gse\_vit:\*

21: em\_gse\_fun:\*

22: em\_gse\_man:\*

23: em\_gse\_mus:\*

24: em\_gse\_pro:\*

25: em\_gse\_rtd:\*

26: em\_gse\_phg:\*

27: em\_gse\_vrl:\*

28: gb\_gse1:\*

| Result No. | Score | Query Match | Length | DB ID       | Description        |
|------------|-------|-------------|--------|-------------|--------------------|
| 1          | 510   | 100.0       | 334    | 9 AA297512  | AA297512 EST113061 |
| 2          | 510   | 100.0       | 432    | 13 BX112106 | BX112106 BX112106  |
| 3          | 505   | 99.0        | 424    | 14 W63083   | W63083 zd44b06.b1  |
| 4          | 484   | 94.9        | 334    | 14 W63020   | W63020 zd29g01.b1  |
| 5          | 481   | 94.3        | 432    | 14 W69233   | W69233 zd44c04.r1  |
| 6          | 477   | 93.5        | 431    | 14 W69227   | W69227 zd44b06.r1  |
| 7          | 471.5 | 92.5        | 412    | 14 W60268   | W60268 zd29g01.r1  |
| 8          | 458   | 89.8        | 373    | 9 AA722694  | AA722694 zg82b06.s |
| 9          | 455   | 89.4        | 381    | 14 W63108   | W63108 zd44c04.b1  |
| 10         | 453.5 | 88.9        | 336    | 9 AA297513  | AA297513 EST113062 |
| 11         | 450   | 88.2        | 348    | 9 AA287578  | AA287578 xp03e08.x |
| 12         | 440   | 86.3        | 377    | 9 AA582988  | AA582988 m72h02.s  |
| 13         | 413   | 81.0        | 339    | 9 AA778414  | AA778414 zf39e05.s |
| 14         | 381   | 74.7        | 345    | 9 A1217565  | A1217565 qd43d02.x |
| 15         | 380   | 74.5        | 359    | 10 BE466728 | BE466728 h224g06.x |
| 16         | 380   | 74.5        | 352    | 9 A1140605  | A1140605 qe05f03.x |
| 17         | 379   | 74.3        | 376    | 14 W95920   | W95920 ze08d01.r1  |
| 18         | 375   | 73.5        | 318    | 9 AA586846  | AA586846 m67e11.s  |
| 19         | 374   | 73.3        | 359    | 10 BG150312 | BG150312 7198g03.x |
| 20         | 369   | 72.4        | 378    | 9 A1184682  | A1184682 qd68b02.x |
| 21         | 367   | 72.0        | 413    | 9 AA393296  | AA393296 ze74f05.r |
| 22         | 363   | 71.2        | 330    | 14 W95883   | W95883 ze08d01.b1  |
| 23         | 357   | 70.0        | 358    | 9 AM003825  | AM003825 wq83f12.x |
| 24         | 353   | 69.2        | 436    | 9 AV597545  | AV597545 wq83f12.x |
| 25         | 352   | 69.0        | 345    | 9 AA583942  | AA583942 m644f07.s |
| 26         | 351.5 | 68.9        | 421    | 9 AV618771  | AV618771 AV618771  |
| 27         | 351   | 68.8        | 334    | 9 A1217587  | A1217587 qd43f04.x |
| 28         | 322.5 | 63.2        | 461    | 12 B1285632 | B1285632 UI-R-DDO- |
| 29         | 317.5 | 62.3        | 444    | 12 B1282573 | B1282573 UI-R-DDO- |
| 30         | 313.5 | 61.5        | 458    | 12 B1282568 | B1282568 UI-R-DDO- |
| 31         | 308.5 | 60.5        | 452    | 12 B1277693 | B1277693 UI-R-DDO- |
| 32         | 306.5 | 60.1        | 444    | 12 B1286103 | B1286103 UI-R-DDO- |
| 33         | 306.5 | 60.1        | 446    | 12 B1283220 | B1283220 UI-R-DDO- |
| 34         | 305   | 59.8        | 368    | 9 AM260965  | AM260965 E0K0243   |
| 35         | 303.5 | 59.5        | 346    | 13 BY137356 | BY137356 BY137356  |
| 36         | 303.5 | 59.5        | 409    | 9 AA572239  | AA572239 v151g12.x |
| 37         | 303.5 | 59.5        | 457    | 14 BY703646 | BY703646 BY703646  |
| 38         | 303.5 | 59.5        | 467    | 9 AM105901  | AM105901 um28f02.x |
| 39         | 303.5 | 59.5        | 459    | 14 W30505   | W30505 mc21f12.r1  |
| 40         | 303.5 | 59.5        | 470    | 9 AV007306  | AV007306 AV007306  |
| 41         | 301   | 59.0        | 339    | 14 W52030   | W52030 zd13b01.b1  |
| 42         | 300.5 | 58.9        | 938    | 14 CB192967 | CB192967 AGENCOURT |
| 43         | 300   | 58.8        | 241    | 9 AA595989  | AA595989 m644f08.s |
| 44         | 298.5 | 58.5        | 327    | 13 BY140130 | BY140130 BY140130  |
| 45         | 290.5 | 57.0        | 466    | 12 B1277761 | B1277761 UI-R-CZO- |

## ALIGNMENTS

RESULT 1

AA297512 334 bp mRNA EST 18-APR-1997

LOCUS EST113061 Fetal skin Homo sapiens cDNA 5' end, mRNA sequence.

DEFINITION AA297512

ACCESSION AA297512

VERSION AA297512.1 GI:1949866

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 334)

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult









Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.  
The WashU-Merck EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert Length: 466 Std Error: 0.00  
Seq primer: mob.REGA+ET

High quality sequence stop: 410.

#### FEATURES

source

1. 431  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1268850"  
/db\_xref="taxon:9606"  
/clone="IMAGE:343475"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal heart NBH19W"  
/note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTCCACATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBH19W."

BASE COUNT 106 a 127 c 94 g 102 t 2 others  
ORIGIN

Alignment Scores:  
Pred. No.: 4.67e-52 Length: 431  
Score: 477.00 Matches: 98  
Percent Similarity: 97.03% Conservative: 0  
Best Local Similarity: 97.03% Mismatches: 1  
Query Match: 93.53% Indels: 2  
DB: 14 Gaps: 0

US-10-059-395-142 (1-99) x W69227 (1-431)

QY 1 MetLysIleProValIleuProAla-ValValIleuSerLeuValIleuHisSerAl 20  
Db 12 ATGAAGATCCCGGCTCTCTGCGCGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 71  
QY 20 agInGlyAlaThrlLeuGlyGlyProGluGluGluSerThrIleGluAsnTyrAlaSerAr 40  
Db 72 CAGGAGGCCACCTGGGTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 111  
QY 40 g-ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysA 60  
Db 132 ACCCGAGGCGCTTAAACCCCGTCTGAACATCGAACAATTGCGATCGCGTTAAAG 191  
QY 60 laLeuGluPheLeuAsnThrHisAlaLeuPheGluSerIleLysArgLysLeuProPhe 80  
Db 192 CTATGAGTCTCGAAGTGCACGCCCTCTTGAAGTCTATCAAAAGAACTTCTCTCTCC 251  
QY 80 eubAsnTPAspAlaPheProLysLeuArgSerAlaThrlProAspAlaGln 99  
Db 252 TCAACTGGAGTGCCTTCTTAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 310

RESULT 7  
W60268

LOCUS W60268 412 bp mRNA linear EST 15-OCT-1996  
DEFINITION z229601.r1 Soares fetal heart NBH19W Homo sapiens cDNA clone  
ACCESSION IMAGE:342096 5', mRNA sequence.  
VERSION W60268.1 GI:1367169  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

#### REFERENCE

1 (bases 1 to 412)

Hillier, L., Clark, N., Dubuque, T., Eliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Merra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.

The WashU-Merck EST Project

#### COMMENT

Unpublished

#### TITLE

Washington University School of Medicine

#### JOURNAL

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

#### FEATURES

source

1. 412  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1267471"  
/db\_xref="taxon:9606"  
/clone="IMAGE:342096"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal heart NBH19W"  
/note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTCCACATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBH19W."

#### FEATURES

High quality sequence stop: 385.

BASE COUNT 96 a 127 c 88 g 98 t 3 others  
ORIGIN

Alignment Scores:  
Pred. No.: 2.29e-51 Length: 412  
Score: 471.50 Matches: 97  
Percent Similarity: 97.98% Conservative: 0  
Best Local Similarity: 97.98% Mismatches: 2  
Query Match: 92.45% Indels: 1  
DB: 14 Gaps: 0

US-10-059-395-142 (1-99) x W60268 (1-412)

QY 1 MetLysIleProValIleuProAlaValValIleuSerLeuValIleuHisSerAla 20  
Db 15 ATGAAGATCCCGGCTCTCTGCGCGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 74  
QY 21 gInGlyAlaThrlLeuGlyGlyProGluGluGluSerThrIleGluAsnTyrAlaSerAr 40  
Db 75 CAGGAGGCCACCTGG--TGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 132

QY 41 ProGU1a1aPheAasThrProPheLeuAan11eApLyLeuArgSer1aPhe1yala 60  
 Db 133 CCCGAGGCCCTTTAACACCCCGTTCCTGAACATGCACAAATTCGATCTCGTTTAAGGCT 192  
 QY 61 AaPgiuPheLeuAasThrPhe1a1aPheG1uSer11eLyAArgLyLeuProPheLeu 80  
 Db 193 GAGTATCAAAAGGAACCTTCCTCAACCTGAGATGATCAAAAGGAACCTTCCTTCCTC 252  
 QY 81 AaNTTPaSPa1aPheProLyLeuLySG1yLeuArgSer1aThrProaSPa1aG1n 99  
 Db 253 AACTGGAGATCGCTTTCCTTAAGCTGAAGACCTGAGAGGCCAATCTCTATGCTCCAG 309  
 RESULT 8  
 AA722694 373 bp mRNA linear EST 02-JAN-1998  
 LOCUS z982b06.s1 Soares fetal heart NBH19W Homo sapiens cDNA clone  
 DEFINITION IMAGE:399827 3', mRNA sequence.  
 ACCESSION AA722694  
 VERSION AA722694.1 GI:2740401  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 373)  
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,  
 J., Moore, B., Scheinberg, K., Stepien, M., Tan, F., Theisling, B.,  
 White, Y., Wylie, T., Waterston, R. and Wilson, R.  
 WashU-NCI human EST Project  
 TITLE Unpublished  
 JOURNAL  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: -40m3 fwd. ET from Amersham.  
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 1..373  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:1307650"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:399827"  
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 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_1lb="Soares fetal heart NBH19W"  
 /note="Organ: heart; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTTCACATCTGAGTGGAGCGCCGCGATCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by  
 M. Fatima Bonaldo. This library was constructed from the  
 same fetus as the fetal lung library, Soares fetal lung  
 NBH19W."
 BASE COUNT 89 a 81 c 113 g 90 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.15e-49 Length: 373  
 Score: 458.00 Matches: 88  
 Percent Similarity: 96.88% Conservative: 0  
 Best Local Similarity: 98.88% Mismatches: 1  
 Query Match: 89.80% Indels: 0  
 DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x AA722694 (1-373)  
 QY 11 LeuAasThrLeuValLeuHisSer1aG1ng1yA1aThrLeuG1yG1yProG1uG1u 30  
 Db 373 CTCCTCTCCCTCGGTGCTCTCCATCTTCGCCAGGAGTCCACCCCTGGGTGCTCGAAGAA 314  
 QY 31 G1uSerThr11eG1uAasThr1a1aSerArgProG1ua1aPheAasThrProPheLeuAa 50  
 Db 313 GAAGACCACTTGAATATATGCGTCACAGCCCGGCTTTAACCCTTCCTGAAC 254  
 QY 51 11aAPLyLeuArgSer1aPhe1y1a1aPgiuPheLeuAasThrPhe1a1aPhe 70  
 Db 253 ATCGACAAATTCGATCGCTTTAAGGCTGATGATGCTCGAATCGGACGCCCTCTTT 194  
 QY 71 G1uSer11eLyAArgLyLeuProPheLeuAasThrPaSPa1aPheProLyLeuLySG1y 90  
 Db 193 GAGTATCAAAAGGAACCTTCCTCAACCTGAGATGCTTCCTTAAGCTGAAGGA 134  
 QY 91 LeuArgSer1aThrProaSPa1aG1n 99  
 Db 133 CTGAGAGCGCACTCTCGATGCCAG 107  
 RESULT 9  
 W69108/c 381 bp mRNA linear EST 16-OCT-1996  
 LOCUS zd44c04.s1 Soares fetal heart NBH19W Homo sapiens cDNA clone  
 DEFINITION IMAGE:343394 3', mRNA sequence.  
 ACCESSION W69108  
 VERSION W69108.1 GI:1378389  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 381)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,  
 M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaks, E., Waterston,  
 R., Williamson, A., Wohlmann, P. and Wilson, R.  
 The WashU-Merck EST Project  
 TITLE Unpublished  
 JOURNAL  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Inert Length: 442 Std Error: 0.00  
 Seq primer: mob. REGA+ET  
 High quality sequence stop: 347.  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:343494"  
 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_1lb="Soares fetal heart NBH19W"  
 /note="Organ: heart; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTTCACATCTGAGTGGAGCGCCGCGATCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by

M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."

BASE COUNT 91 a 86 c 114 g 89 t 1 others

## Alignment Scores:

Pred. No.: 2,16e-49 Length: 381  
Score: 456.00 Matches: 91  
Percent Similarity: 97.85% Conservative: 0  
Best Local Similarity: 97.85% Mismatches: 1  
Query Match: 89.41% Indels: 1  
DB: 14 Gaps: 0

US-10-059-395-142 (1-99) x W69108 (1-381)

QY 8 A1AValValLeuLeuSerLeuLeuValLeuHisSer-AlaGlnGlyAlaThrLeuGlyG1 27  
DB 381 GCGGTGTGNTCTCTCCCTCCGTGCTCCACTTCTTCCAGGAGGAGCCACTGAGTGG 322  
QY 27 YProGluGluGluSerThrIleGluSerThrAlaSerArgProGluAlaPheAsnThrP 47  
DB 321 TCTGTAG 262  
QY 47 OPhelLeuAniLeuAspLeuLeuArgSerAlaPheLeuAlaAspGluPheLeuAsnThrP 67  
DB 261 GTTCTCGAAGCATGCAAAATTCGATCTGCTTAAGCTGATGATCTTCTGAACTGGCA 202  
QY 67 SAlaLeuPheGluSerIleLeuArgLeuLeuProPheLeuAsnThrPAspAlaPhePro 87  
DB 201 CCGCCCTTGTGAGTATCAAAAGAACTTCTTCTTCACTGAGGAGGATGCTTCTTCA 142  
QY 87 SLeuLeuGlyLeuArgSerAlaThrProAspAlaGln 99  
DB 141 GCTGAAG 105

RESULT 10  
AA297513 326 bp mRNA linear EST 18-APR-1997  
LOCUS AA297513 Fetal skin Homo sapiens cDNA 5' end, mRNA sequence.  
DEFINITION AA297513  
ACCESSION AA297513.1 GI:1949867  
VERSION  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 326)  
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirschner,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wei,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Barle-Hughes,J., Fink,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodex,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanges,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Seudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uteback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrite,A., Fischer,C., Hastings,G.A., He,M.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseeltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)  
MEDLINE 96026280  
PUBMED 7560098  
COMMENT Other\_ESTs: TH0151622  
Contact: Kerlavage, AR  
Bioinformatics

The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@icgr.org  
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgt/hgt.html>)  
Seq primer: M13 Reverse.  
Location/Qualifiers

## FEATURES

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/db\_xref="taxon:9606"  
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/dev\_stage="fetus"  
/clone\_lib="Fetal skin"  
/note="Organ: skin; Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI"  
BASE COUNT 76 a 95 c 76 g 77 t 2 others  
ORIGIN

Alignment Scores:  
Pred. No.: 3.67e-49 Length: 326  
Score: 453.50 Matches: 91  
Percent Similarity: 92.86% Conservative: 0  
Best Local Similarity: 92.86% Mismatches: 6  
Query Match: 88.92% Indels: 1  
DB: 9 Gaps: 1

US-10-059-395-142 (1-99) x AA297513 (1-326)

QY 2 LysIleProValLeuProAlaValLeuLeuSerLeuLeuValLeuHisSerAlaGln 21  
DB 1 AAGATCCCGGTCTCTTCCGCGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60  
QY 22 GlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnThrAlaSerArgPro 41  
DB 61 GGAGCCACCTGTGGGTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
QY 42 GluAlaPheAsnThrProPheLeuAsnIleAspLeuLeuArgSerAlaPheLeuAlaAsp 61  
DB 121 GAGGCTTTAAACACCCCGCTCTGAAACATGCAAAATTCGATCTGCTTAAAGGCTGAT 180  
QY 62 GluPheLeuAsnThrPheAlaLeuPheGluSerIleLeuArgLeuProPheLeuAsn 81  
DB 181 GAGTCTCGAAGTGCAGACGCTCTTTGAGTCTTCAAAAGAGAACTTCTTCTCTCAAC 240  
QY 82 TTPAAlaPheProLeuLeuLeuArgSerAla--ThrProAspAla 98  
DB 241 TGGATGCTTCTTCTTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 294

RESULT 11  
AM238758 348 bp mRNA linear EST 13-DEC-1999  
LOCUS AM238758 xp03e08.x1 NCI CGAP\_HN8 Homo sapiens cDNA clone IMAGE:2739302 3'  
DEFINITION AM238758  
ACCESSION AM238758  
VERSION AM238758.1 GI:6571147  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 348)  
TITLES NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

Tissue Procurement: Edward Shillitoe Ph.D., Silvio Gutkind Ph.D.,  
Chidchanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.,  
CDNA Library Preparation: David B. Krizman, Ph.D.,  
CDNA Library Arrayed by: Greg Lennon, Ph.D.,  
DNA Sequencing by: Washington University Genome Sequencing Center  
clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LML at:  
www-bio.lml.gov/bdrip/image/image.html

Possible reversed clone: polyt not found  
Seq primer: -40bp from Gibco  
High quality sequence stop: 331.

## FEATURES

## SOURCE

Location/Qualifiers

1. .348

/organism="Homo sapiens"

/mol type="mRNA"

/db xref="taxon:9606"

/clone="IMAGE:2739302"

/tissue\_type="well-differentiated invasive carcinoma,  
floor of mouth"

/lab host="DH10B"

/clone lib="NCI CGAP HN8"

/note="Vector: PAMPI0; CDNA made by oligo-dT priming.  
Non-directionally cloned into the UDG sites of PAMPI0.  
Size-selected on agarose gel, average insert size 500 bp.  
Primary library; non-amplified. CDNA library  
Preparation: David B. Krizman, Ph.D (NCI). Reference:  
Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 82 a 104 c 84 g 78 t

## ORIGIN

## Alignment Scores:

Pred. No.: 1.15e-48 Length: 348  
Score: 450.00 Matches: 86  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 88.24% Indels: 0  
DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x AW238758 (1-348)

Qy 14 LeuLeuValLeuHisSerAlaGlnGlyAlaThrLeuGlyGlyProGlnGlnGlnSerThr 33  
Db 36 CTCCTGGTCTCCCTCTGCGAGGAGCCACCCCTGGGTGTCTCTGAAGAGAAAGCACC 95  
Qy 34 IleGlnSerTyrAlaSerArgProGlnAlaPheAsnThrProPheLeuAsnIleAspLys 53  
Db 96 ATTGAGATTATGATCAGACCCGAGGCTTTAAACCCCGTCTTGAAGATGACAAA 155  
Qy 54 LeuArgSerAlaPheLeuAlaAspGlnPheLeuAsnThrPheAlaLeuPheGlnSerIle 73  
Db 156 TTGGGATCTGCGTTTAAAGGTGATGAGTCTTGAAGTGGACGCCCTCTTGAAGTCATC 215  
Qy 74 LysArgLysLeuProPheLeuAsnThrAspAlaPhePhePheLeuLysGlyLeuArgSer 93  
Db 216 AAAAGAGAACTTCTTCTTCTCACTGGGATGCTTTCTTAAGCTGAAGAGACTGAGAGC 275  
Qy 94 AlaThrProAspAlaGln 99  
Db 276 GCAACTCTGTAGTCCAG 293

## RESULT 12

AA582988 377 bp mRNA linear EST 26-SEP-1997

LOCUS n72h02.e1 NCI\_CGAP\_lart Homo sapiens cDNA clone IMAGE:1089459 3',

DEFINITION mRNA sequence.

ACCESSION AA582988

VERSION AA582988.1 GI:2360348

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 377)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Straubeberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.  
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Stratagene, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LML at:  
www-bio.lml.gov/bdrip/image/image.html

Insert Length: 526 Std Error: 0.00

Seq primer: -40ml3 fwd. RT from Amersham.

## FEATURES

## SOURCE

Location/Qualifiers

1. .377

/organism="Homo sapiens"

/mol type="mRNA"

/db xref="taxon:9606"

/clone="IMAGE:1089459"

/tissue\_type="larynx"

/lab host="SOLR (kanamycin resistant)"

/clone lib="NCI CGAP Lart1"

/note="Organ: larynx; Vector: Bluescript SK-; Site 1:  
EcoRI; Site 2: XhoI; cloned unidirectionally. Primer:  
Oligo dT. Larynx. 5' adaptor sequence: 5' GATTGGGACGAG  
3' 3' adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3'  
Average insert size: 0.9 kb."

BASE COUNT 90 a 84 c 114 g 89 t

## ORIGIN

## Alignment Scores:

Pred. No.: 2.61e-47 Length: 377  
Score: 440.00 Matches: 91  
Percent Similarity: 98.91% Conservative: 0  
Best Local Similarity: 98.91% Mismatches: 1  
Query Match: 86.27% Indels: 1  
DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x AA582988 (1-377)

Qy 8 AlaValLeuLeuSerLeuLeuValLeuHisSerAlaGlnGlyAlaThrLeuGlyGly 27  
Db 377 GCCGTGTGCTCTCTCTCTCTGCTGCTCCTCCAGGAGCCACCTGGGTGT 318  
Qy 28 ProGlnGlnSerThrIleGlnSerTyrAlaSerArgProGlnAlaPheAsnThrPro 47  
Db 317 CTTGAGGAAAGAAACACATTGAGATTATGCGTCAGACCCGAGGCTTTAAACACCCCG 258  
Qy 48 PheLeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGlnPheLeuAsnThrPhe 67  
Db 257 TTCTGGAACATCGAACAATTGCGATCTGCGTTTAAAGGTGATGAGTCTTGAAGTGC 199  
Qy 68 AlaLeuPheGlnSerIleLysArgLysLeuProPheLeuAsnThrAspAlaPheProLys 87  
Db 198 GCCCTTTAGTGTATCAAAAGAACTTCTTCTCACTGAGTGGATGCTTTCTTAAG 139  
Qy 88 LeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
Db 138 CTGAAGAGACTGAGAGAGCGCACTCTGATGCCAG 103

## RESULT 13

AA778414 339 bp mRNA linear EST 05-FEB-1998

LOCUS zf39e05.e1 Soares fetal heart\_NDH19W Homo sapiens cDNA clone

DEFINITION IMAGE:379328 3', mRNA sequence.

ACCESSION AA778414

VERSION AA778414.1 GI:2837745

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 339)  
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,  
 Kitzman, D., Kucada, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin,  
 J., Moore, B., Schellenger, K., Stepien, M., Tan, F., Theising, B.,  
 White, Y., Wylie, T., Waterston, R. and Wilson, R.  
 WASHU-NCI human EST Project  
 Unpublished  
 TITLE JOURNAL  
 COMMENT Contact: Wilson, R.  
 Washington University School of Medicine  
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 This clone is available royalty-free through LML; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: -40m3 fwd. ET from Amersham.  
 Location/Qualifiers  
 1..339  
 /organism="Homo sapiens"  
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 /db\_xref="GDB:1287584"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:379328"  
 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_1lb="Soares\_fetal\_heart\_NbH19W"  
 /note="Organ: heart; Vector: pTZ19 (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTTCACATCTGAGTGGAGCGCCGCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pTZ19 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by  
 M.Fatima Bonaldo. This library was constructed from the  
 same fetus as the fetal lung library, Soares fetal lung  
 NbH19W."  
 BASE COUNT 79 a 77 c 96 g 87 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 7,52e-44 Length: 339  
 Score: 413.00 Matches: 78  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 80.98% Indels: 0  
 DB: 9 Gaps: 0  
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 QY 42 G1A1AphASnThrProPhelEuaSn11eAp1YsLeuARsER1A1PhelYsA1aSp 61  
 DB 277 GAGGCGCTTTAACAACCCGCTCTGAAACATCGACAATTCGATCTGCGTTAAAGCTAT 218  
 QY 62 G1UphELeuASnThrPh1A1aLeuPhEg1USer11eLYsAR1YsLeuPProPhelEuaSn 81  
 DB 217 GAGTTCCTGAAGTGGACCCCTCTTGTGCTATCAAAAGGAACTCTTCTCTCAAC 158  
 QY 82 TTPAaPa1AphPProLYsLeuYsG1YLeuARsER1A1ThrProAsPa1aG1n 99  
 DB 157 TGGGATGCTTCTTAAGCTGAAGAGACTGAGAGCGCACTCTGATGCCAG 104  
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 A1217565/c

LOCUS A1217565 345 bp mRNA linear EST 10-NOV-1998  
 DEFINITION g43d02.x1 Soares\_fetal\_heart\_NbH19W Homo sapiens cDNA clone  
 IMAGE:1732227 3', mRNA sequence.  
 ACCESSION A1217565  
 VERSION A1217565.1 GI:3797380  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 345)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-rc@mail.nih.gov  
 This clone is available royalty-free through LML; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert length: 451 Std Error: 0.00  
 Seq primer: -40UP from Glpco  
 High quality sequence stop: 320.  
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 /lab\_host="DH10B (ampicillin resistant)"  
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 /note="Organ: heart; Vector: pTZ19 (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTTCACATCTGAGTGGAGCGCCGCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pTZ19 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by  
 M.Fatima Bonaldo. This library was constructed from the  
 same fetus as the fetal lung library, Soares fetal lung  
 NbH19W."  
 BASE COUNT 79 a 77 c 99 g 89 t 1 others  
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 Alignment Scores:  
 Pred. No.: 1.16e-39 Length: 345  
 Score: 361.00 Matches: 77  
 Percent Similarity: 96.25% Conservative: 0  
 Best Local Similarity: 96.25% Mismatches: 1  
 Query Match: 74.71% Indels: 2  
 DB: 9 Gaps: 0  
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 DB 342 GGAGCCACCCCTGGG1GCTCTGAGAGAGAACACCATTAATGCGTCAGACCC 283  
 QY 41 CG1U-1A1AphASnThrProPhelEuaSn11eAp1YsLeuARsER1A1PhelYsA1aSp 61  
 DB 282 GAGGCGCTTTAACAACCCGCTCTGAAACATCGACAATTCGATCTGCGTTAAAGGCTG 223  
 QY 61 SPGLUphELeuASnThrPh1A1aLeuPhEg1USer11eLYsAR1YsLeuPProPhelEua 81  
 DB 222 ATGAGTTCCTGAAGTGGACCCCTCTTGTGCTATCAAAAGGAACTCTTCTCTCA 163  
 QY 81 SNTTPAaPa1AphPProLYsLeuYsG1YLeuARsER1A1ThrProAsPa1aG1n 99  
 DB 162 ACTGGATGCTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCAG 107

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RESULT 15
BE466728/c 359 bp mRNA linear EST 27-JUN-2000
LOCUS h224g06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3208954 3',
DEFINITION mRNA sequence.
ACCESSION BE466728
VERSION BE466728.1 GI:9512503
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 359)
NCI-CCGAP http://www.nci.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbbs-rc@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL, send email to:
info@image.lnl.gov
Seq primer: -40bp from Gibco.
FEATURES
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Location/Qualifiers
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/mol_type="mRNA"
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/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_id="NCI_CGAP_GC6"
/notes="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI_CGAP GC4 was prepared, and
as circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonids
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 77 a 80 c 96 g 106 t
ORIGIN
Alignment Scores:
Pred. No.: 1.66e-39 Length: 359
Score: 380.00 Matches: 73
Percent Similarity: 96.05% Conservative: 0
Best Local Similarity: 96.05% Mismatches: 3
Query Match: 74.51% Indels: 0
DB: 10 Gaps: 0
US-10-059-395-142 (1-99) x BE466728 (1-359)
QY 24 ThrleuglyglyProgluglugluserThrllegluantYrAlaserArgProgluAla 43
Db 347 ACCGGGGGAGACGGCGAGAGAAAGACCAATTGGAATTATGCGTCAAGACCGAGGCC 288
QY 44 PheAsnThrProPheLeuAsn11eAspYsLeuArgSerAlaPheYsAlaAspGluPhe 63
Db 287 TTTAAcACCCCGTTCCTGACATCGACAAATTGCGATCTGCGTTTAAGCTGATGAGTTC 228
QY 64 LeuAsnTPhAlaAlaLeuPheGluSer11eYsArgYsLeuProPheLeuAsnTPhAsp 83
Db 227 CTGAACCTGGCAACGCCCTTTGAGCTATCAAAAGAAACTTCCTTCTCAACTGGGAT 168
QY 84 AlapheProYsLeuYsGlyLeuArgSerAlaThrProAspAlaGln 99

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Db 167 GCCCTTCTTAAGCTGAAGAGACTGAGAGCGCCAACTCTGATGCCAG 120

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Search completed: November 28, 2003, 09:26:31
Job time : 1723 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 13:41:33 Search time 17 Seconds

(without alignments)  
176.710 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Sequence: 1 EESTETENASREAFNTPF.....LNMDFPKLGRSAPDAQ 71

Scoring table: OLIGO

Gapop 60.0 , Gapept 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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2: /cgn2\_6/ptodata/2/1aa/5R COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6R COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID                     | Description       |
|------------|-------|-------------|--------|------------------------|-------------------|
| 1          | 71    | 100.0       | 99     | 4 US-09-996-243-201    | Sequence 201, App |
| 2          | 7     | 12.7        | 344    | 4 US-09-252-991A-22286 | Sequence 22286, A |
| 3          | 7     | 9.9         | 254    | 4 US-09-107-532A-4795  | Sequence 4795, Ap |
| 4          | 7     | 9.9         | 257    | 4 US-09-252-991A-26002 | Sequence 26002, A |
| 5          | 6     | 8.5         | 18     | 1 US-08-285-085-3      | Sequence 3, Appl1 |
| 6          | 6     | 8.5         | 18     | 1 US-08-285-085-4      | Sequence 4, Appl1 |
| 7          | 6     | 8.5         | 18     | 1 US-08-285-085-5      | Sequence 5, Appl1 |
| 8          | 6     | 8.5         | 18     | 5 PCT-US95-10741-3     | Sequence 3, Appl1 |
| 9          | 6     | 8.5         | 18     | 5 PCT-US95-10741-4     | Sequence 4, Appl1 |
| 10         | 6     | 8.5         | 18     | 5 PCT-US95-10741-5     | Sequence 5, Appl1 |
| 11         | 6     | 8.5         | 45     | 4 US-08-469-260A-483   | Sequence 483, App |
| 12         | 6     | 8.5         | 45     | 4 US-08-468-446-483    | Sequence 483, App |
| 13         | 6     | 8.5         | 45     | 4 US-08-467-344A-483   | Sequence 483, App |
| 14         | 6     | 8.5         | 105    | 4 US-09-252-991A-26885 | Sequence 26885, A |
| 15         | 6     | 8.5         | 117    | 4 US-09-252-991A-19208 | Sequence 19208, A |
| 16         | 6     | 8.5         | 132    | 2 US-09-109-265-8      | Sequence 8, Appl1 |
| 17         | 6     | 8.5         | 136    | 4 US-09-690-454-131    | Sequence 131, App |
| 18         | 6     | 8.5         | 177    | 4 US-09-252-991A-28186 | Sequence 28186, A |
| 19         | 6     | 8.5         | 178    | 4 US-09-328-352-5593   | Sequence 5593, Ap |
| 20         | 6     | 8.5         | 213    | 4 US-09-134-001C-3969  | Sequence 3969, Ap |
| 21         | 6     | 8.5         | 218    | 1 US-08-470-837-26     | Sequence 26, Appl |
| 22         | 6     | 8.5         | 218    | 4 US-08-868-452-26     | Sequence 26, Appl |
| 23         | 6     | 8.5         | 220    | 4 US-09-480-675A-4     | Sequence 4, Appl1 |
| 24         | 6     | 8.5         | 229    | 4 US-09-327-984A-8     | Sequence 8, Appl1 |
| 25         | 6     | 8.5         | 231    | 4 US-08-129-722A-2     | Sequence 2, Appl1 |
| 26         | 6     | 8.5         | 232    | 4 US-08-337-874A-6     | Sequence 6, Appl1 |
| 27         | 6     | 8.5         | 232    | 5 PCT-US94-09700-6     | Sequence 6, Appl1 |

#### ALIGNMENTS

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| 29 | 6 | 8.5 | 245 | 4 US-09-613-303-23    | Sequence 23, Appl |
| 30 | 6 | 8.5 | 272 | 3 US-08-910-820-4     | Sequence 4, Appl1 |
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| 32 | 6 | 8.5 | 272 | 4 US-09-844-908-4     | Sequence 4, Appl1 |
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| 37 | 6 | 8.5 | 282 | 4 US-09-844-908-5     | Sequence 5, Appl1 |
| 38 | 6 | 8.5 | 291 | 1 US-08-102-757-9     | Sequence 9, Appl1 |
| 39 | 6 | 8.5 | 291 | 1 US-08-102-757-11    | Sequence 11, Appl |
| 40 | 6 | 8.5 | 307 | 2 US-08-216-894-6     | Sequence 6, Appl1 |
| 41 | 6 | 8.5 | 307 | 3 US-09-115-746-6     | Sequence 6, Appl1 |
| 42 | 6 | 8.5 | 310 | 4 US-09-646-075-1     | Sequence 1, Appl1 |
| 43 | 6 | 8.5 | 324 | 4 US-09-613-303-25    | Sequence 25, Appl |
| 44 | 6 | 8.5 | 331 | 4 US-09-217-228-6     | Sequence 6, Appl1 |
| 45 | 6 | 8.5 | 346 | 2 US-08-476-254-2     | Sequence 2, Appl1 |

#### RESULT 1

US-09-996-243-201  
Sequence 201, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Batton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28

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|---------------------------|------------|
| PRIOR FILING DATE:        | 1998-06-17 |
| PRIOR APPLICATION NUMBER: | 60/089653  |
| PRIOR FILING DATE:        | 1998-06-17 |
| PRIOR APPLICATION NUMBER: | 60/089801  |
| PRIOR FILING DATE:        | 1998-06-18 |
| PRIOR APPLICATION NUMBER: | 60/089907  |
| PRIOR FILING DATE:        | 1998-06-18 |
| PRIOR APPLICATION NUMBER: | 60/089908  |
| PRIOR FILING DATE:        | 1998-06-18 |
| PRIOR APPLICATION NUMBER: | 60/089947  |
| PRIOR FILING DATE:        | 1998-06-19 |
| PRIOR APPLICATION NUMBER: | 60/089948  |
| PRIOR FILING DATE:        | 1998-06-19 |
| PRIOR APPLICATION NUMBER: | 60/089952  |
| PRIOR FILING DATE:        | 1998-06-19 |
| PRIOR APPLICATION NUMBER: | 60/090246  |
| PRIOR FILING DATE:        | 1998-06-22 |
| PRIOR APPLICATION NUMBER: | 60/090252  |
| PRIOR FILING DATE:        | 1998-06-22 |
| PRIOR APPLICATION NUMBER: | 60/090254  |
| PRIOR FILING DATE:        | 1998-06-22 |
| PRIOR APPLICATION NUMBER: | 60/090349  |
| PRIOR FILING DATE:        | 1998-06-23 |
| PRIOR APPLICATION NUMBER: | 60/090355  |
| PRIOR FILING DATE:        | 1998-06-23 |
| PRIOR APPLICATION NUMBER: | 60/090429  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090431  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090435  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090444  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090445  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090472  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090535  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090540  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090542  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090557  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090676  |
| PRIOR FILING DATE:        | 1998-06-25 |
| PRIOR APPLICATION NUMBER: | 60/090678  |
| PRIOR FILING DATE:        | 1998-06-25 |
| PRIOR APPLICATION NUMBER: | 60/090690  |
| PRIOR FILING DATE:        | 1998-06-25 |
| PRIOR APPLICATION NUMBER: | 60/090694  |
| PRIOR FILING DATE:        | 1998-06-25 |
| PRIOR APPLICATION NUMBER: | 60/090655  |
| PRIOR FILING DATE:        | 1998-06-25 |
| PRIOR APPLICATION NUMBER: | 60/090656  |
| PRIOR FILING DATE:        | 1998-06-25 |
| PRIOR APPLICATION NUMBER: | 60/090862  |
| PRIOR FILING DATE:        | 1998-06-26 |
| PRIOR APPLICATION NUMBER: | 60/090863  |
| PRIOR FILING DATE:        | 1998-06-26 |
| PRIOR APPLICATION NUMBER: | 60/091360  |
| PRIOR FILING DATE:        | 1998-07-01 |
| PRIOR APPLICATION NUMBER: | 60/091478  |
| PRIOR FILING DATE:        | 1998-07-02 |
| PRIOR APPLICATION NUMBER: | 60/091544  |
| PRIOR FILING DATE:        | 1998-07-01 |
| PRIOR APPLICATION NUMBER: | 60/091519  |
| PRIOR FILING DATE:        | 1998-07-02 |
| PRIOR APPLICATION NUMBER: | 60/091626  |
| PRIOR FILING DATE:        | 1998-07-02 |
| PRIOR APPLICATION NUMBER: | 60/091633  |
| PRIOR FILING DATE:        | 1998-07-02 |



PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match  
Best Local Similarity 100.0%; Score 71; DB 4; Length 99;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EESTIENYASRPEAFNTPEFLNIDKLSAFKADFLNMLALFESIKRKLPLNMDAPPL 60  
Db 29 EESTIENYASRPEAFNTPEFLNIDKLSAFKADFLNMLALFESIKRKLPLNMDAPPL 88

Qy 61 KGLRSATPDAQ 71  
Db 89 KGLRSATPDAQ 99

RESULT 2  
US-09-252-991A-22286

Sequence 22286, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22286

LENGTH: 344

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22286

Query Match

Best Local Similarity 12.7%; Score 9; DB 4; Length 344;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 GLRSATPDA 70  
Db 210 GLRSATPDA 218

RESULT 3  
US-09-107-532A-4795

Sequence 4795, Application US/09107532A  
Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A. Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESS: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781) 893-5007

TELEFAX: (781) 893-8277

INFORMATION FOR SEQ ID NO: 4795:

SEQUENCE CHARACTERISTICS:

LENGTH: 254 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...254

SEQUENCE DESCRIPTION: SEQ ID NO: 4795:

US-09-107-532A-4795

Query Match

Best Local Similarity 9.9%; Score 7; DB 4; Length 254;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 KRKLPL 52  
Db 33 KRKLPL 39

RESULT 4  
US-09-252-991A-26002

Sequence 26002, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26002

LENGTH: 257

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-26002

Query Match

Best Local Similarity 9.9%; Score 7; DB 4; Length 257;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 LKGLRSA 66  
Db 247 LKGLRSA 253

RESULT 5  
US-08-295-085-3

Sequence 3, Application US/08295085  
Patent No. 5582997

GENERAL INFORMATION:  
APPLICANT: Blondelle, Sylvie E.  
APPLICANT: Perez-Paya, Enrique  
APPLICANT: Houghten, Richard A.  
TITLE OF INVENTION: Lysine/leucine Polypeptides, Mixture  
TITLE OF INVENTION: Sets and Libraries Thereof  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edward P. Gamson  
STREET: 135 South LaSalle Street, Suite 1625  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,085  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Gamson, Edward P.  
REGISTRATION NUMBER: 29,381  
REFERENCE/DOCKET NUMBER: IMS017.OB 3418/61275  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 781-9470  
TELEFAX: (312) 781-9548  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-295-085-3

Query Match 8.5%; Score 6; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.5;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 PKLQGL 63  
|||||  
DB 9 PKLQGL 14

RESULT 6  
US-08-295-085-4  
Sequence 4, Application US/08295085  
Patent No. 5582997  
GENERAL INFORMATION:  
APPLICANT: Blondelle, Sylvie E.  
APPLICANT: Perez-Paya, Enrique  
APPLICANT: Houghten, Richard A.  
TITLE OF INVENTION: Lysine/leucine Polypeptides, Mixture  
TITLE OF INVENTION: Sets and Libraries Thereof  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edward P. Gamson  
STREET: 135 South LaSalle Street, Suite 1625  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,085  
FILING DATE:

CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Gamson, Edward P.  
REGISTRATION NUMBER: 29,381  
REFERENCE/DOCKET NUMBER: IMS017.OB 3418/61275  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 781-9470  
TELEFAX: (312) 781-9548  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-295-085-4

Query Match 8.5%; Score 6; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.5;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 PKLQGL 63  
|||||  
DB 9 PKLQGL 14

RESULT 7  
US-08-295-085-5  
Sequence 5, Application US/08295085  
Patent No. 5582997  
GENERAL INFORMATION:  
APPLICANT: Blondelle, Sylvie E.  
APPLICANT: Perez-Paya, Enrique  
APPLICANT: Houghten, Richard A.  
TITLE OF INVENTION: Lysine/leucine Polypeptides, Mixture  
TITLE OF INVENTION: Sets and Libraries Thereof  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edward P. Gamson  
STREET: 135 South LaSalle Street, Suite 1625  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,085  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Gamson, Edward P.  
REGISTRATION NUMBER: 29,381  
REFERENCE/DOCKET NUMBER: IMS017.OB 3418/61275  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 781-9470  
TELEFAX: (312) 781-9548  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-295-085-5

Query Match 8.5%; Score 6; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.5;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 PKLQGL 63  
|||||

Db 9 PKLKG 14

## RESULT 8

PCT-US95-10741-3

Sequence 3, Application PC/TUS9510741

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Lysine/leucine Polypeptides, Mixture

TITLE OF INVENTION: Sets and Libraries Thereof

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Edward P. Gamson

STREET: 135 South Lasalle Street, Suite 1625

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/10741

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: IMS017.0B 3418/61275

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 781-9470

TELEFAX: (312) 781-9548

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US95-10741-3

Query Match 8.5%; Score 6; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 8.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 PKLKG 63

Db 9 PKLKG 14

## RESULT 9

PCT-US95-10741-4

Sequence 4, Application PC/TUS9510741

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Lysine/leucine Polypeptides, Mixture

TITLE OF INVENTION: Sets and Libraries Thereof

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Edward P. Gamson

STREET: 135 South Lasalle Street, Suite 1625

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/10741

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: IMS017.0B 3418/61275

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 781-9470

TELEFAX: (312) 781-9548

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US95-10741-4

Query Match 8.5%; Score 6; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 8.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 PKLKG 63

Db 9 PKLKG 14

## RESULT 10

PCT-US95-10741-5

Sequence 5, Application PC/TUS9510741

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Lysine/leucine Polypeptides, Mixture

TITLE OF INVENTION: Sets and Libraries Thereof

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Edward P. Gamson

STREET: 135 South Lasalle Street, Suite 1625

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/10741

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: IMS017.0B 3418/61275

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 781-9470

TELEFAX: (312) 781-9548

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US95-10741-5

Query Match 8.5%; Score 6; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 8.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 PKLKG 63

Db 9 PKLKG 14

RESULT 11  
US-08-469-260A-483  
Sequence 483, Application US/08469260A  
Patent No. 6451578  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMM J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUEHROFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,260A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 483:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-469-260A-483  
Query Match 8.5%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 60 LKGLRS 65  
Db 37 LKGLRS 42  
RESULT 12  
US-08-488-446-483  
Sequence 483, Application US/08488446  
Patent No. 6556898  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMM J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY

APPLICANT: ANTHONY SCOTT MUEHROFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,446  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 483:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-446-483  
Query Match 8.5%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 60 LKGLRS 65  
Db 37 LKGLRS 42  
RESULT 13  
US-08-467-344A-483  
Sequence 483, Application US/08467344A  
Patent No. 6586568  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMM J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUEHROFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL

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; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,344A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 483:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 483:
US-08-467-344A-483
```

## Query Match

```

8.5%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 60 LKGLRS 65
DB 37 LKGLRS 42
```

## RESULT 14

```

US-09-252-991A-26885
; Sequence 26885, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26885
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26885
```

## Query Match

```

8.5%; Score 6; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 63 LRSATP 68
DB 2 LRSATP 7
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## RESULT 15

```

US-09-252-991A-19208
; Sequence 19208, Application US/09252991A
```

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; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19208
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19208
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## Query Match

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8.5%; Score 6; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 10 ASRPEA 15
DB 7 ASRPEA 12
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Search completed: November 28, 2003, 13:44:08  
Job time : 19 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 12:12:50 / Search time 53 seconds  
(without alignments)  
591.287 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99  
Sequence: 1 EESTIENYASRPEANTPE.....LNMWAPFKLGRSATPAQ 71

Scoring table:  
OLIGO  
Xgapop 60.0, Xgapext 60.0  
Ygapop 60.0, Ygapext 60.0  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1135135

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/usfto.spool/US10059395/rnatc.25112003.140941.8076/app\_query.fasta-1.263  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=011.rn1 -MINMATCH=0.1 -LOOPT=0  
-LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NOR=ext -HEATSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10059395.QCEN.1.1.56@rnatc.25112003.140941.8076 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WANT TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database:

Issued Patents NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/6C\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/6D\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID                  | Description        |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1          | 71    | 100.0       | 415    | US-09-996-243-200   | Sequence 200, App  |
| 2          | 9     | 12.7        | 666    | US-09-252-991A-5754 | Sequence 5754, App |
| 3          | 9     | 12.7        | 837    | US-09-252-991A-5702 | Sequence 5702, App |
| 4          | 9     | 12.7        | 1035   | US-09-252-991A-5715 | Sequence 5715, App |
| 5          | 9     | 12.7        | 1245   | US-09-252-991A-5725 | Sequence 5725, App |
| 6          | 9     | 12.7        | 1245   | US-09-252-991A-5725 | Sequence 5725, App |
| 7          | 9     | 12.7        | 1245   | US-09-252-991A-5725 | Sequence 5725, App |
| 8          | 9     | 12.7        | 1245   | US-09-252-991A-5725 | Sequence 5725, App |
| 9          | 9     | 12.7        | 1245   | US-09-252-991A-5725 | Sequence 5725, App |
| 10         | 9     | 12.7        | 1245   | US-09-252-991A-5725 | Sequence 5725, App |
| 11         | 9     | 12.7        | 1245   | US-09-252-991A-5725 | Sequence 5725, App |
| 12         | 9     | 12.7        | 1245   | US-09-252-991A-5725 | Sequence 5725, App |

|      |   |     |         |   |                      |                    |
|------|---|-----|---------|---|----------------------|--------------------|
| C 13 | 7 | 9.9 | 1230025 | 4 | US-09-198-452A-1     | Sequence 1, Appl   |
| C 14 | 7 | 9.9 | 1664976 | 4 | US-08-916-421B-1     | Sequence 1, Appl   |
| C 15 | 6 | 8.5 | 20      | 1 | US-08-335-583C-20    | Sequence 20, Appl  |
| C 16 | 6 | 8.5 | 20      | 4 | US-09-668-313A-170   | Sequence 170, App  |
| C 17 | 6 | 8.5 | 31      | 1 | US-08-383-743A-9     | Sequence 9, Appl   |
| C 18 | 6 | 8.5 | 31      | 3 | US-08-808-881-9      | Sequence 9, Appl   |
| C 19 | 6 | 8.5 | 31      | 3 | US-09-017-631-9      | Sequence 9, Appl   |
| C 20 | 6 | 8.5 | 31      | 4 | US-09-520-118-9      | Sequence 9, Appl   |
| C 21 | 6 | 8.5 | 31      | 5 | PCT-US93-07116-9     | Sequence 9, Appl   |
| C 22 | 6 | 8.5 | 38      | 6 | 5165431-28           | Patent No. 5165431 |
| C 23 | 6 | 8.5 | 46      | 3 | US-09-252-292-22     | Sequence 22, Appl  |
| C 24 | 6 | 8.5 | 62      | 3 | US-08-483-511-13     | Sequence 13, Appl  |
| C 25 | 6 | 8.5 | 62      | 5 | PCT-US93-01009-13    | Sequence 13, Appl  |
| C 26 | 6 | 8.5 | 74      | 3 | US-08-258-287B-11    | Sequence 11, Appl  |
| C 27 | 6 | 8.5 | 74      | 3 | US-08-368-704C-11    | Sequence 11, Appl  |
| C 28 | 6 | 8.5 | 75      | 3 | US-09-060-756-146    | Sequence 146, App  |
| C 29 | 6 | 8.5 | 75      | 4 | US-09-670-314-146    | Sequence 146, App  |
| C 30 | 6 | 8.5 | 164     | 1 | US-08-480-552-1      | Sequence 1, Appl   |
| C 31 | 6 | 8.5 | 164     | 1 | US-08-039-385-1      | Sequence 1, Appl   |
| C 32 | 6 | 8.5 | 164     | 3 | US-08-929-208-1      | Sequence 1, Appl   |
| C 33 | 6 | 8.5 | 164     | 3 | US-09-158-469-1      | Sequence 1, Appl   |
| C 34 | 6 | 8.5 | 164     | 3 | US-09-561-844-1      | Sequence 1, Appl   |
| C 35 | 6 | 8.5 | 164     | 4 | US-09-568-315-1      | Sequence 1, Appl   |
| C 36 | 6 | 8.5 | 164     | 4 | US-09-562-226-1      | Sequence 1, Appl   |
| C 37 | 6 | 8.5 | 164     | 5 | PCT-US91-07492-1     | Sequence 1, Appl   |
| C 38 | 6 | 8.5 | 165     | 3 | US-08-836-261A-95    | Sequence 95, Appl  |
| C 39 | 6 | 8.5 | 240     | 6 | 5173308-2            | Patent No. 5173308 |
| C 40 | 6 | 8.5 | 255     | 4 | US-09-134-001C-82    | Sequence 82, Appl  |
| C 41 | 6 | 8.5 | 277     | 1 | US-08-391-339-12     | Sequence 12, Appl  |
| C 42 | 6 | 8.5 | 277     | 1 | US-08-484-274A-12    | Sequence 12, Appl  |
| C 43 | 6 | 8.5 | 277     | 3 | US-08-746-111-54     | Sequence 54, Appl  |
| C 44 | 6 | 8.5 | 305     | 4 | US-09-313-294A-7107  | Sequence 7107, App |
| C 45 | 6 | 8.5 | 318     | 4 | US-09-252-991A-10314 | Sequence 10314, A  |

#### ALIGNMENTS

RESULT 1  
US-09-996-243-200  
Sequence 200, Application US/0996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996, 243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16

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|---------------------------|------------|
| PRIOR FILING DATE:        | 1998-06-16 |
| PRIOR APPLICATION NUMBER: | 60/089512  |
| PRIOR FILING DATE:        | 1998-06-16 |
| PRIOR APPLICATION NUMBER: | 60/089514  |
| PRIOR FILING DATE:        | 1998-06-16 |
| PRIOR APPLICATION NUMBER: | 60/089532  |
| PRIOR FILING DATE:        | 1998-06-17 |
| PRIOR APPLICATION NUMBER: | 60/089538  |
| PRIOR FILING DATE:        | 1998-06-17 |
| PRIOR APPLICATION NUMBER: | 60/089558  |
| PRIOR FILING DATE:        | 1998-06-17 |
| PRIOR APPLICATION NUMBER: | 60/089599  |
| PRIOR FILING DATE:        | 1998-06-17 |
| PRIOR APPLICATION NUMBER: | 60/089600  |
| PRIOR FILING DATE:        | 1998-06-17 |
| PRIOR APPLICATION NUMBER: | 60/089653  |
| PRIOR FILING DATE:        | 1998-06-17 |
| PRIOR APPLICATION NUMBER: | 60/089908  |
| PRIOR FILING DATE:        | 1998-06-18 |
| PRIOR APPLICATION NUMBER: | 60/089947  |
| PRIOR FILING DATE:        | 1998-06-18 |
| PRIOR APPLICATION NUMBER: | 60/089801  |
| PRIOR FILING DATE:        | 1998-06-19 |
| PRIOR APPLICATION NUMBER: | 60/089948  |
| PRIOR FILING DATE:        | 1998-06-19 |
| PRIOR APPLICATION NUMBER: | 60/089952  |
| PRIOR FILING DATE:        | 1998-06-19 |
| PRIOR APPLICATION NUMBER: | 60/090246  |
| PRIOR FILING DATE:        | 1998-06-22 |
| PRIOR APPLICATION NUMBER: | 60/090252  |
| PRIOR FILING DATE:        | 1998-06-22 |
| PRIOR APPLICATION NUMBER: | 60/090254  |
| PRIOR FILING DATE:        | 1998-06-22 |
| PRIOR APPLICATION NUMBER: | 60/090349  |
| PRIOR FILING DATE:        | 1998-06-23 |
| PRIOR APPLICATION NUMBER: | 60/090355  |
| PRIOR FILING DATE:        | 1998-06-23 |
| PRIOR APPLICATION NUMBER: | 60/090429  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090431  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090435  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090444  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090445  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090472  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090535  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090540  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090542  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090557  |
| PRIOR FILING DATE:        | 1998-06-24 |
| PRIOR APPLICATION NUMBER: | 60/090676  |
| PRIOR FILING DATE:        | 1998-06-25 |
| PRIOR APPLICATION NUMBER: | 60/090678  |
| PRIOR FILING DATE:        | 1998-06-25 |
| PRIOR APPLICATION NUMBER: | 60/090686  |
| PRIOR FILING DATE:        | 1998-06-25 |
| PRIOR APPLICATION NUMBER: | 60/090862  |
| PRIOR FILING DATE:        | 1998-06-26 |





Query Match: 12.68% Indels: 0  
DB: 4 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-5715 (1-1035)  
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DB 628 GGGCTGGCGAGCGCCACGCCGACGCT 654  
RESULT 5  
US-09-252-991A-5725/C  
Sequence 5725, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 5725  
LENGTH: 1245  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5725  
Alignment Scores:  
Pred. No.: 0.935 Length: 1245  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 12.68% Indels: 0  
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US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-5725 (1-1245)  
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DB 631 GGGCTGGCGAGCGCCACGCCGACGCT 605  
RESULT 6  
US-09-107-532A-1141  
Sequence 1141, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Maitland  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 1141:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 765 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...765  
SEQUENCE DESCRIPTION: SEQ ID NO: 1141:  
US-09-107-532A-1141  
Alignment Scores:  
Pred. No.: 80.3 Length: 765  
Score: 7.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.86% Indels: 0  
DB: 4 Gaps: 0  
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QY 46 LysAlGlyLeuProPheLeu 52  
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DB 97 AAAAGAAATTAACCTTCTTG 117  
RESULT 7  
US-09-252-991A-9431  
Sequence 9431, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 9431  
LENGTH: 774  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9431  
Alignment Scores:  
Pred. No.: 81.2 Length: 774  
Score: 7.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.86% Indels: 0  
DB: 4 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-9431 (1-774)  
QY 60 LeuYsG1YLeuAArgSerAla 66  
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Db 739 CTCAGGCGCTGCTAGCGCT 759

## RESULT 8

US-09-221-017B-272/C

Sequence 272, Application US/09221017B

Patent No. 6444799

GENERAL INFORMATION:

APPLICANT: Rose, Bruce C.

TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF

NUMBER OF SEQUENCES: 1120

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON &amp; FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/221,017B

FILING DATE: 23-DEC-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: P1182

FILING DATE: 31-DEC-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: P1546

FILING DATE: 30-JAN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: P2911

FILING DATE: 09-APR-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/AU98/01023

FILING DATE: 10-DEC-1998

ATTORNEY/AGENT INFORMATION:

NAME: Monroy, Gladys H

REGISTRATION NUMBER: 32,430

REFERENCE/DOCKET NUMBER: 27340-20021.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-813-5600

TELEFAX: 650-494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 272:

SEQUENCE CHARACTERISTICS:

LENGTH: 2397 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: UNKNOWN

ORIGINAL SOURCE:

ORGANISM: PORYPHYROMONAS GINGIVALIS

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1...2397

US-09-221-017B-272

Alignment Scores:

Pred. No: 244

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 9.86%

DB: 4

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-221-017B-272 (1-2397)

QY 20 Phleubani1leaplyLieu 26

Db 647 TTCTAAATATAGTAAATTA 627

## RESULT 9

US-09-620-312D-128

Sequence 128, Application US/09620312D

Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyan

APPLICANT: Chen, Rui-hong

APPLICANT: Zhao, Qing A.

APPLICANT: Wehrman, Tom

APPLICANT: Xue, Aldong J.

APPLICANT: Yang, Yonghong

APPLICANT: Wang, Jian-Rui

APPLICANT: Zhou, Ping

APPLICANT: Ma, Yungting

APPLICANT: Wang, Dunrui

APPLICANT: Wang, Zhiwei

APPLICANT: John Tillinghaast

APPLICANT: Drmanac, Radote T.

TITLE OF INVENTION: No. 6569662el Nucleic Acids and

FILE REFERENCE: 784CIP2B

CURRENT APPLICATION NUMBER: US/09/620,312D

CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1105

SOFTWARE: pc\_Fl\_genes Version 1.0

SEQ ID NO 128

LENGTH: 3964

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (174)..(2540)

US-09-620-312D-128

Alignment Scores:

Pred. No: 399

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 9.86%

DB: 4

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-620-312D-128 (1-3964)

QY 10 AlaserArpProgluaIaphe 16

DB 2273 GCTTCCAGGCCAGAGCCTTT 2293

RESULT 10

US-09-369-364A-12

Sequence 12, Application US/09369364A

Patent No. 6391610

GENERAL INFORMATION:

APPLICANT: Apte, Suneel

APPLICANT: Hurskainen, Tiina L.

APPLICANT: Hirohata, Satoshi

TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases

FILE REFERENCE: 26473/4007/10-30-00

CURRENT APPLICATION NUMBER: US/09/369,364A

CURRENT FILING DATE: 1999-08-06

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin Ver. 2.1

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/ SEQ ID NO 12
/ LENGTH: 5804
/ TYPE: DNA
/ ORGANISM: Homo sapiens ADAMTS-9
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (3)..(5648)
/ NAME/KEY: misc_feature
/ LOCATION: (1406)
/ OTHER INFORMATION: n=T
/ NAME/KEY: misc_feature
/ LOCATION: (1563)
/ OTHER INFORMATION: n=T
US-09-369-364A-12

Alignment Scores:
Pred. No.: 578 Length: 5804
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.86% Indels: 0
DB: 4 Gaps: 0

US-10-059-395-142_COPY_29_99 (1-71) x US-09-369-364A-12 (1-5804)

QY 45 11elysarglysleuprophe 51
DB 2959 ATCAAGAGAAAGTACCATTC 2979

RESULT 11
US-09-852-067-3
/ Sequence 3, Application US/09852067
/ Patent No. 6531297
/ GENERAL INFORMATION:
/ APPLICANT: MERKULOV, Gennady et al
/ TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
/ TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
/ TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,
/ TITLE OF INVENTION: AND USES THEREOF
/ FILE REFERENCE: CL000897-CIP
/ CURRENT APPLICATION NUMBER: US/09/852,067
/ CURRENT FILING DATE: 2001-05-10
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 31208
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(31208)
/ OTHER INFORMATION: n = A,T,C or G
US-09-852-067-3

Alignment Scores:
Pred. No.: 2.97e+03 Length: 31208
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.86% Indels: 0
DB: 4 Gaps: 0

US-10-059-395-142_COPY_29_99 (1-71) x US-09-852-067-3 (1-31208)

QY 46 1ysarglysleupropheleu 52
DB 24241 AAGAGAAAGTCCCTTCTTG 24261

RESULT 12
US-09-103-330-35
/ Sequence 35, Application US/09103330A
/ Patent No. 6319716
/ GENERAL INFORMATION:

/ APPLICANT: TIKOO, SURESH K.
/ APPLICANT: BABIUK, LOREN A.
/ APPLICANT: REDDY, POLICE S.
/ TITLE OF INVENTION: ISOLATION OF MUTANTS IN THE E3 REGION OF THE
/ TITLE OF INVENTION: BOVINE ADENOVIRUS GENOME AND THEIR USE IN VACCINES
/ FILE REFERENCE: 293102002121
/ CURRENT APPLICATION NUMBER: US/09/103,330A
/ CURRENT FILING DATE: 1998-06-23
/ EARLIER APPLICATION NUMBER: 08/880,234
/ EARLIER FILING DATE: 1997-06-23
/ EARLIER APPLICATION NUMBER: 08/164,292
/ EARLIER FILING DATE: 1993-12-09
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 35
/ LENGTH: 34446
/ TYPE: DNA
/ ORGANISM: Bovine adenovirus type 3
US-09-103-330-35

Alignment Scores:
Pred. No.: 3.28e+03 Length: 34446
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.86% Indels: 0
DB: 4 Gaps: 0

US-10-059-395-142_COPY_29_99 (1-71) x US-09-103-330-35 (1-34446)

QY 62 Glyleuargseralathpro 68
DB 14923 GGCCACGCGTACGACACACCG 14943

RESULT 13
US-09-198-452A-1/C
/ Sequence 1, Application US/09198452A
/ Patent No. 6559294
/ GENERAL INFORMATION:
/ APPLICANT: Griffels, R.
/ TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
/ TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
/ TITLE OF INVENTION: and treatment of infection
/ FILE REFERENCE: 9710-003-999
/ CURRENT APPLICATION NUMBER: US/09/198,452A
/ CURRENT FILING DATE: 1998-11-24
/ NUMBER OF SEQ ID NOS: 6849
/ SEQ ID NO 1
/ LENGTH: 1230025
/ TYPE: DNA
/ ORGANISM: Chlamydia pneumoniae
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(15000)
/ OTHER INFORMATION: n=a or c or g or t
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/ LOCATION: (15001)..(30000)
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[illegible]

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Pred. No.: 1.02e+05 Length: 1230025
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.86% Indels: 0
DB: 4 Gaps: 0

US-10-059-395-142_COPY_29_99 (1-71) x US-09-198-452A-1 (1-1230025)

QY 16 PheAerThProPhaeuSen 22
Db 391689 TTCACACACCATTTTGAT 391669

RESULT 14
US-08-916-421B-1/C
/ Sequence 1, Application US/08916421B
/ Patent No. 6503729
/ GENERAL INFORMATION:
/ APPLICANT: Bult et al.
/ TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco
/ Patent No. 6503729
/ TITLE OF INVENTION: jannaschii
/ FILE REFERENCE: PB275
/ CURRENT APPLICATION NUMBER: US/08/916,421B
/ PRIOR FILING DATE: 1997-08-22
/ PRIOR APPLICATION NUMBER: US 60/024,428
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 1664976
/ TYPE: DNA
/ ORGANISM: Methanococcus jannaschii
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (1637998) ..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1664854) ..(1664854)
OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

Alignment Scores:
Pred. No.: 1.34e+05
Score: 7.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 9.86%
DB: 4
Length: 1664976
Matches: 7
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

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US-10-059-395-142_COPY_29_99 (1-71) x US-08-916-421B-1 (1-1664976)
QY 44 SerTleYArgYleuPro 50
DB 1134223 AGCATAAAGAGAAAGTTACT 1134203

RESULT 15
US-08-335-583C-20
Sequence 20, Application US/08335583C
Patent No. 5693779
GENERAL INFORMATION:
APPLICANT: Moos Jr., Malcolm
APPLICANT: Wang, Shouwan
APPLICANT: Kinks, Marie
TITLE OF INVENTION: PRODUCTION AND USE OF
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,583C
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH104.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
IMMEDIATE SOURCE:
LIBRARY: GENWORKS, X57234
US-08-335-583C-20

Alignment Scores:
Pred. No.: 27.1
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 8.45%
DB: 1
Length: 20
Matches: 6
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-059-395-142_COPY_29_99 (1-71) x US-08-335-583C-20 (1-20)
QY 62 GYleuArgSerAlaThr 67
DB 3 GGACTTCGAAGTCAACC 20

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Sat Nov 29 17:52:38 2003

us-10-059-395-142\_copy\_29\_99.011.rtf

Page 10

Search completed: November 28, 2003, 13:11:13  
Job time : 311 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 13:41:08 ; Search time 18 Seconds  
(without alignments)  
379.332 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99  
Perfect score: 71  
Sequence: 1 EESTIENTASREAFNTPF.....LMDAPFKLGKLSRATPDQ 71

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|-------------|
| 1          | 8     | 11.3          | 184    | 2     | AF0298      |
| 2          | 8     | 11.3          | 428    | 2     | D97010      |
| 3          | 7     | 9.9           | 202    | 2     | A83448      |
| 4          | 7     | 9.9           | 311    | 1     | BYEBT       |
| 5          | 7     | 9.9           | 329    | 2     | AG0942      |
| 6          | 7     | 9.9           | 361    | 2     | I50505      |
| 7          | 7     | 9.9           | 372    | 1     | WMVZCN      |
| 8          | 7     | 9.9           | 372    | 2     | C72155      |
| 9          | 7     | 9.9           | 372    | 2     | H36840      |
| 10         | 7     | 9.9           | 372    | 2     | T28475      |
| 11         | 7     | 9.9           | 437    | 2     | D69519      |
| 12         | 7     | 9.9           | 451    | 2     | A38099      |
| 13         | 7     | 9.9           | 451    | 2     | A38099      |
| 14         | 7     | 9.9           | 867    | 2     | D86393      |
| 15         | 6     | 8.5           | 25     | 2     | S74108      |
| 16         | 6     | 8.5           | 52     | 2     | S52069      |
| 17         | 6     | 8.5           | 99     | 2     | A41605      |
| 18         | 6     | 8.5           | 116    | 1     | B46279      |
| 19         | 6     | 8.5           | 128    | 2     | UC6092      |
| 20         | 6     | 8.5           | 131    | 2     | AG2115      |
| 21         | 6     | 8.5           | 164    | 2     | B36951      |
| 22         | 6     | 8.5           | 172    | 2     | T02229      |
| 23         | 6     | 8.5           | 178    | 2     | F64931      |
| 24         | 6     | 8.5           | 178    | 2     | H90932      |
| 25         | 6     | 8.5           | 178    | 2     | D85781      |
| 26         | 6     | 8.5           | 178    | 2     | AB0707      |
| 27         | 6     | 8.5           | 185    | 2     | T08279      |
| 28         | 6     | 8.5           | 186    | 2     | H90182      |
| 29         | 6     | 8.5           | 187    | 2     | AG0662      |

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|----|---|-----|-----|---|--------|--------------------|
| 30 | 6 | 8.5 | 190 | 2 | T31661 | hypothetical prote |
| 31 | 6 | 8.5 | 197 | 2 | C95290 | hypothetical prote |
| 32 | 6 | 8.5 | 203 | 2 | G86785 | acetyltransferase  |
| 33 | 6 | 8.5 | 204 | 2 | E95896 | probable transcrip |
| 34 | 6 | 8.5 | 219 | 2 | A26484 | glutathione transf |
| 35 | 6 | 8.5 | 227 | 2 | F96777 | germin-like protei |
| 36 | 6 | 8.5 | 231 | 2 | A82084 | MTA/SAH nucleosid  |
| 37 | 6 | 8.5 | 239 | 2 | C81935 | probable ribonucle |
| 38 | 6 | 8.5 | 239 | 2 | E81169 | ribonuclease III N |
| 39 | 6 | 8.5 | 239 | 2 | E70800 | probable transport |
| 40 | 6 | 8.5 | 240 | 2 | T25299 | hypothetical prote |
| 41 | 6 | 8.5 | 240 | 2 | AG0857 | hypothetical prote |
| 42 | 6 | 8.5 | 244 | 2 | T26265 | hypothetical prote |
| 43 | 6 | 8.5 | 245 | 2 | F96913 | glutamine ABC tran |
| 44 | 6 | 8.5 | 261 | 2 | C84776 | hypothetical prote |
| 45 | 6 | 8.5 | 261 | 2 | E96036 | probable phenylace |

#### ALIGNMENTS

RESULT 1  
AF0298  
Probable yfeABCD locus regulator yfeE [imported] - Versinia peatis (strain CO92)  
C/Species: Versinia peatis  
C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #ext\_change 09-Nov-2001  
C/Accession: AF0298  
R/Parikh, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,  
Nature 413, 523-527, 2001  
A/Title: Genome sequence of Versinia peatis, the causative agent of plague.  
A/Reference number: AB0001; MID:21470413; PMID:11586360  
A/Accession: AF0298  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-184 <KUR>  
A/Cross-references: GB:AL590842; PIDN:CAC91250.1; PID:G15980433; GSPDB:GN00175  
C/Genetics:  
A/Gene: yfeE  
C/Superfamily: Escherichia coli probable membrane protein bi726

Query Match  
Best Local Similarity 11.3%; Score 8; DB 2; Length 184;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 FMTPLNTI 23  
DB 63 FMTPLNTI 70

RESULT 2  
D97010  
5-enolpyruvylshikimate-3-phosphate synthase [imported] - Clostridium acetobutylicum  
C/Species: Clostridium acetobutylicum  
C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #ext\_change 30-Sep-2001  
C/Accession: D97010  
R/Nolling, U.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C  
A/Reference number: A96900; MID:21359325; PMID:21359325  
A/Accession: D97010  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-428 <KUR>  
A/Cross-references: GB:AE001437; PIDN:AAK78871.1; PID:G15023793; GSPDB:GN00168  
A/Experimental source: Clostridium acetobutylicum ATCC824  
C/Genetics:  
A/Gene: CAC0895  
C/Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carboxy

Query Match  
11.3%; Score 8; DB 2; Length 428;



Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTTEN 8  
|||||  
Db 35 EESTTEN 42

## RESULT 3

AG3448  
hypothetical protein PA1579 (imported) - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C/Accession: A83448

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Vyan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lardig, K.; Lim,

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: A83448

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-202 <STO>

A/Cross-references: GB:AE004586; GB:AE004091; NID:99947536; PIDN:AAG04968.1; GSPDB:GN001

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA1579

Query Match 9.9%; Score 7; DB 2; Length 202;  
Best Local Similarity 100.0%; Pred. No. 8.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 LKGLRSA 66  
|||||  
Db 192 LKGLRSA 198

## RESULT 4

BYEBT  
sulfate-binding protein - Salmonella typhimurium

C/Species: Salmonella typhimurium

C/Date: 24-Sep-1981 #sequence\_revision 09-Aug-1997 #text\_change 09-Aug-1997

C/Accession: A03403; S09675

R/Isihara, H.; Hogg, R.W.

J. Biol. Chem. 255, 4614-4618, 1980

A/Title: Amino acid sequence of the sulfate-binding protein from Salmonella typhimurium

A/Reference number: A03403; MUID:80182123; PMID:6989815

A/Accession: A03403

A/Molecule type: protein

A/Residues: 1-230,232-300, 'D',302-311 <ISI>

A/Experimental source: strain LT2

R/Garrett, A.R.; Johnson, L.A.; Beacham, I.R.

Mol. Microbiol. 3, 177-186, 1989

A/Title: Isolation, molecular characterization and expression of the ushB gene of Salmon

A/Accession: S09675

A/Status: translation not shown

A/Molecule type: DNA

Query Match 9.9%; Score 7; DB 1; Length 311;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 DAFPKLK 61  
|||||  
Db 274 DAFPKLK 280

## RESULT 5

AG0942  
periplasmic sulphate binding protein (imported) - Salmonella enterica subsp. enterica s

C/Species: Salmonella enterica subsp. enterica serovar Typh

A/Note: This species has also been called Salmonella typh

C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C/Accession: AG0942

R/Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar

, S.; Moutle, S.; O'Garra, P.

Nature 413, 848-852, 2001

A/Author: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serc

A/Reference number: AB0502; MUID:21534947; PMID:11677608

A/Accession: AG0942

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-329 <PAR>

A/Cross-references: GB:AL513382; PIDN:CAD09561.1; PID:G16504675; GSPDB:GN00176

C/Genetics:

A/Gene: STY3808

C/Superfamily: sulfate-binding protein

Query Match 9.9%; Score 7; DB 2; Length 329;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 DAFPKLK 61  
|||||  
Db 292 DAFPKLK 298

## RESULT 6

150505  
gene wnt8 protein - zebra fish

C/Species: Brachydanio rerio (zebra fish)

C/Date: 13-Mar-1997 #sequence\_revision 13-Mar-1997 #text\_change 24-Nov-1999

C/Accession: 150505

R/Kelly, G.M.; Greenstein, P.; Erezylmaz, D.F.; Moon, R.T.

Development 121, 1787-1799, 1995

A/Title: Zebrafish wnt8 and wnt8b share a common activity but are involved in distinct

A/Reference number: 150505; MUID:95324404; PMID:7600994

A/Accession: 150505

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-361 <KER>

A/Cross-references: EMBL:U10869; NID:9968914; PID:9968915

C/Genetics:

A/Gene: wnt8

C/Superfamily: int-1 transforming protein

Query Match 9.9%; Score 7; DB 2; Length 361;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 KGLRSAT 67  
|||||  
Db 77 KGLRSAT 83

## RESULT 7

WNVZCN  
major envelope antigen - vaccinia virus (strain Copenhagen)

C/Species: vaccinia virus

A/Note: host Homo sapiens (man)

C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Jul-1999

C/Accession: 142507

R/Goebel, S.O.; Johnson, G.P.; Perkins, M.E.; Winslow, J.P.; Paolletti, E.

Virology 179, 517-563, 1990

A/Title: Appendix to "The complete DNA sequence of vaccinia virus".

A/Reference number: A42501

A/Accession: 142507

A.Molecule type: DNA  
A.Residues: 1-372 <GOE>  
A.Cross-references: GB:M35027; NID:G335317; PIDN:AAA8031.1; PID:G335379  
R.Goebel, S.J.; Johnson, G.F.; Perkins, M.E.; Davis, S.W.; Winslow, J.P.; Paolietti, E.  
Virology 179, 247-266, 1990  
A.Title: The complete DNA sequence of vaccinia virus.  
A.Reference number: A42531; MUID:91021027; PMID:2219722  
A.Contents: annotation, possible protein-coding frames  
A.Note: neither amino acid nor nucleotide sequence is given  
C.Superfamily: vaccinia virus major envelope antigen  
C.Keywords: envelope protein; transmembrane protein

Query Match 9.9%; Score 7; DB 1; Length 372;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 IDKLSA 29  
DB 224 IDKLSA 230

RESULT 8  
C72155  
E13L protein - variola minor virus (strain Garcia-1966)  
C.Species: variola minor virus  
C.Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 20-Jun-2000  
C.Accession: C72155  
R.Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Sifronov, P.F.; Massung, R.F.; Lopat  
submitted to GenBank, March 1998  
A.Description: Analysis of the complete coding sequence of DNA of alastrim variola minor  
A.Reference number: A72150  
A.Accession: C72155  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-372 <SHC>  
A.Cross-references: GB:Y16780; NID:G5830555; PIDN:CAB54637.1; PID:G5830598  
A.Experimental source: strain Garcia-1966  
C.Genetics:  
A.Gene: E13L  
C.Superfamily: vaccinia virus major envelope antigen

Query Match 9.9%; Score 7; DB 2; Length 372;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 IDKLSA 29  
DB 224 IDKLSA 230

RESULT 9  
H56840  
C17L protein - variola virus (strain India-1967)  
C.Species: variola virus  
C.Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 23-Mar-2001  
C.Accession: H56840  
R.Blinov, V.M.  
submitted to GenBank, November 1992  
A.Reference number: A36859  
A.Accession: H56840  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-372 <BLI>  
A.Cross-references: GB:X69198; NID:G456758; PIDN:CAA48978.1; PID:G297218  
C.Superfamily: vaccinia virus major envelope antigen  
C.Keywords: transmembrane protein

Query Match 9.9%; Score 7; DB 2; Length 372;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 IDKLSA 29  
DB 224 IDKLSA 230

DB 224 IDKLSA 230

RESULT 10  
T28475  
hypothetical protein C17L - variola major virus  
C.Species: variola major virus  
C.Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
C.Accession: T28475  
R.Masung, R.F.; Bepkoito, J.J.; Liu, L.I.; Qi, J.; Uteback, T.R.; Knight, J.C.; Audin  
Nature 366, 748-751, 1993  
A.Title: Potential virulence determinants in terminal regions of variola smallpox virus  
A.Reference number: Z20488; MUID:94088747; PMID:8264798  
A.Accession: T28475  
A.Status: preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: DNA  
A.Residues: 1-372 <MAS>  
A.Cross-references: EMBL:L22579; NID:G623595; PIDN:AAA60785.1; PID:G438955  
A.Experimental source: strain Bangladesh-1975  
C.Superfamily: vaccinia virus major envelope antigen

Query Match 9.9%; Score 7; DB 2; Length 372;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 IDKLSA 29  
DB 224 IDKLSA 230

RESULT 11  
D69519  
cRNA nucleotidyltransferase (cca) homolog - Archaeoglobus fulgidus  
C.Species: Archaeoglobus fulgidus  
C.Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 06-Jan-2003  
C.Accession: D69519  
R.Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
J. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirtress, B.F.  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A.Authors: Uteback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.F.; Sykes, S.J.  
Smith, H.O.; Weese, C.R.; Venter, J.C.  
A.Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo:  
A.Reference number: A69250; MUID:96049343; PMID:9389475  
A.Accession: D69519  
A.Status: preliminary; nucleic acid sequence not shown; translation not shown  
A.Molecule type: DNA  
A.Residues: 1-437 <KLE>  
A.Cross-references: GB:AE000955; GB:AE000782; NID:G2689278; PIDN:AB89084.1; PID:G264835.  
C.Superfamily: cRNA nucleotidyltransferase (CCA-adding enzyme)

Query Match 9.9%; Score 7; DB 2; Length 437;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 LRSAPKA 32  
DB 316 LRSAPKA 322

RESULT 12  
A38099  
glycylpeptide N-tetradecanoyltransferase (EC 2.3.1.97) - yeast (Candida albicans)  
C.Species: Candida albicans  
C.Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 28-Jul-2000  
C.Accession: A38099  
R.Wiegand, R.C.; Carr, C.; Mimerly, J.C.; Paulay, A.M.; Carron, C.P.; Langner, C.A.; Du  
J. Biol. Chem. 267, 8591-8598, 1992  
A.Title: The Candida albicans myristoyl-CoA:protein N-myristoyltransferase gene. Isolatic  
A.Reference number: A38099; MUID:92235090; PMID:1569105  
A.Accession: A38099  
A.Status: preliminary; not compared with conceptual translation  
A.Molecule type: DNA

A:Residues: 1-451 <MIF>  
A:Cross-references: GB:M80544; NID:g170883; PIDN:AAA34351.1; PID:g170884  
C:Superfamily: Yeast glycylylpeptide N-cetradecanoyltrifunctionase  
C:Keywords: acyltransferase; coenzyme A

Query Match 9.9%; Score 7; DB 2; Length 451;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 PKLKGRLR 64  
DB 262 PKLKGRLR 268

## RESULT 13

hypothetical protein C17H11.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T25555

R:Johnson, D.

Submitted to the EMBL Data Library, December 1996  
A:Description: The sequence of C. elegans cosmid C17H11.

A:Reference number: Z20049

A:Accession: T25555

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-816 <JOH>

A:Cross-references: EMBL:U80847; PIDN:AA37987.1; GSPDB:GN00028; CESP:C17H11.6

A:Experimental source: strain Bristol N2; clone C17H11

A:Genetics: CESP:C17H11.6

A:Map position: X

A:Introns: 47/3; 85/3; 122/3; 150/2; 187/2; 260/1; 331/1; 399/1; 448/1; 497/1; 534/3; 59

Query Match 9.9%; Score 7; DB 2; Length 816;  
Best Local Similarity 100.0%; Pred. No. 28;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 AFPKLG 62  
DB 104 AFPKLG 110

## RESULT 14

D86393

hypothetical protein TIK7.1 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2001

C:Accession: D86393

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Malt, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Yu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D86393

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-867 <STO>

A:Cross-references: GB:AE005172; NID:g9797740; PIDN:AAF98558.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 9.9%; Score 7; DB 2; Length 867;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 LKGRSA 66  
DB 457 LKGRSA 463

## RESULT 15

S74108

hemolysin A - Vibrio cholerae (fragments)

C:Species: Vibrio cholerae

C:Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999

C:Accession: S74108

R:Menzl, K.; Maier, E.; Chakraborty, T.; Benz, R.

Eur. J. Biochem. 240, 646-654, 1996

A:Title: HlyA hemolysin of Vibrio cholerae O1 biotype El Tor. Identification of the hem

A:Reference number: S74108; MUID:97008956; PMID:8856066

A:Accession: S74108

A:Molecule type: protein

A:Residues: 1-15,16-25 <MEN>

A:Experimental source: strain O1 biotype El Tor

C:Keywords: channel-forming protein; toxin

Query Match 8.5%; Score 6; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 SATPDA 70  
DB 9 SATPDA 14

Search completed: November 28, 2003, 13:43:46  
Job time : 21 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model1

Run on: November 28, 2003, 13:40:38 / Search time 11 Seconds

(without alignments)  
303.536 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Sequence: 1 EESTIENVASRPEAFNTPF.....LNDAPPKKGLASATPDAQ 71

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description         |
|------------|-------|-------------|--------|--------------|---------------------|
| 1          | 8     | 11.3        | 184    | 1 YFEE_YERPE | Q6956 Yersinia pe   |
| 2          | 8     | 11.3        | 428    | 1 AROA_CLOAB | Q97km2 Clostridium  |
| 3          | 7     | 9.9         | 202    | 1 YF79_PSEAB | Q9348 Pseudomonas   |
| 4          | 7     | 9.9         | 205    | 1 EF18_YEAST | P32471 Saccharomyc  |
| 5          | 7     | 9.9         | 239    | 1 GIDB_CLOAB | Q8xh2 Clostridium   |
| 6          | 7     | 9.9         | 325    | 1 CYK2_ORISA | Q8xe8 Oryza sativ   |
| 7          | 7     | 9.9         | 329    | 1 SUBI_SALTY | P2906 Salimoneilla  |
| 8          | 7     | 9.9         | 359    | 1 WNT8_BRARE | P51028 brachydanio  |
| 9          | 7     | 9.9         | 372    | 1 VENV_VACCC | P20638 vaccinia vi  |
| 10         | 7     | 9.9         | 372    | 1 VENV_VACCC | P33815 variola vir  |
| 11         | 7     | 9.9         | 437    | 1 CCA_ARCRU  | Q88126 archaeoglob  |
| 12         | 7     | 9.9         | 451    | 1 NNT_CANLU  | P30418 candida alb  |
| 13         | 6     | 8.5         | 116    | 1 GUAN_MOUSE | P33680 mus musculu  |
| 14         | 6     | 8.5         | 164    | 1 YGAE_ERWAB | P35675 erwinia amy  |
| 15         | 6     | 8.5         | 178    | 1 YNIB_ECOLI | P76208 escherichia  |
| 16         | 6     | 8.5         | 189    | 1 MOBA_PASMU | P57971 pasteurella  |
| 17         | 6     | 8.5         | 191    | 1 AMPN_PASMU | P79143 canis fami1  |
| 18         | 6     | 8.5         | 218    | 1 GT26_SCHJA | P08515 schistosoma  |
| 19         | 6     | 8.5         | 227    | 1 G1T3_ARATV | Q98772 arabidopsis  |
| 20         | 6     | 8.5         | 234    | 1 AMPN_BOVIN | P79008 bos taurus   |
| 21         | 6     | 8.5         | 239    | 1 RNC_NEIMA  | Q9jv43 neisseria m  |
| 22         | 6     | 8.5         | 239    | 1 RNC_NEIMA  | Q9jv43 neisseria m  |
| 23         | 6     | 8.5         | 249    | 1 KDXA_XANAC | Q8pnh3 xanthomonas  |
| 24         | 6     | 8.5         | 263    | 1 SURE_CHUTE | Q8k69 chlorobium    |
| 25         | 6     | 8.5         | 289    | 1 HXDB_MOUSE | P23463 mus musculu  |
| 26         | 6     | 8.5         | 306    | 1 YZ05_AQUAE | O66401 aquifex aeo  |
| 27         | 6     | 8.5         | 313    | 1 ENVI_MOUSE | P10404 mus musculu  |
| 28         | 6     | 8.5         | 313    | 1 Y135_TREPA | O83171 treponema    |
| 29         | 6     | 8.5         | 323    | 1 CYCH_XENLA | P51947 xenopus lae  |
| 30         | 6     | 8.5         | 329    | 1 SUBI_ECOLI | P06997 escherichia  |
| 31         | 6     | 8.5         | 334    | 1 ARGC_BUCAI | P57156 buchneria ap |
| 32         | 6     | 8.5         | 343    | 1 APL6_HUMAN | Q9bww8 homo sapien  |
| 33         | 6     | 8.5         | 344    | 1 YD33_MYCTU | Q10644 mycobacteri  |

## ALIGNMENTS

| RESULT 1 | YFEE_YERPE   | STANDARD | PRT | 184 AA. |
|----------|--|----------|-----|---------|
| AC       | Q6956;   |          |     |         |
| DT       | 15-JUL-1998 (Rel. 36, Created)   |          |     |         |
| DT       | 15-JUL-1998 (Rel. 36, Last sequence update)                                |          |     |         |
| DT       | 28-FEB-2003 (Rel. 41, Last annotation update)                              |          |     |         |
| DE       | Putative yfEABCD regulator yfE.  |          |     |         |
| GN       | YFEE OR YF02445 OR Y1891.  |          |     |         |
| OS       | Yersinia pestis.   |          |     |         |
| OC       | Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;          |          |     |         |
| CC       | Enterobacteriaceae; Yersinia.  |          |     |         |
| OX       | NCBI_Taxid=632;  |          |     |         |
| RN       | [1]  |          |     |         |
| RP       | SEQUENCE FROM N.A.   |          |     |         |
| RC       | STRAIN=KIM6;   |          |     |         |
| RA       | Bearden S.W.;  |          |     |         |
| RL       | Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.                    |          |     |         |
| RN       | [2]  |          |     |         |
| RP       | SEQUENCE FROM N.A.   |          |     |         |
| RC       | STRAIN=CO-92 / Biovar Orientalis;  |          |     |         |
| RX       | MEDLINE=21470413; PubMed=11586360;   |          |     |         |
| RA       | Parikhil J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,         |          |     |         |
| RA       | Prentice M.B., Sepahia M., James K.D., Church C., Mungall K.L.,            |          |     |         |
| RA       | Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,        |          |     |         |
| RA       | Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,             |          |     |         |
| RA       | Peltwell T., Hamlin N., Holroyd S., Jørgen K., Karlyshev A.V.,             |          |     |         |
| RA       | Leather S., Mould S., Oyston P.C.F., Quail M., Rutherford K.,              |          |     |         |
| RA       | Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;           |          |     |         |
| RT       | "Genome sequence of Yersinia pestis, the causative agent of plague.";      |          |     |         |
| RL       | Nature 413:523-527(2001).  |          |     |         |
| RN       | [3]  |          |     |         |
| RP       | SEQUENCE FROM N.A.   |          |     |         |
| RC       | STRAIN=KIM5 / Biovar Mediaevalis;  |          |     |         |
| RX       | MEDLINE=22137863; PubMed=12142430;   |          |     |         |
| RA       | Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liles P.,    |          |     |         |
| RA       | Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,                     |          |     |         |
| RA       | Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,                  |          |     |         |
| RA       | Straley S.C., McDonough K.A., Nilles M.L., Watson J.S., Blattner F.R.,     |          |     |         |
| RA       | Perry R.D.;  |          |     |         |
| RT       | "Genome sequence of Yersinia pestis KIM.";                                 |          |     |         |
| RL       | J. Bacteriol. 184:4601-4611(2002).   |          |     |         |
| CC       | - FUNCTION: PUTATIVE REGULATOR OF YFEBABD, AN ABC TRANSPORTER LOCUS        |          |     |         |
| CC       | INVOLVED IN INORGANIC IRON TRANSPORT.                                      |          |     |         |
| CC       | - SUBCELLULAR LOCATION: Integral membrane protein (Potential).             |          |     |         |
| CC       | - SIMILARITY: STRONG, TO E.COLI YNIB.                                      |          |     |         |
| CC       |  |          |     |         |
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| CC       | or send an email to license@isb-sib.ch).                                   |          |     |         |
| CC       |  |          |     |         |
| DR       | EMBL, U50903; AAC46151.1; -  |          |     |         |

DR EMBL: AJ414152: CAC91250.1; -  
 DR EMBL: AE013792: AAM85458.1; -  
 DR PIR: AF0298: AF0298.  
 KW Transmembrane; Complete proteome.  
 FT TRANSMEM 15 35 POTENTIAL.  
 FT TRANSMEM 84 104 POTENTIAL.  
 FT TRANSMEM 162 182 POTENTIAL.  
 SQ SEQUENCE 184 AA; 20913 MW; 99860ED024E8A51A CRC64;

Query Match 11.3%; Score 8; DB 1; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 0.37;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 EMTPLNT 23  
 DB 63 EMTPLNT 70

## RESULT 2

ARO\_CLOAB STANDARD; PRT; 428 AA.

AC 097KM2;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).  
 GN AROA OR CAC0895.  
 OS Clostridium acetobutylicum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 NC NCB1\_TaxID=1488;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
 RX MEDLINE=21359325; PubMed=1466286;  
 RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,  
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitt J., Wolf Y.T.,  
 RA Tatuov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
 RA Bennett G.N., Koonin E.V., Smith D.R.;  
 RT "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum";  
 RT J. Bacteriol. 183:4823-4838(2001).  
 CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =  
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.  
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;  
 CC sixth step.  
 CC -1- SUBUNIT: Monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
 CC -1- SIMILARITY: Belongs to the EPSP synthase family.

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CC EMBL: AE007605; AAK78871.1; -  
 DR PIR: D97010; D97010.  
 DR HAMAP: MF\_00210; -; 1.  
 DR InterPro: IPR006264; AROA.  
 DR InterPro: IPR001986; EPSP synthase.  
 DR Pfam: PF00275; EPSP synthase; 1.  
 DR ProDom: PD001867; EPSP synthase; 1.  
 DR TIGRfam: TIGR01356; aroA; 1.  
 DR PROSITE: PS00104; EPSP SYNTHASE 1; FALSE\_NEG.  
 DR PROSITE: PS00885; EPSP SYNTHASE 2; 1.  
 KW Aromatic amino acid biosynthesis; transferase; Complete proteome.  
 SQ SEQUENCE 428 AA; 46960 MW; D3A9BF1F46E9C547 CRC64;

Query Match 11.3%; Score 8; DB 1; Length 428;

Best Local Similarity 100.0%; Pred. No. 0.77;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EESTIEN 8  
 DB 35 EESTIEN 42

## RESULT 3

YF79\_PSEAE STANDARD; PRT; 202 AA.

AC 0913D8;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Hypothetical protein PA1579.  
 GN PA1579.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 NC NCB1\_TaxID=287;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,  
 RA Hickey M.C., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltser L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Iasbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.";  
 RT Nature 406:959-964(2000).  
 RN (2)

## POTENTIAL FUNCTION.

RX MEDLINE=21173595; PubMed=11276083;  
 RA Ayer L.W., Koonin E.V., Aravind L.;  
 RT "Adaptations of the helix-grip fold for ligand binding and catalysis in the START domain superfamily.";  
 RT Proteins 43:134-144(2001).  
 CC -1- FUNCTION: May play a role in the interaction of the bacterium with animal cells.

CC -1- SIMILARITY: Contains 1 START domain.  
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CC EMBL: AB04586; AAG04968.1; -  
 DR PIR: AB3448; AB3448.  
 DR InterPro: IPR002913; START.  
 DR Pfam: PF01852; START; 1.  
 DR PROSITE: PS50848; START; 1.  
 KW Hypothetical protein; Complete proteome.  
 FT DOMAIN 1 202 START.  
 SQ SEQUENCE 202 AA; 22110 MW; 9F1C9B7161ED95E CRC64;

Query Match 9.9%; Score 7; DB 1; Length 202;  
 Best Local Similarity 100.0%; Pred. No. 4.4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 LKGLRSA 66  
 DB 192 LKGLRSA 198

## RESULT 4

EF1B\_YEAST

ID EF1B\_YEAST STANDARD; PRT; 205 AA.  
 AC P32471;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Elongation factor 1-beta (EF-1-beta).  
 GN EF1B OR TEF5 OR YAL003W.  
 OS Saccharomyces cerevisiae (Baker's Yeast).  
 OC Saccharomycetes; Saccharomycetaceae; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;  
 OC NCB1\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93131037; PubMed=8420802;  
 RA Hiraga K., Suzuki K., Tsuchiya E., Miyakawa T.,  
 RT Cloning and characterization of the elongation factor EF-1 beta  
 RT homologue of Saccharomyces cerevisiae. EF-1 beta is essential for  
 RT growth.";  
 RL FEBS Lett. 316:165-169(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=8288c / AB972;  
 MEDLINE=95028152; PubMed=7941740;  
 RA Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,  
 RA Delaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H.,  
 RT Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of  
 RT the 42 kbp SPOT-CENT-CDC15 region.";  
 RL Yeast 10:535-541(1994).  
 RN [3]  
 RP SEQUENCE OF 167-177.  
 RX STRAIN=8288c;  
 MEDLINE=95203288; PubMed=7895733;  
 RA Garrels J.I., Putcher B., Kobayashi R., Latter G.I., Schwender B.,  
 RA Volpe I., Warner J.R., McLaughlin C.S.,  
 RT Protein identifications for a Saccharomyces cerevisiae protein  
 RT database.";  
 RL Electrophoresis 15:1466-1486(1994).  
 RN [4]  
 RP SEQUENCE OF 13-21 AND 50-55.  
 RX STRAIN=ATCC 38531 / Y41;  
 MEDLINE=97089742; PubMed=8935650;  
 RA Norbeck J., Blomberg A.,  
 RT Protein expression during exponential growth in 0.7 M NaCl medium of  
 RT Saccharomyces cerevisiae.";  
 RL PEMS Microbiol. Lett. 137:1-8(1996).  
 RN [5]  
 RP ACETYLATION, PUTCHER B., KOBAYASHI R., LATTER G.I., SCHWENDER B.,  
 RA GARRELS J.I., WARNER J.R., MCLAUGHLIN C.S.,  
 RA VOLPE I., PUTCHER B., KOBAYASHI R., LATTER G.I., SCHWENDER B.,  
 RT Submitted (SEP-1994) to the SWISS-PROT data bank.  
 RL FUNCTION: EF-1-BETA AND EF-1-DELTA STIMULATE THE EXCHANGE OF  
 CC GDP BOUND TO EF-1-ALPHA TO GTP.  
 CC -1- SUBUNIT: EF-1 IS COMPOSED OF FOUR SUBUNITS: ALPHA, BETA,  
 CC DELTA, AND GAMMA.  
 CC -1- PTM: PHOSPHORYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE EF-1-BETA/EF-1-DELTA FAMILY.  
 CC  
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 CC  
 CC -----  
 CC EMBL: D14080; BAA03165.1; -;  
 DR EMBL: I22015; AAC04954.1; -;  
 DR PIR: S43445; S43445.  
 DR PDB: 1F60; 22-NOV-00.  
 DR PDB: 1G7C; 30-MAY-01.  
 DR PDB: 1J0B; 06-JUN-01.  
 DR PDB: 1J0F; 06-JUN-01.  
 DR SWISS-2DPAGE; P32471; YEAST.

DR SGD: S0000003; EF1B.  
 DR InterPro: IPR001326; EF1\_BD.  
 DR InterPro: IPR004046; GST\_Cterm.  
 DR Pfam: PF00736; EF1BD.1.  
 DR PROSITE: PS00824; EF1BD.1; 1.  
 DR PROSITE: PS00825; EF1BD.2; 1.  
 KW Elongation factor; Protein biosynthesis; Acetylation; Phosphorylation;  
 KM 3D-structure.  
 FT INIT MET 0  
 FT MOD RES 1 1 ACETYLATION.  
 FT CONFLICT 48 48 F -> S (IN REF. 2).  
 FT CONFLICT 56 56 F -> S (IN REF. 2).  
 FT CONFLICT 97 97 W -> L (IN REF. 2).  
 FT CONFLICT 167 167 L -> E (IN REF. 3).  
 SQ SEQUENCE 205 AA; 22689 MW; E47782908998DE6 CRC64;  
 Query Match 9.9%; Score 7; DB 1; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 29 AFKADF 35  
 DB 55 AFKADF 61  
 ID GIBB\_CLOPE STANDARD; PRT; 239 AA.  
 AC 08XH32;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Methyltransferase glibb (EC 2.1.1.-) (Glucose inhibited division  
 DE protein B).  
 GN GIBB OR CPE2653.  
 OS Clostridium perfringens.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCB1\_TaxID=1502;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=13 / Type A;  
 MEDLINE=21664373; PubMed=11792842;  
 RA Shimizu T., Ohtani K., Hirakawa H., Onshima K., Yamashita A.,  
 RA Shiba T., Ogasawara N., Hattori M., Kohara S., Hayashi H.,  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
 RT flesh-eater.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
 CC -1- FUNCTION: Probable S-adenosyl-L-methionine dependent  
 CC methyltransferase specific for a sterol and/or lipid substrate (By  
 CC similarity).  
 CC -1- SIMILARITY: BELONGS TO THE GIBB FAMILY.  
 CC  
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 CC  
 CC -----  
 CC EMBL: AB003194; BAB82359.1; -;  
 DR HAMAP: MF\_00074; -; 1.  
 DR InterPro: IPR003682; Glibb.  
 DR Pfam: PF02527; Glibb.1.  
 DR PRODOM: PD004441; Glibb.1.  
 DR TIGRPFAM: TIGR00138; Glibb.1.  
 KW Transferase; Methyltransferase; Complete proteome.  
 SQ SEQUENCE 239 AA; 26886 MW; 5F10243A3E3C1C71B CRC64;  
 Query Match 9.9%; Score 7; DB 1; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 AFRADEF 35  
 DB 62 AFRADEF 68

RESULT 6  
 CYR2\_ORYSA STANDARD; PRT; 325 AA.

ID CYR2\_ORYSA  
 AC Q9XEA8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cysteine synthase (EC 4.2.99.8) (O-acetylserine sulphydrylase)  
 GN RCSI3.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 NC NCB1\_Taxid=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare;  
 RX MEDLINE=99196994; PubMed=10095115;  
 RA Nakamura T., Yamaguchi Y., Sano H.;  
 RT "Four rice genes encoding cysteine synthase: isolation and  
 RL differential responses to sulfur, nitrogen and light.";  
 CC Gene 229:155-161(1999).  
 CC -1- CATALYTIC ACTIVITY: O(3)-acetyl-L-serine + H(2)S = L-cysteine +  
 CC acetate.  
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).  
 CC -1- PATHWAY: Cysteine biosynthesis.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE CYSTEINE SYNTHASE/CYSTATHIONINE BETA-  
 CC SYNTHASE FAMILY.

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 CC -----

DR EMBL; AF073697; AJ23909.1; -.  
 DR HSSP; P12674; 1FCJ.  
 DR ANU-2DPAGE; Q9XEA8; -.  
 DR Gramene; Q9XEA8; -.  
 DR InterPro; IPR001926; B6\_enzyme\_beta.  
 DR InterPro; IPR001216; Cys\_synthase.  
 DR InterPro; IPR005859; Cys\_synthase.  
 DR InterPro; IPR005856; Cys\_synthase.  
 DR Pfam; PF00291; PALP; 1.  
 DR TIGRfam; TIGR01139; cy8K; 1.  
 DR TIGRfam; TIGR01136; cy8K; 1.  
 DR PROSITE; PS00901; CYS\_SYNTHASE; 1.  
 DR Lyase; Cysteine biosynthesis; Pyridoxal phosphate.  
 FT BINDING 49 49  
 FT DOMAIN 275 280 POLY-ALA.  
 SQ SEQUENCE 325 AA; 34306 MW; 8F6B0CCDCD7DCAC4 CRG64;

Query Match 9.9%; Score 7; DB 1; Length 325;  
 Best Local Similarity 100.0%; Pred. No. 6.7;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 LPESTIKR 47  
 DB 310 LPESTIKR 316

RESULT 7

SUBI SALTY  
 ID SUBI SALTY STANDARD; PRT; 329 AA.  
 AC P02906;  
 DT 21-JUL-1966 (Rel. 01, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Sulfate-binding protein precursor.  
 GN SBP OR STM4063.  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 NC NCB1\_Taxid=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;  
 RX MEDLINE=21534948; PubMed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
 RL LT2.";  
 RN Nature 413:852-856(2001).  
 RN [2]  
 RP SEQUENCE OF 20-329.  
 RC STRAIN=LT2;  
 RX MEDLINE=80182123; PubMed=6989815;  
 RA Ishihara H., Hogg R.W.;  
 RT "Amino acid sequence of the sulfate-binding protein from Salmonella  
 RL typhimurium LT2.";  
 RN J. Biol. Chem. 255:4614-4618(1980).  
 RN [3]  
 RP SEQUENCE OF 246-329 FROM N.A.  
 RC STRAIN=LT2;  
 RX MEDLINE=89343621; PubMed=2548058;  
 RA Garrett A.R., Johnson L.A., Beacham I.R.;  
 RT "Isolation, molecular characterization and expression of the ushB  
 RL gene of Salmonella typhimurium which encodes a membrane-bound  
 RN UDP-sugar hydrolase.";  
 RN Mol. Microbiol. 3:177-186(1989).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=85163724; PubMed=3885043;  
 RA Pfelegrath J.W., Quijcho F.A.;  
 RT "Sulphate sequestered in the sulphate-binding protein of Salmonella  
 RL typhimurium is bound solely by hydrogen bonds.";  
 RN Nature 314:257-260(1985).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=88245181; PubMed=3288756;  
 RA Pfelegrath J.W., Quijcho F.A.;  
 RT "The 2-A resolution structure of the sulfate-binding protein involved  
 RL in active transport in Salmonella typhimurium.";  
 RN J. Mol. Biol. 200:163-180(1988).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).  
 RX MEDLINE=94073079; PubMed=8251939;  
 RA He J.J., Quijcho F.A.;  
 RT "Dominant role of local dipoles in stabilizing uncompensated charges  
 RL on a sulfate sequestered in a periplasmic active transport protein.";  
 CC Protein Sci. 2:1643-1644(1993).  
 CC -1- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS SULFATE AND IS INVOLVED  
 CC IN ITS TRANSMEMBRANE TRANSPORT.  
 CC -1- SUBCELLULAR LOCATION: Periplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC SULFATE BINDING PROTEIN  
 CC FAMILY.

-----  
 CC -1- CAUTION: There are conflicts with the sequence stored in PDB.  
 CC -----  
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 CC -----  
 DR EMBL; AE008889; AAL22903.1; -;  
 DR EMBL; X13380; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; A03403; BYEBT.  
 DR StvGene; SG10382; sbp.  
 DR InterPro; IPR000957; Thiolupn\_bind.  
 DR InterPro; IPR005669; Thiolupn\_bind.  
 DR Pfam; PF01547; SBP\_bac\_1; 1.  
 DR ProDom; PD008688; Sulfate\_bind; 1.  
 DR TIGRFAMs; TIGR00971; 3a0106s03; 1.  
 DR PROSITE; PS00401; PROK\_SULFATE\_BIND\_1; 1.  
 DR PROSITE; PS00757; PROK\_SULFATE\_BIND\_2; 1.  
 KW Sulfate transport; Transport; Periplasmic; Signal; 3D-structure;  
 KW Complete proteome.  
 FT SIGNAL 1 19  
 FT CHAIN 20 329  
 FT CONFLICT 58  
 FT CONFLICT 63 64  
 FT CONFLICT 70 79  
 FT CONFLICT 79 79  
 FT CONFLICT 89 89  
 FT CONFLICT 129 129  
 FT CONFLICT 175 175  
 FT CONFLICT 249 249  
 FT CONFLICT 319 319  
 FT STRAND 21 28  
 FT TURN 31 32  
 FT HELIX 33 51  
 FT STRAND 54 61  
 FT HELIX 64 69  
 FT HELIX 71 73  
 FT TURN 74 75  
 FT STRAND 80 83  
 FT HELIX 86 94  
 FT TURN 95 96  
 FT TURN 100 101  
 FT HELIX 102 105  
 FT HELIX 107 110  
 FT STRAND 113 115  
 FT STRAND 117 122  
 FT TURN 123 124  
 FT TURN 126 127  
 FT HELIX 132 136  
 FT TURN 138 139  
 FT STRAND 142 143  
 FT TURN 147 149  
 FT HELIX 151 167  
 FT TURN 168 170  
 FT HELIX 172 184  
 FT TURN 185 185  
 FT STRAND 186 188  
 FT HELIX 193 201  
 FT TURN 202 202  
 FT STRAND 208 212  
 FT HELIX 213 221  
 FT TURN 222 227  
 FT STRAND 228 231  
 FT STRAND 235 237  
 FT STRAND 239 239  
 FT STRAND 242 245  
 FT HELIX 247 253  
 FT TURN 254 254  
 FT HELIX 256 267  
 FT HELIX 269 277  
 FT TURN 278 279  
 FT STRAND 281 282  
 FT HELIX 285 290  
 FT TURN 291 291  
 FT HELIX 292

SULFATE-BINDING PROTEIN.  
 R -> D (IN REF. 2).  
 GS -> SQ (IN REF. 2).  
 S -> SS (IN REF. 2).  
 V -> T (IN REF. 2).  
 D -> N (IN REF. 2).  
 H -> T (IN REF. 2).  
 O -> E (IN REF. 2).  
 MISSING (IN REF. 2).  
 N -> D (IN REF. 2).

FT STRAND 299 301  
 FT HELIX 303 307  
 FT HELIX 310 317  
 FT TURN 318 318  
 FT TURN 320 321  
 FT HELIX 323 328  
 FT SEQUENCE 329 AA; 36540 MW; AFP2481D758CAFD CRC64;  
 SQ  
 Query Match 9.9%; Score 7; DB 1; Length 329;  
 Best Local Similarity 100.0%; Pred. No. 6.8;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 55 DAPFKK 61  
 Db 292 DAPFKK 298  
 RESULT 8  
 WNT8 BRARE STANDARD; PRT; 359 AA.  
 ID PS1028; Q90YL9;  
 AC 01-OCT-1996 (Rel. 34, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Wnt-8 protein precursor.  
 GN WNT8.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_Taxid=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RA MEDLINE=95324404; PubMed=7600994;  
 RA Kelly G.M., Erezylimaz D.F., Greenstein P.E., Moon R.T.;  
 RT "Zebrafish wnt8 and wnt8b share a common activity but are involved in  
 RT distinct developmental pathways.";  
 RL Development 121:1787-1791(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.; REVISIONS, AND DEVELOPMENTAL STAGE.  
 RA MEDLINE=21563308; PubMed=11703928;  
 RA Lekven A.C., Thorpe C.J., Waxman J.S., Moon R.T.;  
 RT "Zebrafish wnt8 encodes two wnt8 proteins on a bicistronic transcript  
 RT and is required for mesoderm and neuroectoderm patterning.";  
 RL Dev. Cell 1:103-114(2001).  
 CC -1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN  
 CC TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN, IS LIKELY  
 CC TO SIGNAL OVER ONLY FEW CELL DIAMETERS. MAY BE INVOLVED IN THE  
 CC SPECIFICATION OF THE SPATIAL PATTERNS OF EXPRESSION OF GSC AND  
 CC OTHER REGULATORY GENES LEADING TO THE ESTABLISHMENT OF THE  
 CC EMBRYONIC AXIS.  
 CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the  
 CC extracellular matrix.  
 CC -1- TISSUE SPECIFICITY: IN FUTURE MESODERM.  
 CC -1- DEVELOPMENTAL STAGE: Required for mesoderm and neural ectoderm  
 CC patterning during gastrulation.  
 CC -1- SIMILARITY: Belongs to the Wnt family.  
 CC  
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 CC -----  
 DR EMBL; U10869; AAC59697.2; -;  
 DR EMBL; AY032749; AKR70223.1; -;  
 DR ZFIN; ZDB-GENE-980526-332; wnt8.  
 DR InterPro; IPR005817; Wnt.  
 DR InterPro; IPR005816; Wnt\_gthfactor.  
 DR Pfam; PF00110; wnt; 1.



```

DR PRINTS: PRO1349; WNTPROTEIN.
DR SMART: SM00097; WNT1.1.
DR PROSITE: PS00246; WNT1.1.
KM Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 359
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 359 AA; 40289 MW; C192475B9D48C3C2 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 7.3; Length 359;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 KGLRSAT 67
Db 77 KGLRSAT 83

RESULT 9
VENV_VACCC STANDARD; PRT; 372 AA.
AC P20638;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Major envelope protein (37 kDa protein) (p37K).
GN F31L.
OS Vaccinia virus (strain Copenhagen).
OC Viruses; deDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_Taxid=10249;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91021027; PubMed=2219722;
RA Goebel S.J., Johnson G.P., Perkins M.E., Winslow J.P.,
RA Paolletti E.;
RT "The complete DNA sequence of vaccinia virus.";
RT Virology 179:247-266(1990).
RL [2]
CC COMPLETE GENOME.
CC Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
CC Paolletti E.;
CC "Appendix to 'The complete DNA sequence of vaccinia virus.'";
CC Virology 179:517-563(1990).
CC -1- FUNCTION: THIS PROTEIN IS THE MAJOR ANTIGEN ON THE ENVELOPE OF
CC EXTRACELLULAR VACCINIA VIRUS.
CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
CC -1- SIMILARITY: Contains 1 PLD phosphodiesterase domain.
CC -----
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CC -----
CC EMBL: M35027; AAA48031.1; -
CC PIR: I42507; MNVZCN.
CC InterPro: IPR001736; PLD.
CC Pfam: PF00614; PLDC; 2.
CC SMART: SM00155; PLDC; 2.
CC PROSITE: PS50035; PLDC; 1.
CC late protein; Antigen; Lipoprotein; Palmitate.
FT DOMAIN 307 334 PLD PHOSPHODIESTERASE.
SQ SEQUENCE 372 AA; 41823 MW; B488783DC82BFB83 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 372;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 23 IDKLRSA 29
Db 224 IDKLRSA 230

RESULT 10
VENV_VARV STANDARD; PRT; 372 AA.
AC P33815;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Major envelope protein (37 kDa protein) (p37K).
GN F31L OR C17L.
OS Variola virus.
OC Viruses; deDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_Taxid=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=India-1967 / Isolate Ind3;
RX MEDLINE=94152154; PubMed=8109158;
RA Shchelkunov S.N., Blinov V.M., Sandakhchlev L.S.,
RA Sandakhchlev L.S.;
RT "Analysis of the nucleotide sequence of a 43 kbp segment of the
RT genome of variola virus India-1967 strain.";
RT Virus Res. 30:239-258(1993).
RN [2]
CC COMPLETE GENOME.
CC STRAIN=India-1967 / Isolate Ind3;
CC MEDLINE=93202281; PubMed=8384129;
CC Shchelkunov S.N., Blinov V.M., Sandakhchlev L.S.;
CC "Genes of variola and vaccinia viruses necessary to overcome the host
CC protective mechanisms.";
CC FEBS Lett. 319:80-83(1993).
CC -1- FUNCTION: THIS PROTEIN IS THE MAJOR ANTIGEN ON THE ENVELOPE OF
CC EXTRACELLULAR VACCINIA VIRUS.
CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
CC -1- SIMILARITY: Contains 1 PLD phosphodiesterase domain.
CC -----
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CC -----
CC EMBL: X69198; CAA48978.1; -
CC PIR: H36840; H36840.
CC InterPro: IPR001736; PLD.
CC Pfam: PF00614; PLDC; 2.
CC SMART: SM00155; PLDC; 2.
CC PROSITE: PS50035; PLDC; 1.
CC late protein; Antigen; Lipoprotein; Palmitate.
FT DOMAIN 307 334 PLD PHOSPHODIESTERASE.
SQ SEQUENCE 372 AA; 41902 MW; C769B05DD48EC944 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 372;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 IDKLRSA 29
Db 224 IDKLRSA 230

RESULT 11
CCA_ARCFU STANDARD; PRT; 437 AA.
AC O28126;
DT 15-DEC-1998 (Rel. 37, Created)

```

DT 15-DEC-1998 (Rel. 37, last sequence update)  
 DT 16-OCT-2001 (Rel. 40, last annotation update)  
 DE tRNA nucleotidyltransferase (EC 2.7.7.25) (tRNA adenylyltransferase)  
 DE (tRNA CCA-pyrophosphorylase) (CCA-adding enzyme).  
 GN CCA OR A22156.  
 OS Archaeoglobus fulgidus.  
 OC Archaeaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;  
 OC Archaeoglobaceae; Archaeoglobus.  
 NCBI\_TaxID=2234.  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
 RX MEDLINE=98049343; PubMed=9389475;  
 RA Klein H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
 RA Richardson K.A., Dodson R.J., Gilm M., Hickey E.K., Peterson J.D.,  
 RA Fleischmann D.L., Kerlavage A.R., Graham D.E., Kyte J.S.,  
 RA Kirness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,  
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,  
 RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,  
 RA Sadow P.W., DAndrea K.P., Bowmen C., Fujii C., Garland K.A.,  
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
 RA Venter J.C.;  
 RT "The complete genome sequence of the hyperthermophilic, sulphate-  
 RT reducing archaeon Archaeoglobus fulgidus.";  
 RL Nature 380:364-370(1997).  
 CC -1- FUNCTION: THIS ENZYME CARRIES OUT SYNTHESIS OF THE TRNA CCA  
 CC TERMINUS.  
 CC -1- CATALYTIC ACTIVITY: ATP + (tRNA)(N) = diphosphate + (tRNA)(N+1).  
 CC -1- SIMILARITY: BELONGS TO THE TRNA NUCLEOTIDYLTRANSFERASE / POLY(A)  
 CC POLYMERASE FAMILY.  
 CC CC  
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 CC -----  
 CC EMBL; AB000955; AAB89084.1; -.  
 DR PIR; D69519; D69519.  
 DR TIGR; AF2156; -.  
 DR InterPro: IPR002934; NTP transf.  
 DR Pfam; PF01909; NTP\_transf\_2; 1.  
 DR PROSITE; PS00975; CCA-adding enz; 1.  
 DR PIRSF; PIRSF005335; CCA-adding enz; 1.  
 KM Transferase; Nucleotidyltransferase; RNA-binding; rRNA processing;  
 KM Complete proteome.  
 SQ SEQUENCE 437 AA; 51385 MW; CSD57122F63CAC97 CRC64;  
 QY 26 LRSAPKA 32  
 Db 316 LRSAPKA 322  
 Query Match 9.9%; Score 7; DB 1; Length 437;  
 Best Local Similarity 100.0%; Pred. No. 8.7;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 NCBI\_TaxID=5476;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92235090; PubMed=1569105;  
 RA Wiegand R.C., Carr C., Minnerly J.C., Pauley A.M., Carron C.P.,  
 RA Langer C.A., Duronio R.J., Gordon J.I.,  
 RT "The Candida albicans myristoyl-CoA:protein N-myristoyltransferase  
 RT gene, isolation and expression in Saccharomyces cerevisiae and  
 RT Escherichia coli.";  
 RL J. Biol. Chem. 267:8591-8598(1992).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS).  
 RX MEDLINE=98162557; PubMed=9501915;  
 RA Weston S.A., Camble R., Colls J., Rosenbrock G., Taylor I.,  
 RA Egerton M., Tucker A.D., Tunnicliffe A., Mistry A., Mancila F.,  
 RA de la Portelle B., Irwin J., Brice G., Paupit R.A.;  
 RT "Crystal structure of the anti-fungal target N-myristoyl  
 RT transferase.";  
 RL Nat. Struct. Biol. 5:213-221(1998).  
 CC -1- FUNCTION: Adds a myristoyl group to the N-terminal glycine residue  
 CC of certain cellular proteins.  
 CC -1- CATALYTIC ACTIVITY: Tetradecanoyl-CoA + glycyl-peptide = CoA + N-  
 CC tetradecanoylglycyl-peptide.  
 CC -1- SUBUNIT. Monomer.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE NMT FAMILY.  
 CC CC  
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 CC -----  
 CC EMBL; M80544; AAA34351.1; -.  
 DR PIR; A38099; A38099.  
 DR PDB; INMT; 16-FEB-99.  
 DR PDB; 1IVL; 30-DEC-02.  
 DR InterPro: IPR000903; Nmt.  
 DR Pfam; PF01233; NMT; 1.  
 DR Pfam; PF02799; NMT\_C; 1.  
 DR PROSITE; PS00975; NMT\_1; 1.  
 DR PROSITE; PS00976; NMT\_2; 1.  
 KM Transferase; Acyltransferase; 3D-structure.  
 FT STRAND 61 62  
 FT HELIX 69 71  
 FT TURN 81 82  
 FT STRAND 83 87  
 FT TURN 90 91  
 FT HELIX 93 106  
 FT TURN 109 110  
 FT TURN 113 114  
 FT STRAND 115 117  
 FT HELIX 121 128  
 FT TURN 131 132  
 FT HELIX 135 137  
 FT STRAND 138 143  
 FT TURN 144 146  
 FT STRAND 149 162  
 FT TURN 163 166  
 FT STRAND 167 179  
 FT HELIX 181 183  
 FT TURN 184 185  
 FT HELIX 189 202  
 FT TURN 203 204  
 FT STRAND 208 212  
 FT STRAND 221 229  
 FT HELIX 232 237  
 FT TURN 238 239  
 FT TURN 245 246

FT HELIX 249 256  
 FT TURN 265 266  
 RA STRAND 267 269  
 FT HELIX 272 274  
 FT HELIX 275 285  
 FT HELIX 286 288  
 FT STRAND 291 294  
 FT HELIX 297 305  
 FT TURN 309 310  
 FT STRAND 316 322  
 FT TURN 324 325  
 FT STRAND 328 336  
 FT STRAND 339 341  
 FT STRAND 349 350  
 FT STRAND 352 360  
 FT HELIX 361 364  
 FT TURN 365 367  
 FT HELIX 368 383  
 FT HELIX 384 386  
 FT TURN 387 387  
 FT STRAND 390 394  
 FT TURN 397 398  
 FT HELIX 399 401  
 FT TURN 402 402  
 FT HELIX 403 406  
 FT TURN 407 407  
 FT STRAND 409 420  
 FT TURN 421 421  
 FT STRAND 422 423  
 FT TURN 431 431  
 FT STRAND 433 435  
 FT STRAND 438 438  
 FT TURN 440 441  
 FT STRAND 446 446  
 SQ SEQUENCE 451 AA; 51877 MW; 7D107CB05458D2D CRC64;

Query Match  
 Best Local Similarity 9.9%; Score 7; DB 1; Length 451;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 58 PTKKGLR 64  
 DB 262 PTKKGLR 268

RESULT 13  
 ID GUAN\_MOUSE STANDARD; PRT; 116 AA.  
 AC P33660;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Guanylin precursor (Guanylate cyclase activator 2A).  
 GN GUCY2A OR GUCY2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Small intestine;  
 RX MEDLINE=93028409; PubMed=1409606;  
 RA de Sauvage F.J., Keshav S., Kuang W.J., Gillett N., Henzel W.,  
 RA Goeddel D.V.;  
 RT "Precursor structure, expression, and tissue distribution of human  
 RT guanylin."  
 RT Guanylin.  
 RT Proc. Natl. Acad. Sci. U.S.A. 89:9089-9093 (1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Kato J., Wiegand R.C., Currie M.G.;  
 RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.

RC STRAIN=129/Sv;  
 RX MEDLINE=95229161; PubMed=7713512;  
 RA Sciaky D., Koshida J.L., Cohen M.B.;  
 RT "Genomic sequence of the murine guanylin gene."  
 RL Genomics 24:583-587(1994).  
 CC -!- FUNCTION: ENDOGENOUS ACTIVATOR OF INTESTINAL GUANYLATE CYCLASE.  
 CC IT STIMULATES THIS ENZYME THROUGH THE SAME RECEPTOR BINDING REGION  
 CC AS THE HEAT-STABLE ENTEROTOXINS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: LOCALIZED IN BOTH CRYPTS AND VILLI IN THE  
 CC SMALL INTESTINE AND TO SUPERFICIAL EPITHELIAL CELLS IN THE COLON.  
 CC -!- SIMILARITY: BELONGS TO THE GUANYLIN FAMILY. ALSO SIMILAR TO HEAT-  
 CC STABLE ENTEROTOXINS.  
 CC -----  
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 CC -----  
 DR EMBL; M95175; AAA37758.1; -;  
 DR EMBL; L05516; AAA37715.1; -;  
 DR EMBL; U60528; AAB05758.1; -;  
 DR PIR; A55643; B46279.  
 DR HSSP; Q02747; IGNA.  
 DR MGD; MGI:102738; Gucy2.  
 DR InterPro; IPR000879; Guanylin.  
 DR Pfam; PF02058; Guanylin.1.  
 DR PRINTS; PR00774; GUANYLIN.  
 DR ProDom; PD005588; Guanylin.1.  
 KW SIGNAL.  
 FT SIGNAL. 1 23 POTENTIAL.  
 FT PROPEP 24 101  
 FT PERIDE 102 116 GUANYLIN.  
 FT DISULFD 105 113 BY SIMILARITY.  
 FT DISULFD 108 116 BY SIMILARITY.  
 SQ SEQUENCE 116 AA; 12466 MW; 272E0D87C20869C7 CRC64;

Query Match  
 Best Local Similarity 8.5%; Score 6; DB 1; Length 116;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 59 KTKGLR 64  
 DB 38 KTKGLR 43

RESULT 14  
 ID YGAE\_ERWAM STANDARD; PRT; 164 AA.  
 AC P35675;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DB Hypothetical protein in galb 3' region (fragment).  
 OS Erythra amylovora.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Erythra.  
 OC NCBI\_TaxID=552;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EA7/74;  
 RX MEDLINE=94117381; PubMed=7507102;  
 RA Metzger M., Bellemann P., Bugert P., Geider K.;  
 RT "Genetics of galactose metabolism of Erythra amylovora and its  
 RT influence on polysaccharide synthesis and virulence of the fire  
 RT blight pathogen."  
 RT J. Bacteriol. 176:450-459 (1994).  
 CC -!- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY.  
 CC -----  
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DR EMBL; X76172; CAA53768.1; -  
 DR PIR; B36951; B36951.  
 DR HSSP; P27830; 1BXK.  
 DR InterPro: IPR001509; Epimerase\_Dh.  
 DR Pfam: PF01370; Epimerase; 1.  
 KW Hypothetical protein.  
 FT NON TER 164  
 SQ SEQUENCE 164 AA; 18161 MW; A817B62C1F5580AC CRC64;

Query Match 8.5%; Score 6; DB 1; Length 164;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 LNIDKL 26  
 Db 29 LNIDKL 34

RESULT 15  
 YNIB\_ECOLI STANDARD; PRT; 178 AA.

AC P76208;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein yniB.  
 GN YNIB OR B1726.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=9742617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: STRONG, TO Y.PBSTIS YPRE.

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CC -----  
 CC EMBL; AB000267; AAC74796.1; -  
 DR PIR; F64931; F64931.  
 DR EcoGene; EG13987; yniB.  
 KW Hypothetical protein; Transmembrane; Complete proteome.  
 FT TRANSMEM 15 35 POTENTIAL.  
 FT TRANSMEM 80 100 POTENTIAL.  
 FT TRANSMEM 158 178 POTENTIAL.  
 SQ SEQUENCE 178 AA; 20367 MW; 2BAB684D37E9E36 CRC64;

Query Match 8.5%; Score 6; DB 1; Length 178;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NTPFLN 22

Db 64 NTPFLN 69

Search completed: November 28, 2003, 13:43:20  
 Job time: 14 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:42:24 ; Search time 29 Seconds  
(without alignments)  
631.784 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Sequence: 1 EESTIENVASRPEAFVTFP.....LNDAPPKLGLRSATPDQA 71

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
|------------|-------|-------------|--------|-------|---------------------|
| 1          | 8     | 11.3        | 390    | 16    | OBETM3 oceanobac11  |
| 2          | 7     | 9.9         | 173    | 16    | OBED808 vibrio vuln |
| 3          | 7     | 9.9         | 238    | 10    | Q9LTX0 arabidops1s  |
| 4          | 7     | 9.9         | 282    | 10    | OBW313 oryza sativ  |
| 5          | 7     | 9.9         | 284    | 5     | Q9BLQ8              |
| 6          | 7     | 9.9         | 329    | 16    | OBZ2W5              |
| 7          | 7     | 9.9         | 354    | 10    | Q9FHE9              |
| 8          | 7     | 9.9         | 354    | 13    | Q90YL8              |
| 9          | 7     | 9.9         | 354    | 13    | Q90YU8              |
| 10         | 7     | 9.9         | 372    | 12    | Q8V2W9              |
| 11         | 7     | 9.9         | 372    | 12    | Q85369              |
| 12         | 7     | 9.9         | 437    | 11    | Q9D496              |
| 13         | 7     | 9.9         | 477    | 2     | Q9AOL1              |
| 14         | 7     | 9.9         | 541    | 12    | Q9EMJ0              |
| 15         | 7     | 9.9         | 793    | 5     | Q95083              |
| 16         | 7     | 9.9         | 796    | 5     | Q95084              |

|    |   |     |      |    |        |                    |
|----|---|-----|------|----|--------|--------------------|
| 17 | 7 | 9.9 | 867  | 10 | Q9FZB6 | Q9fze6 arabidops1s |
| 18 | 7 | 9.9 | 1077 | 13 | Q8UWA5 | Q8uwa5 tribolodon  |
| 19 | 7 | 9.9 | 1088 | 13 | Q8AXH7 | Q8axh7 oncorhynch  |
| 20 | 7 | 9.9 | 1566 | 5  | Q8WZD0 | Q8wzd0 drosophila  |
| 21 | 7 | 9.9 | 1566 | 5  | Q9VOT4 | Q9vot4 drosophila  |
| 22 | 7 | 9.9 | 1577 | 5  | Q9NKC7 | Q9nkc7 drosophila  |
| 23 | 6 | 8.5 | 69   | 12 | Q912H0 | Q912h0 human echov |
| 24 | 6 | 8.5 | 76   | 4  | Q9PIC0 | Q9pic0 homo sapien |
| 25 | 6 | 8.5 | 76   | 12 | Q912I5 | Q912i5 human coxa  |
| 26 | 6 | 8.5 | 85   | 12 | Q912F8 | Q912f8 human echov |
| 27 | 6 | 8.5 | 90   | 12 | Q912I7 | Q912i7 human coxa  |
| 28 | 6 | 8.5 | 96   | 12 | Q912G3 | Q912g3 human echov |
| 29 | 6 | 8.5 | 96   | 15 | Q83374 | Q83374 murine leuk |
| 30 | 6 | 8.5 | 99   | 12 | Q912I6 | Q912i6 human coxa  |
| 31 | 6 | 8.5 | 101  | 2  | Q9Z5F2 | Q9z5f2 pseudomonas |
| 32 | 6 | 8.5 | 102  | 12 | Q9U462 | Q9u462 human coxa  |
| 33 | 6 | 8.5 | 103  | 12 | Q912G2 | Q912g2 human echov |
| 34 | 6 | 8.5 | 106  | 12 | Q912G1 | Q912g1 human echov |
| 35 | 6 | 8.5 | 112  | 5  | Q9VFU2 | Q9vf42 drosophila  |
| 36 | 6 | 8.5 | 127  | 16 | Q8FKP9 | Q8fkp9 escherichia |
| 37 | 6 | 8.5 | 129  | 11 | Q9CQ03 | Q9cqd3 mus musc    |
| 38 | 6 | 8.5 | 131  | 5  | Q9VUZ9 | Q9vuz9 drosophila  |
| 39 | 6 | 8.5 | 131  | 16 | Q8YU76 | Q8yu76 anabaena sp |
| 40 | 6 | 8.5 | 132  | 16 | Q8NSE0 | Q8nse0 corynebacte |
| 41 | 6 | 8.5 | 133  | 5  | Q9GYU7 | Q9gyu7 drosophila  |
| 42 | 6 | 8.5 | 137  | 4  | Q96EW8 | Q96ew8 homo sapien |
| 43 | 6 | 8.5 | 144  | 9  | Q8W766 | Q8w766 bacterioph  |
| 44 | 6 | 8.5 | 145  | 2  | Q9EW39 | Q9ew39 streptococ  |
| 45 | 6 | 8.5 | 149  | 10 | Q9F5N5 | Q9fens oryza sativ |

## ALIGNMENTS

RESULT 1  
ID OBETM3 PRELIMINARY, PRT, 390 AA.

AC OBETM3;  
DT 01-MAR-2003 (T-EMBLrel. 23, Created)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
DE Hypothetical protein.  
GN OB0237.  
OS Oceanobacillus iheyensis.  
OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.  
OX NCBI\_TaxID=182710;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;  
RX MEDLINE=22280767; PubMed=12235376;  
RA Takami H., Takaki Y., Uchiyama I.;  
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya  
RT Ridge and its unexpected adaptive capabilities to extreme  
RT environments.";  
RL Nucleic Acids Res. 30:3927-3935(2002).  
DR EMBL; AP004593; BAC12193.1; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 390 AA; 43262 MW; B2CE189BE0A63D2B CRC64;

Query Match 11.3%; Score 8; DB 16; Length 390;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 PFLNIDKL 26  
DB 200 PFLNIDKL 207

RESULT 2  
ID OBED808 PRELIMINARY, PRT, 173 AA.  
AC OBED808;  
DT 01-MAR-2003 (T-EMBLrel. 23, Created)

DT 01-MAR-2003 (T-EMBLrel. 23, last sequence update)  
 DT 01-MAR-2003 (T-EMBLrel. 23, last annotation update)  
 GN Hypothetical protein.  
 GN V13186.  
 OS Vibrio vulnificus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrrio.  
 NCBI\_TaxID=672;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CMCP6;  
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
 RA Choy H.E.;  
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6."  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB016807; AA011501.1; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 173 AA; 19836 MW; EE70E83D96A7CE3F CRC64;  
 QY Query Match 9.9%; Score 7; DB 16; Length 173;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 23 IDKLRSA 29  
 59 IDKLRSA 65  
 RESULT 3  
 ID 09LTX0 PRELIMINARY; PRT; 238 AA.  
 AC 09LTX0;  
 DT 01-OCT-2000 (T-EMBLrel. 15, Created)  
 DT 01-OCT-2000 (T-EMBLrel. 15, last sequence update)  
 DT 01-OCT-2002 (T-EMBLrel. 22, last annotation update)  
 DE Hypothetical protein (ATG312650/T2822\_103).  
 GN T2822.4.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu B., Tabata S.;  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RA MEDLINE=20277480; PubMed=10819329;  
 RA Nakamura Y.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC  
 RT clones."  
 RL DNA Res. 7:131-135(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA MEDLINE=21016720; PubMed=11130713;  
 RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unefeld M.,  
 RA Scharnau B., Valle G., Bloecher H., Perez-Alonso M., Obermaier B.,  
 RA Delannay M., Boutry M., Givelli L.A., Mache R., Pulgomech P.,  
 RA De Simone V., Choiane N., Artiguenave F., Robert C., Brotier P.,  
 RA Wincker P., Catolico L., Weissenbach J., Saurin W., Queller F.,  
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
 RA Wurmacher E., Dzzonek H., Erfle H., Jordan N., Bangert S.,  
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,  
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Stomati B.,  
 RA Conrad A., Hornischer K., Kauer G., Loehner T.H., Nordstiek G.,  
 RA Reichelt J., Scharte M., Schoen O., Baryshev M., Terol J., Climent J.,  
 RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,  
 RA Cooke R., Landie M., Berger-Ilauro C., Purnelle B., Maury D.,

RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,  
 RA Montfort A., Argilou A., Flores M., Lignori R., Vitale D.,  
 RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,  
 RA Mayer K.F.X., Kaul S., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,  
 RA Rooney T., Rizzo M., Wals A., Uterback T., Fujii C.Y., Shea T.P.,  
 RA Cressy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,  
 RA Pal G., Miltscher J., Sellers P., Gill U.B., Feldlyum T.V.,  
 RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,  
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu B.,  
 RA Sasamoto S., Kimura T., Ideasa K., Kawashima K., Kishida Y.,  
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakayama S., Nakazaki N., Shino S., Takuchi C., Wada T.,  
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;  
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis  
 RT thaliana."  
 RL Nature 408:820-822(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,  
 RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,  
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,  
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,  
 RA Satou M., Seki M., Southwick A., Tang C.C., Tortum M., Yamada K.,  
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
 RA Ecker J.R.;  
 RT "Arabidopsis cDNA clones."  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Kim C.J., Chen H., Cheuk R., Shim P., Banh J., Bowser L.,  
 RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,  
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
 RA Tang C.C., Tortum M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,  
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
 RT "Arabidopsis ORF clones."  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB024033; BAB02408.1; -  
 DR EMBL; AC069474; AAG51037.1; -  
 DR EMBL; AY057658; AAL15289.1; -  
 DR EMBL; AY113015; AAM47323.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 238 AA; 26887 MW; EE2A551E3C005D7C CRC64;  
 QY Query Match 9.9%; Score 7; DB 10; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 22 NIDKRS 28  
 57 NIDKRS 63  
 RESULT 4  
 ID 08W313 PRELIMINARY; PRT; 282 AA.  
 AC 08W313;  
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)  
 DT 01-MAR-2002 (T-EMBLrel. 20, last sequence update)  
 DT 01-MAR-2003 (T-EMBLrel. 23, last annotation update)  
 DE Cysteine synthase, 5'-partial (fragment).  
 GN OSUNBA0069E14.1.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhacoidae; Oryzaceae; Oryza.  
 NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare;  
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,

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RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Taitlin T., Riggs F., Hsiao J., Zisman V., Blunt E., Pat G.,
RA Vanaken S.E., Utterback T.R., Feldblum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNBa0069E14 genomic sequence.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC091811; AAL58961.1; -.
DR Gramene; Q8W313; -.
DR InterPro: IPR001926; B6_enzyme_beta.
DR InterPro: IPR005859; Cys_synchr.
DR InterPro: IPR005856; Cys_synchr.
DR Pfam: PF00291; PALP; 1.
DR TIGRPFAMs: TIGR01139; cysK; 1.
DR TIGRPFAMs: TIGR01136; cysK; 1.
FT NON_TER
SQ
Query Match 282 AA; 29892 MW; 350302F3CA80EF85 CRC64;
Best Local Similarity 100.0%; Score 7; DB 10; Length 282;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 LFSIKR 47
Db 267 LFSIKR 273

RESULT 5
Q9BLQ8 PRELIMINARY; PRT; 284 AA.
ID Q9BLQ8
AC Q9BLQ8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 6-pass transmembrane protein L654.12.
GN L654.12.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Tosato V., Ciaroni L., Bianchetti G., Brusch C.V., Ivens A.C.,
RA Quail M., Rajadream M.A., Barrell B.G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RL "A physical map of the Leishmania major Friedlin genome.";
EMBL: AL512294; CAC29460.1; -.
DR InterPro: IPR002076; GNS1_SUR4.
DR Pfam: PF01151; ELO; 1.
KW Transmembrane.
SQ
SEQUENCE 284 AA; 32575 MW; E845BE811DC6E9A0 CRC64;

Query Match 9.9%; Score 7; DB 5; Length 284;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 KRKLPL 52
Db 137 KRKLPL 143

RESULT 6
Q8Z2W5 PRELIMINARY; PRT; 329 AA.
ID Q8Z2W5
AC Q8Z2W5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Periplasmic sulphate binding protein.
GN STY3808.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=1167608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagers K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
DR EMBL: AL627279; CAD09561.1; -.
DR InterPro: IPR006059; SBP_bac_1.
DR InterPro: IPR000957; Sulphate_bind.
DR InterPro: IPR005669; Thiosulph_bind.
DR Pfam: PF01547; SBP_bac_1; 1.
DR ProDom: PD008688; Sulphate_bind; 1.
DR TIGRPFAMs: TIGR00971; 3a0106a03; 1.
DR PROSITE: PS00401; PROK_SULFATE_BIND_1; 1.
DR PROSITE: PS00757; PROK_SULFATE_BIND_2; 1.
KW Complete proteome.
SQ
SEQUENCE 329 AA; 36496 MW; 100FD9CC32C050AF CRC64;

Query Match 9.9%; Score 7; DB 16; Length 329;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 DAFPKL 61
Db 292 DAFPKL 298

RESULT 7
Q9FHE9 PRELIMINARY; PRT; 354 AA.
ID Q9FHE9
AC Q9FHE9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Similarity to disease resistance protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asanizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones."
RL DNA Res. 7:31-63(2000).
DR EMBL: AB019224; BAB09490.1; -.
DR InterPro: IPR000157; TIR_domain.
DR Pfam: PF01582; TIR; 1.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS50104; TIR; 1.
SQ
SEQUENCE 354 AA; 40106 MW; 2E2A1B525B377997 CRC64;

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Query Match 58 PKLKGSR 64  
 Best Local Similarity 100.0%; Score 7; DB 10; Length 354;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 149 PKLKGSR 155

RESULT 8  
 ID 090YL8 PRELIMINARY; PRT; 354 AA.  
 AC 090YL8;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 GN Wnt8-like protein 2.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NCBI\_Taxid=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lekven A.C., Thorpe C.J., Waxman J.S., Moon R.T.;  
 RT "Zebrafish wnt8 encodes two Wnt proteins on a bicistronic transcript  
 and is required for mesoderm and neuroectoderm patterning.";  
 RL Dev. Cell 1:0-0(2001).  
 DR EMBL; AY032749; AAK70224.1; -.  
 DR InterPro; IPR005817; Wnt.  
 DR InterPro; IPR005816; Wnt\_growthfactor.  
 DR Pfam; PF00110; Wnt; 1.  
 DR PRINTS; PR01349; WNTPROTEIN.  
 DR SMART; SM00097; WNT1; 1.  
 SQ SEQUENCE 354 AA; 40109 MW; F42951A27AC38A67 CRC64;

Query Match 61 KGLRSAT 67  
 Best Local Similarity 100.0%; Score 7; DB 13; Length 354;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 76 KGLRSAT 82

RESULT 9  
 ID 090YL8 PRELIMINARY; PRT; 354 AA.  
 AC 090YL8;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 GN Wnt8-like protein 2.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NCBI\_Taxid=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lekven A.C., Thorpe C.J., Waxman J.S., Moon R.T.;  
 RT "Zebrafish wnt8 encodes two Wnt proteins on a bicistronic transcript  
 and is required for mesoderm and neuroectoderm patterning.";  
 RL Dev. Cell 1:0-0(2001).  
 DR EMBL; AY032749; AAK70224.1; -.  
 DR InterPro; IPR005817; Wnt.  
 DR InterPro; IPR005816; Wnt\_growthfactor.  
 DR Pfam; PF00110; Wnt; 1.  
 DR PRINTS; PR01349; WNTPROTEIN.  
 DR SMART; SM00097; WNT1; 1.  
 SQ SEQUENCE 354 AA; 40109 MW; F42951A27AC38A67 CRC64;

DR InterPro; IPR005816; Wnt\_growthfactor.  
 DR Pfam; PF00110; Wnt; 1.  
 DR PRINTS; PR01349; WNTPROTEIN.  
 DR SMART; SM00097; WNT1; 1.  
 SQ SEQUENCE 354 AA; 40065 MW; B25CEDEB7453FD37 CRC64;

Query Match 61 KGLRSAT 67  
 Best Local Similarity 100.0%; Score 7; DB 13; Length 354;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 76 KGLRSAT 82

RESULT 10  
 ID 08VZW9 PRELIMINARY; PRT; 372 AA.  
 AC 08VZW9;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 GN Putative EBV envelope lipase (CMP48L).  
 OS Camelpox virus (strain CP-1).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 NCBI\_Taxid=203174;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Aforso C.L., Tulman E.R., Lu Z., Zsak L., Zaifeev V.L.,  
 RA Kerebekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;  
 RT "The genome of camelpox virus.";  
 RL Submitted (Oct-2001) to the EMBL/genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=CMS;  
 RX PubMed=11907336;  
 RA Gubser C., Smith G.L.;  
 RT "The sequence of camelpox virus shows it is most closely related to  
 variola virus, the cause of smallpox.";  
 RL J. Gen. Virol. 83:855-872(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=CMS;  
 RA Gubser C., Smith G.L.;  
 RL Submitted (Oct-2000) to the EMBL/genbank/DBJ databases.  
 DR EMBL; AF438165; AAL73755.1; -.  
 DR EMBL; AY009089; AAG37509.1; -.  
 DR InterPro; IPR01736; PLD.  
 DR Pfam; PF00614; PLDC; 2.  
 DR SMART; SM00155; PLDC; 2.  
 DR PROSITE; PS50035; PLD; 1.  
 SQ SEQUENCE 372 AA; 41914 MW; DFC025644501B151 CRC64;

Query Match 23 IDKLRSA 29  
 Best Local Similarity 100.0%; Score 7; DB 12; Length 372;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 224 IDKLRSA 230

RESULT 11  
 ID 085369 PRELIMINARY; PRT; 372 AA.  
 AC 085369;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 GN Homolog of VACCINIA virus CDS F13L.



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GN C17L OR B13L.
OS Variola virus, and
OS Variola minor virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255, 53258;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Variola virus; STRAIN=BANGLADESH-1975;
RX MEDLINE=94088747; PubMed=8264798;
RA Masung R.F., Esposito J.J., Liu L.I., Qi J., Uteback T.R.,
RA Knight J.C., Aubin L., Yuran T.B., Parsons J.M., Loparev V.N.;
RT "Potential virulence determinants in terminal regions of variola
RT smallpox virus genome";
RL Nature 366:748-751 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Variola minor virus; STRAIN=GARCIA-1966;
RA Shchelkunov S.N., Tolmenin A.V., Gutov V.V., Safonov P.F.,
RA Masung R.F., Loparev V.N., Knight J.C., Chizhkov V.B., Parsons J.M.,
RA Esposito J.J., Sosnovtsev S.;
RT "Analysis of the complete coding sequence of DNA of alastrim variola
RT minor virus strain Garcia-1966";
RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; L22579; AAA60785.1; -
DR EMBL; Y16780; CAB5437.1; -
DR InterPro; IPR001736; PLD.
DR Pfam; PF00614; PLDC; 2.
DR SMART; SM00155; PLDC; 2.
DR PROSITE; PS50035; PLD; 1.
SQ SEQUENCE 372 AA; 41929 MW; C7711FBA9C212E14 CRC64;

Query Match 9.9%; Score 7; DB 12; Length 372;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 IDKLRS 29
DB 224 IDKLRS 230

RESULT 12
O9D496 PRELIMINARY; PRT; 437 AA.
AC O9D496.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE 4930548H2ARik protein.
GN 4930548H2ARik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,
RA Akawa K., Irawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kankawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guenichon S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzaletti U., Mombauts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

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RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690 (2001).
DR EMBL; AK016690; BAB30382.1; -
DR MED; MGI:1914905; 4930548H2ARik.
SQ SEQUENCE 437 AA; 50470 MW; F1C862ED6B16526B CRC64;

Query Match 9.9%; Score 7; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 ESTXKL 49
DB 384 ESTXKL 390

RESULT 13
O9AQL1 PRELIMINARY; PRT; 477 AA.
AC O9AQL1.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE DNA gyrase B subunit (fragment).
GN GYB.
OS Porphyromonas levii.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=28114;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29147;
RA Suzuki M., Takadera T., Harayama S., Yamamoto S.;
RT "Diversity of marine Cytophaga-like bacteria: Phylogenetic analysis
RT using gyrB sequences and their carotenoid profiles";
RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
DE EMBL; AB048189; BAB33156.1; -
DR HSSP; P06982; 1A6.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR001241; DNA_topoisom.
DR InterPro; IPR006171; Toprim_dom.
DR Pfam; PF00204; DNA_gyrase; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF01751; Toprim; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR SMART; SM00433; TOR2C; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
KW ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1
FT TER 477
SQ SEQUENCE 477 AA; 53457 MW; C88E7FA1536E16ED CRC64;

Query Match 9.9%; Score 7; DB 2; Length 477;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 LINDKLR 27
DB 388 LINDKLR 394

RESULT 14
O9EMJ0 PRELIMINARY; PRT; 541 AA.
AC O9EMJ0.
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE AMW216.
GN AMW216.

```

OS Amsacta moorei entomopoxvirus (AMEPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;  
 OC Entomopoxvirus B.  
 OX NCBI\_TaxID=28321;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2036550; PubMed=10936094;  
 RA Bawden A.L., Glasberg K.J., Digane J., Shaw R., Farmerie W.,  
 RA Moyer R.W.;  
 RT "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:  
 RT Analysis and Comparison with Other Poxviruses";  
 RL Virology 274:120-139(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Bawden A.L., Glasberg K.J., Digane J., Shaw R., Farmerie W.,  
 RA Moyer R.W.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF250284; AAC02922.1; -.  
 SQ SEQUENCE 541 AA; 63508 MW; 669A703BA055EF84 CRC64;

Query Match 9.9%; Score 7; DB 12; Length 541;  
 Best Local Similarity 100.0%; Pred. No. 52;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ESTENTY 9  
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Db 477 ESTENTY 483

RESULT 15

Q95Q83 PRELIMINARY; PRT; 793 AA.  
 AC Q95Q83;  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
 DE Hypothetical 87.4 kDa protein.  
 GN C17H11.6.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
 OC Rhabditidae; Peioderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";   
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Johnson D.;  
 RT "The sequence of C. elegans cosmid C17H11.";   
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Waterston R.;  
 RT "Direct Submission.";   
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL; U80847; AAK68189.1; -.  
 DR WormPep; C17H11.6a; CE27704.  
 DR InterPro; IPR006895; zf-Sec23\_Sec24.  
 DR InterPro; IPR002867; Znf\_C6HC.  
 DR InterPro; IPR001841; Znf\_ring.  
 DR Pfam; PF01485; IIR; 1.  
 DR Pfam; PF00097; zf-C3HC4; 1.  
 DR Pfam; PF04810; zf-Sec23\_Sec24; 1.  
 DR SMART; SM00647; IIR; 2.  
 DR SMART; SM00184; RING; 2.

DR PROSITE; P550089; ZF\_RING\_2; 1.  
 KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.  
 SQ SEQUENCE 793 AA; 87408 MW; 6FD1C98F1809C9D4 CRC64;

Query Match 9.9%; Score 7; DB 5; Length 793;  
 Best Local Similarity 100.0%; Pred. No. 73;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 APPKLG 62  
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Db 96 APPKLG 102

Search completed: November 28, 2003, 13:44:48  
 Job time : 34 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 12:18:06 / Search time 1605 seconds

(without alignments)  
1075.151 Million cell updates/sec

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Title: US-10-059-395-142\_COPY\_29\_99  
Sequence: 1 EESTIENYASRPEAFNTPF.....LNMWAPKXKGLRSATPPAQ 71  
Scoring table: OLIGO  
Xgapop 60.0, Xgapext 60.0  
Ygapop 60.0, Ygapext 60.0  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Word size: 1

Total number of hits satisfying chosen parameters: 45562437

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Listing first 45 summaries

Command line parameters:  
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-CG2\_1/USFO\_SPOOL/US1005395/runat.25112003.140940.8064/app\_query.fasta.1.263  
-DB=EST -QFMT=fastap -SUFFIX=011.rst -MINMATCH=0.1 -LOOFC=0 -LOOEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=quality -THR MEN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pro  
-NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US1005395 @CCN 1.1.2810 @runat.25112003.140940.8064 -NCPU=6 -ICPU=3  
-NO MAP -LARGEOUTERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST.\*  
1: em\_estba:\*  
2: em\_estchum:\*  
3: em\_estcin:\*  
4: em\_estcmu:\*  
5: em\_estcov:\*  
6: em\_estcpl:\*  
7: em\_estcro:\*  
8: em\_estc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hcc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_hnv:\*  
19: em\_gss\_pin:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_pig:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*

| Result No. | Score | *<br>Query Match | Length | DB | ID       | Description        |
|------------|-------|------------------|--------|----|----------|--------------------|
| 1          | 71    | 100.0            | 318    | 9  | AA586846 | AA586846 nm67611.s |
| 2          | 71    | 100.0            | 334    | 9  | AA297512 | AA297512 EST113061 |
| 3          | 71    | 100.0            | 339    | 9  | AA778414 | AA778414 ZF39605.s |
| 4          | 71    | 100.0            | 348    | 9  | AA738758 | AA738758 xp03608.x |
| 5          | 71    | 100.0            | 359    | 10 | BE466728 | BE466728 hz24906.x |
| 6          | 71    | 100.0            | 362    | 9  | A1140605 | A1140605 qe05f03.x |
| 7          | 71    | 100.0            | 373    | 9  | AA722694 | AA722694 z982b06.s |
| 8          | 71    | 100.0            | 381    | 14 | W69108   | W69108 z444c04.s1  |
| 9          | 71    | 100.0            | 394    | 14 | W60320   | W60320 z429901.s1  |
| 10         | 71    | 100.0            | 412    | 14 | W60268   | W60268 z429901.s1  |
| 11         | 71    | 100.0            | 424    | 14 | W69083   | W69083 z444b06.s1  |
| 12         | 71    | 100.0            | 432    | 13 | EX112106 | EX112106 BX112106  |
| 13         | 71    | 100.0            | 432    | 13 | W69233   | W69233 z444c04.r1  |
| 14         | 59    | 83.1             | 431    | 14 | W69237   | W69237 z444b06.r1  |
| 15         | 58    | 81.7             | 413    | 9  | AA393296 | AA393296 zt74f05.r |
| 16         | 57    | 80.3             | 345    | 9  | A1217565 | A1217565 qd43d02.x |
| 17         | 56    | 78.9             | 241    | 9  | AA595989 | AA595989 nm64508.s |
| 18         | 53    | 74.6             | 359    | 10 | BG150312 | BG150312 7398903.x |
| 19         | 51    | 71.8             | 334    | 9  | A1217587 | A1217587 qd43f04.x |
| 20         | 43    | 60.6             | 345    | 9  | AA583942 | AA583942 nm64f07.s |
| 21         | 43    | 60.6             | 376    | 14 | W95920   | W95920 z608d01.r1  |
| 22         | 39    | 54.9             | 221    | 9  | AA584333 | AA584333 nm73a09.s |
| 23         | 39    | 54.9             | 326    | 9  | AA297513 | AA297513 EST113062 |
| 24         | 37    | 52.1             | 358    | 9  | AA003825 | AA003825 wq83f12.x |
| 25         | 37    | 52.1             | 377    | 9  | AA582988 | AA582988 nm72b02.s |
| 26         | 35    | 49.3             | 330    | 14 | W95883   | W95883 z608d01.s1  |
| 27         | 33    | 46.5             | 218    | 9  | AA398638 | AA398638 zt74f05.s |
| 28         | 33    | 46.5             | 239    | 9  | AA595930 | AA595930 nm66f07.s |
| 29         | 27    | 38.0             | 339    | 14 | W52030   | W52030 z413b01.s1  |
| 30         | 27    | 38.0             | 378    | 9  | A1184682 | A1184682 qd68b02.x |
| 31         | 24    | 33.8             | 436    | 9  | AA260965 | AA260965 EOUK0243  |
| 32         | 24    | 33.8             | 436    | 9  | AV597545 | AV597545 AV597545  |
| 33         | 18    | 25.4             | 163    | 9  | AA776980 | AA776980 zt23d05.s |
| 34         | 15    | 21.1             | 377    | 9  | AA260982 | AA260982 EOUK0196  |
| 35         | 14    | 19.7             | 421    | 9  | AV618771 | AV618771 AV618771  |
| 36         | 12    | 16.9             | 323    | 10 | BE715771 | BE715771 MR2-HT075 |
| 37         | 8     | 11.3             | 271    | 10 | BE701465 | BE701465 PM2-NN017 |
| 38         | 8     | 11.3             | 304    | 9  | AT894297 | AT894297 ms66b04.x |
| 39         | 8     | 11.3             | 310    | 14 | CD036743 | CD036743 mg9a011xd |
| 40         | 8     | 11.3             | 353    | 10 | BF366304 | BF366304 CML-NT008 |
| 41         | 8     | 11.3             | 365    | 10 | BF735391 | BF735391 CML-AN008 |
| 42         | 8     | 11.3             | 378    | 10 | BF522420 | BF522420 UI-R-C3-t |
| 43         | 8     | 11.3             | 382    | 12 | B1881645 | B1881645 fm88905.y |
| 44         | 8     | 11.3             | 399    | 12 | B1881568 | B1881568 fm87c01.y |
| 45         | 8     | 11.3             | 404    | 14 | R80137   | R80137 y495c09.r1  |

#### ALIGNMENTS

RESULT 1  
LOCUS AA586846/c 318 bp mRNA EST 26-SEP-1997  
DEFINITION nm67611.s1 NCI\_CGAP\_Lair1 Homo sapiens cDNA clone IMAGE:1088972 3',  
AA586846  
ACCESSION AA586846  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
1 (bases 1 to 318)



|  |   |   |      |        |                 |
|--|---|---|------|--------|-----------------|
| RESULT 3   | AA778414/c  | 339 bp  | mRNA | linear | EST 05-FEB-1998 |
| LOCUS  | AA778414  |   |      |        |                 |
| DEFINITION   | z139e05.s1 Soares_fetal_heart_NbHH19w Homo sapiens cDNA clone IMAGE:379328 3', mRNA sequence.   |   |      |        |                 |
| ACCESSION  | AA778414  |   |      |        |                 |
| VERSION  | AA778414.1  | GI:2837745  |      |        |                 |
| KEYWORDS   | EST.  |   |      |        |                 |
| SOURCE   | Homo sapiens (human)  |   |      |        |                 |
| ORGANISM   | Homo sapiens  |   |      |        |                 |
| REFERENCE  | Mammalia; Eutelesia; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Carnivora; Homnidae; Homo.   |   |      |        |                 |
| AUTHORS  | 1 (bases 1 to 339)  |   |      |        |                 |
| TITLE  | Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lemon, G., Marra, M., Martin, J., Moore, B., Schellander, K., Stepec, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.  |   |      |        |                 |
| JOURNAL  | WashU-NCI human EST Project   |   |      |        |                 |
| COMMENT  | Unpublished   |   |      |        |                 |
|  | Contact: Wilson RK  |   |      |        |                 |
|  | Washington University School of Medicine  |   |      |        |                 |
|  | 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108   |   |      |        |                 |
|  | Tel: 314 286 1800   |   |      |        |                 |
|  | Fax: 314 286 1810   |   |      |        |                 |
|  | Email: est@watson.wustl.edu   |   |      |        |                 |
|  | This clone is available royalty-free through LMLT; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  |   |      |        |                 |
|  | Seq primer: -40m3 fwd. ET from Amersham.  |   |      |        |                 |
| FEATURES   | Location/Qualifiers   |   |      |        |                 |
| source   | 1..339  |   |      |        |                 |
|  | /organism="Homo sapiens"  |   |      |        |                 |
|  | /mol_type="mRNA"  |   |      |        |                 |
|  | /db_xref="GDB:1287584"  |   |      |        |                 |
|  | /db_xref="taxon:9606"   |   |      |        |                 |
|  | /clone="IMAGE:379328"   |   |      |        |                 |
|  | /sex="unknown"  |   |      |        |                 |
|  | /dev_stage="19 weeks"   |   |      |        |                 |
|  | /lab_host="DH10B (ampicillin resistant)"  |   |      |        |                 |
|  | /clone_idb="Soares_fetal_heart_NbHH19w"   |   |      |        |                 |
|  | /note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGGCCGACATCTTTTCTTTTCTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73D vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Felima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHH19w." |   |      |        |                 |
| BASE COUNT   | 79 a  | 96 g  | 87 c |        |                 |
| ORIGIN   | 77 c  |   |      |        |                 |
| Alignment Scores:                                      |   |   |      |        |                 |
| Pred. No.:   | 5.44e-68  | Length:   | 339  |        |                 |
| Score:   | 71.00   | Matches:  | 71   |        |                 |
| Percent Similarity:                                    | 100.00%   | Conservative:   | 0    |        |                 |
| Best Local Similarity:                                 | 100.00%   | Mismatches:   | 0    |        |                 |
| Query Match:   | 100.00%   | Indels:   | 0    |        |                 |
| DB:  | 9   | Gaps:   | 0    |        |                 |
| US-10-059-395-142_COPY_29_99 (1-71) x AA778414 (1-339) |   |   |      |        |                 |
| Oy   | 1   | GluglugsuSerrTrlllEgluAsntYrYlAsSergPvGluAlpheaNthProphe    | 20   |        |                 |
| Db   | 316   | GAGAGAGAAACACCAATCGAATTAATTCGTCACACCCGAGGCTTTAAACACCCCGTTC  | 257  |        |                 |
| Oy   | 21  | LeuAnllleaPlylSleuAArgSerAlaPheYsAlaAePGluPheLeuAstrPHlSA14 | 40   |        |                 |
| Db   | 256   | CTGAACATCGACAAATTCGCATTCGCCGTTTAAAGCTGATGAGTTCTGAATCGGACGCC | 197  |        |                 |
| Oy   | 41  | LeudhegluSerrllElYsArgYleuBProPheLeuAstrPaPAlaPheProlySleu  | 60   |        |                 |

| Db   | Accession  | Version  | KeyWords | Source | Organism | Reference Authors Title | Journal Comment |
|--|--|--|----------|--------|----------|-------------------------|-----------------|
| Dn   | 196  | CTCTTTAGGCTATCAAAAGAACTTCCTTCTCCTCAACTGGATGCTTCTTAAGCTG        | 137      |        |          |                         |                 |
| Dn   | 61   | LYGSLYLeuAysSera1aThrProASPAlaGln                              | 71       |        |          |                         |                 |
| Dn   | 136  | AAAGGACTGAGAGCGCACTCTGATGCCGAG                                 | 104      |        |          |                         |                 |
| RESULT 4   |  |  |          |        |          |                         |                 |
| LOCUS  | AM238758   |  |          |        |          |                         |                 |
| DEFINITION   | XP030608.X1 NCI_CGAP_HN8 Homo sapiens cDNA clone IMAGE:2739302 3',   |  |          |        |          |                         |                 |
| ACCESSION  | AM238758   |  |          |        |          |                         |                 |
| VERSION  | AM238758.1   |  |          |        |          |                         |                 |
| KEYWORDS   | EST.   |  |          |        |          |                         |                 |
| SOURCE   | Homo sapiens (human)   |  |          |        |          |                         |                 |
| ORGANISM   | Homo sapiens   |  |          |        |          |                         |                 |
| REFERENCE  | Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  |  |          |        |          |                         |                 |
| AUTHORS  | 1 (bases 1 to 348)   |  |          |        |          |                         |                 |
| TITLE  | NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  |  |          |        |          |                         |                 |
| JOURNAL  | National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  |  |          |        |          |                         |                 |
| COMMENT  | Unpublished<br>Contact: Robert Strausberg, Ph.D.<br>Email: rcgabs-remail.nih.gov<br>Tissue Procurement: Edward Shillito Ph.D., Silvio Gutkind Ph.D.,<br>Chidnapok Leebhakul D.D.S., Michael Emmert-Buck M.D. Ph.D.<br>cDNA Library Preparation: David B. Krizman, Ph.D.<br>cDNA Library Arrayed by: Greg Lennon, Ph.D.<br>DNA Sequencing by: Washington University Genome Sequencing Center<br>Clone distribution: NCI-CGAP clone distribution information can be<br>found through the I.M.A.G.E. Consortium/LINL at:<br>www.bio.llnl.gov/bdrip/image/image.html   |  |          |        |          |                         |                 |
| FEATURES   |  |  |          |        |          |                         |                 |
| SOURCE   | Possible reversed clone: polyT not found<br>Seq primer: -40UP from Gibco<br>High quality sequence stop: 331.<br>Location/Qualifiers<br>1. 348<br>/organism="Homo sapiens"<br>/mol_type="mRNA"<br>/db_xref="taxon:9606"<br>/clone="IMAGE:2739302"<br>/tissue_type="well-differentiated invasive carcinoma,<br>floor of mouth"<br>/lab_host="DH10B"<br>/clone_lib="NCI_CGAP_HN8"<br>/notes="Vector: PAMP10; cDNA made by oligo-dT priming.<br>Non-directionally cloned into the UPG sites of PAMP10.<br>Size-selected on agarose gel, average insert size 500 bp.<br>Primary library; non-amplified. cDNA library<br>Preparation: David B. Krizman, Ph.D (NCI). Reference:<br>Krizman et al. (1996) Cancer Research 56:5380-5383." |  |          |        |          |                         |                 |
| BASE COUNT   | 82 a   | 104 c  | 84 g     | 78 t   |          |                         |                 |
| ORIGIN   |  |  |          |        |          |                         |                 |
| Alignment Scores:                                      |  |  |          |        |          |                         |                 |
| Pred. No.:   | 5.6e-68  | Length:  | 348      |        |          |                         |                 |
| Score:   | 71.00  | Matches:   | 71       |        |          |                         |                 |
| Percent Similarity:                                    | 100.00%  | Conservative:  | 0        |        |          |                         |                 |
| Best Local Similarity:                                 | 100.00%  | Mismatches:  | 0        |        |          |                         |                 |
| Query Match:   | 100.00%  | Indels:  | 0        |        |          |                         |                 |
| Db:  | 9  | Gaps:  | 0        |        |          |                         |                 |
| US-10-059-395-142_COPY 29_99 (1-71) x AM238758 (1-348) |  |  |          |        |          |                         |                 |
| Qy   | 1  | GIUGLUGLUGerThrillegiUAenTYrAlaSerArgProGluuAlaPheAenThrProPhe | 20       |        |          |                         |                 |
| Dn   | 81   | GAGGAGAAAGACCAATGAGATTTATGCTACGACCGAGGCTTTAACCCTTC             | 140      |        |          |                         |                 |
| Yy   | 21   | LeuAenlleApyLeuAysSera1aPheLyAlaSpGluPheLeuAenTPPHAla          | 40       |        |          |                         |                 |

Db 141 CTGAACATCGACAATTGGCATCTGCTTAAGCTGATGCTCTGAATCGGACGCC 200

Qy 41 Leuphegiuser11elysarglyseupropheleuasentrpaspalapherprolyseu 60

Db 201 CTTTGTGATCTATCAAAAGAAACTCTTCTCTCAACTGGAGTCCCTTCTTAAGCTG 260

Qy 61 LysgilyleuargseralathrProaspalagin 71

Db 261 AAAGACTGAGAGCGCAACTCTGATGCCAG 293

RESULT 5

BE466728/c 359 bp mRNA linear EST 27-VUL-2000

LOCUS h224906.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:3208954 3'

DEFINITION mRNA sequence.

ACCESSION BE466728

VERSION BE466728.1 GI:9512503

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 359)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

FEATURES

source

1..359

location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3208954"

/tissue\_type="pooled germ cell tumors"

/lab\_host="DH10B"

/clone\_idb="NCI\_CGAP\_GC6"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI\_CGAP\_GC4 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIdb 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 77 a 80 c 96 g 106 t

ORIGIN

Alignment Scores:

Pred. No.: 5,79e-68 Length: 359

Score: 71.00 Matches: 71

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 10 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x BE466728 (1-359)

Qy 1 GIUGLUGuserThrlleglubenryralaserargProglualaphenanthrProphe 20

Db 332 GAGGAAGAAAGACCACTTGAATATATGCTCAACACCCGCTTTAAACACCCGCTTC 273

Qy 21 LeusenilleasplyleuargseralaphelysallapglupheleuasentrpHisla 40

Db 272 CTGAACATCGACAATTGGCATCTGCTTAAGCTGATGCTCTGAATCGGACGCC 213

Qy 41 Leuphegiuser11elysarglyseupropheleuasentrpaspalapherprolyseu 60

Db 212 CTTTGTGATCTATCAAAAGAAACTCTTCTCTCAACTGGAGTCCCTTCTTAAGCTG 153

Qy 61 LysgilyleuargseralathrProaspalagin 71

Db 152 AAAGACTGAGAGCGCAACTCTGATGCCAG 120

RESULT 6

A1140605/c 362 bp mRNA linear EST 29-OCT-1998

LOCUS qe05f03.x1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1738109

DEFINITION 3', mRNA sequence.

ACCESSION A1140605

VERSION A1140605.1 GI:3648062

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 362)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

FEATURES

source

1..362

location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1738109"

/sex="male"

/lab\_host="DH10B"

/clone\_idb="Soares\_testis\_NHT"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories Inc. and primed with a Not I - oligo(dT) primer [5' TGTACCAATCTGAAGTGGAGCGCGCCCAATTTTCTTTTCTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cots, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 77 a 81 c 99 g 105 t

ORIGIN

Alignment Scores:

Pred. No.: 5,84e-68 Length: 362

Score: 71.00 Matches: 71

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x A1140605 (1-362)

|                   |   |   |                 |
|-------------------|---|---|-----------------|
| QY                | 1   | GluglugusertH1161uastHrYr1a6eAr3pR0G1uA1Pha6aHrHrProbe      | 20              |
| Db                | 331   | GAGGAGAAAGACACATTGAGATATATGGTACGACCCGAGGCGCTTTAAACCCCCGTTTC | 272             |
| QY                | 21  | Leu8n11eap1yLeu8Ar3seZ1a1aPhe1ySa1aA6p1uPh1eLeu8AntRph1Sa1a | 40              |
| Db                | 271   | CTGAACATCGACAATTGCGATCTTCGTTTAAAGCTGATGAGTCTCTAATCGGACGCC   | 212             |
| QY                | 41  | LeuPhe1u8er11e1yAr3yLeu8ProPheLeu8AntRPaPa1aPhePro1yLeu     | 60              |
| Db                | 211   | CTCTTGGTCTATCAAAAGGAAATCTCTTCCCAACCTGGAGATCCCTTCTTAAGCTG    | 152             |
| QY                | 61  | Ly8G1yLeuAr3seZ1a1aThPro8p1a1aG1n                           | 71              |
| Db                | 151   | AAAGACTGAGAGCGCAACTCTCATGCCCCAG                             | 119             |
| RESULT 7          |   |   |                 |
| LOCUS             | AA722694/c  |   |                 |
| DEFINITION        | AA722694  | 373 bp  | mRNA            |
| ACCESSION         | AA722694  |   | linear          |
| VERSION           | AA722694.1  |   | EST 02-JAN-1996 |
| KEYWORDS          | EST.  |   |                 |
| SOURCE            | Homo sapiens (human)  |   |                 |
| ORGANISM          | Homo sapiens  |   |                 |
| REFERENCE         | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.   |   |                 |
| AUTHORS           | 1. (bases 1 to 373)<br>Hillier, D., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S., Kitzman, D., Kucaba, T., Lacy, M., Le, N., Lennom, G., Matra, M., Martin, J., Moore, B., Schellenberg, K., Stepcoe, M., Tan, F., Theisling, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.   |   |                 |
| TITLE             | WashU-NCI human EST Project   |   |                 |
| JOURNAL           | Unpublished   |   |                 |
| COMMENT           | Contact: Wilson RK<br>Washington University School of Medicine<br>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108<br>Tel: 314 286 1800<br>Fax: 314 286 1810<br>Email: est@watson.wustl.edu<br>This clone is available royalty-free through LNL; contact the<br>IMAGS Consortium (info@image.lnl.gov) for further information.<br>Seq primer: -40m13 fwd. ET from Amerham.   |   |                 |
| FEATURES          | Location/Qualifiers   |   |                 |
| source            | 1..373  |   |                 |
|                   | /organism="Homo sapiens"  |   |                 |
|                   | /mol_type="mRNA"  |   |                 |
|                   | /db_xref="GDB:1307650"  |   |                 |
|                   | /db_xref="taxon:9606"   |   |                 |
|                   | /clone="IMAGS:399827"   |   |                 |
|                   | /sex="unknown"  |   |                 |
|                   | /dev_stage="19 weeks"   |   |                 |
|                   | /lab_host="DH10B (ampicillin resistant)"  |   |                 |
|                   | /clone_11b="Soares_fetal heart NBH119W"   |   |                 |
|                   | /note="Organ: heart; Vector: pRT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCCGACATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3D vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Facina Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBH119W." |   |                 |
| BASE COUNT        | 89 a  | 81 c  | 113 g 90 t      |
| ORIGIN            |   |   |                 |
| Alignment Scores: |   |   |                 |
| Pred. No.:        | 6.04e-68  | Length:   | 373             |
| Score:            | 71.00   | Matches:  | 71              |

```

Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:    100.00%      Mismatches:       0
Query Match:             100.00%      Indels:           0
DB:                      9              Gaps:            0

US-10-059-395-142_COPY_29_99 (1-71) x AA1726294 (1-373)

QY      1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnTrpProPhe 20
Db      319 GAGGAAGAAGAACACCATTTGAAATTAATTCCTCAGCACCGGCGCTTTAACCCTTTC 260
QY      21 LeuAsnIleLeuPylsLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40
Db      259 CTGAACATCCAGCAAAATTGCATCGCGCTTAAAGCGTGATGATGGTCCGAACCTGCACGCC 200
QY      41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60
Db      199 CTTTGTAGTCTATCAAAAAGAACTTCCTTCTCTCAACTGAGATGCCCTTCTTAAGCTG 140
QY      61 LysGlyLeuArgSerAlaThrProAspAlaGln 71
Db      139 AAAGCACTGAGAGCGCACTCTCGAGGCCAG 107

RESULT 8
W69108      381 bp      mRNA      linear      EST 16-Oct-1996
LOCUS       W69108/c
DEFINITION IMAGE:343494.3', mRNA sequence.
VERSION     W69108
KEYWORDS    W69108.1 GI:1378389
SOURCE      EST.
ORGANISM   Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 381)
AUTHORS    Hillier,L., Clark,N., Dubuque,T., Bliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,S., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE       The Wash-Werck EST Project
JOURNAL     Unpublished
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LML; contact the
            IMAGE Consortium (info@image.lml.gov) for further information.
            Insert Length: 442 Std Error: 0.00
            Seq primer: mod.RBGA+ET
            High quality sequence stop: 347.
FEATURES
         source
         1..381
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="GDB:1268869"
            /db_xref="taxon:9606"
            /clone="IMAGE:343494"
            /sex="unknown"
            /dev_stage="19 weeks"
            /lab_host="DH10B (ampicillin resistant)"
            /clone_id="Soares_fetal_heart_NBH1.9W"
            /note="Organ: heart; Vector: pTV73d (Pharmacia) with a
            modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
            strand cDNA was primed with a Not I - oligo(dT) primer [5'
            TGTACCAATCTGAAGTAGGAGCGCGCATCTTTTTTTTTTTTTT 3'],
            double-stranded cDNA was size selected, ligated to Eco RI
            adapters (Pharmacia), digested with Not I and cloned into
            the Not I and Eco RI sites of a modified pTV73 vector
            (Pharmacia). Library was through one round of
            normalization to a Cot = 5. Library constructed by

```

BASE COUNT 91 a 86 c 114 g 89 t 1 others  
M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."

## ALIGNMENT SCORES:

Pred. No.: 6,18e-68 Length: 381  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x W69108 (1-381)

QY 1 GIUGIUGIUSERThrlleGUANTYrAlaseArpProGIUAlAphaeAnThrProPhe 20  
DB 317 GAGGAGAAAGACCACTTGAGATTATGCGTCACGACCGAGGCCCTTTAAACCCCGTTC 258

QY 21 LeuAnIleAspLySerLeuArgSerAlaPheLyAlaAspGluPheLeuAnThrPhisAla 40  
DB 257 CTGAACATGACAAATTGCGATCTGCGTTTAAAGCTGATGAGTTCTGTAACCTGGACAGCC 198

QY 41 LeuPheGluSerIleLyArGLysLeuProPheLeuAnThrAspAlaPheProLySleu 60  
DB 197 CTTTGAAGTCTATCAAAAGAACTTCCTTCTCACTGGATCCTTCTTAAGCTG 138

QY 61 LySGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 137 AAAGACTGAGAGCGCAACTCTGTATGCCAG 105

RESULT 9 W60320 394 bp mRNA linear EST 15-OCT-1996  
LOCUS zd29g01.s1 Soares fetal heart NBHL19W Homo sapiens cDNA clone  
DEFINITION IMAGE:342096 3', mRNA sequence.  
ACCESSION W60320  
VERSION W60320.1 GI:1367079  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 394)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohldmann, P., and Wilson, R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 476 Std Error: 0.00  
Seq primer: mob.REGA+ET.  
Location/Qualifiers  
1. 394

FEATURES  
source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1267471"  
/db\_xref="taxon:9606"  
/clone="IMAGE:342096"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal heart NBHL19W"  
/note="Organ: heart; Vector: pT73D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTCCATCTGAGTGGAGCGCGGCACTTTTCTTTTCTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."

US-10-059-395-142\_COPY\_29\_99 (1-71) x W60320 (1-394)

QY 1 GIUGIUGIUSERThrlleGUANTYrAlaseArpProGIUAlAphaeAnThrProPhe 20  
DB 320 GAGGAGAAAGACCACTTGAGATTATGCGTCACGACCGAGGCCCTTTAAACCCCGTTC 261

QY 21 LeuAnIleAspLySerLeuArgSerAlaPheLyAlaAspGluPheLeuAnThrPhisAla 40  
DB 260 CTGAACATGACAAATTGCGATCTGCGTTTAAAGCTGATGAGTTCTTAACTGGACAGCC 201

QY 41 LeuPheGluSerIleLyArGLysLeuProPheLeuAnThrAspAlaPheProLySleu 60  
DB 200 CTTTGAAGTCTATCAAAAGAACTTCCTTCTCACTGGATCCTTCTTAAGCTG 141

QY 61 LySGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 140 AAAGACTGAGAGCGCAACTCTGTATGCCAG 108

RESULT 10 W60268 412 bp mRNA linear EST 15-OCT-1996  
LOCUS zd29g01.r1 Soares fetal heart NBHL19W Homo sapiens cDNA clone  
DEFINITION IMAGE:342096 5', mRNA sequence.  
ACCESSION W60268  
VERSION W60268.1 GI:1367169  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 412)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohldmann, P., and Wilson, R.

TITLE The WashU-Merck EST Project  
JOURNAL Unpublished  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
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High quality sequence score: 385.  
Location/Qualifiers  
1. 412

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/note="Organ: heart; Vector: pT73D (Pharmacia) with a





# TITLE JOURNAL COMMENT

Radelof, U., Schneider, D. and Korn, B.  
Human Unigeneset - RZPD3  
Unpublished  
Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD, IMAGP98D01781.  
RZPDLIB, I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No. 972)  
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi?response?libNo=972  
Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Neuenheimer 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de  
This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r, Primer sequence: TTTCACACAGGAAACGCTATGAC.  
Location/Qualifiers

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source

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BASE COUNT 113 a 129 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 7,08e-68 Length: 432  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x BX112106 (1-432)

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QY 21 LeuAenIIeApLySeuArgSeRAlaPheLyAlaApGluPheLeuAsnTrpHisAla 40  
DB 159 CTGAACATCGACAAATTGCGATCTGCTTTAAGCTGAGTGAAGTCTCTGAACCTGGACGCC 218  
QY 41 LeuPheGluSeRlleLyArgLySeuLeuProPheLeuAsnTrpAspAlaPheProLySeu 60  
DB 219 CTTCTTGAAGCTATCAAAAGAACTCTTCTCTCAACTGGAGATGCCCTTTCTTAAGCTG 278  
QY 61 LysGluLeuArgSeRAlaPheProAspAlaGln 71  
DB 279 AAAAGACTAAGAGCCCACTCTGATGCCAG 311  
RESULT 13  
W69233  
LOCUS W69233 432 bp mRNA linear EST 16-OCT-1996

DEFINITION zd44c04.r1 Soares fetal heart NBH19W Homo sapiens cDNA clone  
IMAGE:343494 5', mRNA sequence.  
ACCESSION W69233  
VERSION W69233.1 GI:1378493  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 432)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.  
The Washu-Merk EST Project  
Unpublished

## TITLE JOURNAL COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
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Location/Qualifiers

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/note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBH19W."  
BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN

Alignment Scores:  
Pred. No.: 7,08e-68 Length: 432  
Score: 71.00 Matches: 71  
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US-10-059-395-142\_COPY\_29\_99 (1-71) x W69233 (1-432)

QY 1 GUGUGUGUSeThrlleGUaSnTYrAlaSeRArgProGUAlaPheAsnThrProPhe 20  
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QY 21 LeuAenIIeApLySeuArgSeRAlaPheLyAlaApGluPheLeuAsnTrpHisAla 40  
DB 156 CTGAACATCGACAAATTGCGATCTGCTTTAAGCTGAGTGAAGTCTCTGAACCTGGACGCC 215  
QY 41 LeuPheGluSeRlleLyArgLySeuLeuProPheLeuAsnTrpAspAlaPheProLySeu 60

Db 216 CTCCTTGACTATCAAAAAGAACTTCCTTCGACGAGTCCCTTCTTAAGCTG 275  
 Qy 61 TysgLYleuArgSerAlaThrProAspAlaGln 71  
 Db 276 AAGAGCTGAGAGGCCAAGCTCTGATGCCCA 308  
 RESULT 14  
 W69227 431 bp mRNA linear EST 16-OCT-1996  
 LOCUS z44b06.r1 Soares\_fetal\_heart\_NbH19W Homo sapiens cDNA clone  
 DEFINITION IMAGE:343475.5, mRNA sequence.  
 ACCESSION W69227  
 VERSION W69227.1 GI:1378487  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 431)  
 Hillier, L., Clark, N., Dubuque, T., Ellison, K., Hawkin, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.  
 The WashU-Merck EST Project  
 TITLE Unpublished  
 JOURNAL Contact: Wilson RK  
 COMMENT Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
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BASE COUNT 106 a 127 c 94 g 102 t 2 others

ORIGIN

Alignment Scores:

|                        |          |               |     |
|------------------------|----------|---------------|-----|
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| Score:                 | 59.00    | Matches:      | 59  |
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| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
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US-10-059-395-142\_COPY\_29\_99 (1-71) x W69227 (1-431)

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 Db 194 GATGAGTTCCTGAACTGGACAGCCCTCTTTGAGTCTATCAAAAAGAACTTCCTTCCTC 253  
 Qy 53 AenTPaAPAlaPheProLYleuLeuLYleuArgSerAlaThrProAspAlaGln 71  
 Db 254 AACTGGATGCTTCCTTAAGCTGAAGAGTGAAGAGCGCAACTCTGATGCCAG 310  
 RESULT 15  
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 LOCUS zc74f05.r1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:728097  
 DEFINITION 5', mRNA sequence.  
 ACCESSION AA393296  
 VERSION AA393296.1 GI:2046264  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 413)  
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Scheinberg, K., Stepien, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
 WashU-Merck EST Project 1997  
 TITLE Unpublished  
 JOURNAL Contact: Wilson RK  
 COMMENT Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: -28mJ3 rev2 ET from Amerham  
 High quality sequence stop: 386.  
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BASE COUNT 96 a 113 c 125 g 79 t

ORIGIN

Alignment Scores:

|                        |          |               |     |
|------------------------|----------|---------------|-----|
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US-10-059-395-142\_COPY\_29\_99 (1-71) x AA393296 (1-413)

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OY 20 eLeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpIAsp 40
Db 224 CCTGAACATTCGACAAATTGCCATCTGCCCTTTAAGGCTGATGAGTTCTGAACTGGCACGC 283
OY 40 aLeuPheGlnSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLe 60
Db 284 CCTCTTGAGTCTATCAAAAGAAACTTCTTCTCAACTGGGATGCTTCTCTTAAGCT 343
OY 60 uLysGlyLeuArgSerAlaThrProAspAlaGln 71
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Search completed: November 28, 2003, 13:33:49  
Job time : 1606 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

# OM protein - nucleic search, using frame\_plus\_p2n model

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(Without alignments)  
580.337 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99  
Sequence: 1 EBBSTIENASREAFNTPF.....LMDAPKKGKRSATPDQ 71

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Searched: 569978 seqs, 220691566 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1135135

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query | Match length | ID                  | Description        |
|------------|-------|-------|--------------|---------------------|--------------------|
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| 2          | 9     | 12.7  | 666          | US-09-252-991A-5754 | Sequence 5754, App |
| 3          | 9     | 12.7  | 837          | US-09-252-991A-5702 | Sequence 5702, App |
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| 6          | 9     | 12.7  | 765          | US-09-107-532A-1141 | Sequence 1141, App |
| 7          | 9     | 9.9   | 774          | US-09-252-991A-9431 | Sequence 9431, App |
| 8          | 9     | 9.9   | 2397         | US-09-221-017B-272  | Sequence 272, App  |
| 9          | 9     | 9.9   | 3964         | US-09-620-912D-128  | Sequence 128, App  |
| 10         | 9     | 9.9   | 5804         | US-09-369-364A-12   | Sequence 12, App1  |
| 11         | 9     | 9.9   | 31208        | US-09-852-067-3     | Sequence 3, App1   |
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| 27 | 6 | 8.5 | 74     | 3 | US-08-368-704C-11    | Sequence 11, App1   |
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| 29 | 6 | 8.5 | 75     | 4 | US-09-670-314-146    | Sequence 146, App   |
| 30 | 6 | 8.5 | 164    | 1 | US-08-480-552-1      | Sequence 1, App1    |
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| 34 | 6 | 8.5 | 164    | 3 | US-09-561-844-1      | Sequence 1, App1    |
| 35 | 6 | 8.5 | 164    | 4 | US-09-568-315-1      | Sequence 1, App1    |
| 36 | 6 | 8.5 | 164    | 4 | US-09-562-226-1      | Sequence 1, App1    |
| 37 | 6 | 8.5 | 164    | 5 | PCT-US91-07492-1     | Sequence 1, App1    |
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| 42 | 6 | 8.5 | 277    | 1 | US-08-484-274A-12    | Sequence 12, App1   |
| 43 | 6 | 8.5 | 277    | 3 | US-08-484-111-54     | Sequence 54, App1   |
| 44 | 6 | 8.5 | 305    | 4 | US-09-313-294A-7107  | Sequence 7107, App  |
| 45 | 6 | 8.5 | 318    | 4 | US-09-252-991A-10314 | Sequence 10314, App |

## ALIGNMENTS

RESULT 1  
US-09-996-243-200  
Sequence 200, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, David  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16

[illegible]



Query Match: 12.68% Indels: 0  
DB: 4 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-5715 (1-1035)  
QY 62 GYLeuArgSerAlaThrProAspAla 70  
DB 628 GGGCTGGGAGCGCCACGCGGACGCT 654  
RESULT 5  
US-09-252-991A-5725/C  
Sequence 5725, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 5725  
LENGTH: 1245  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5725  
Alignment Scores:  
Pred. No.: 0.935 Length: 1245  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 12.68% Indels: 0  
DB: 4 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-5725 (1-1245)  
QY 62 GYLeuArgSerAlaThrProAspAla 70  
DB 631 GGGCTGGGAGCGCCACGCGGACGCT 605  
RESULT 6  
US-09-107-532A-1141  
Sequence 1141, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 1141:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 765 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...765  
SEQUENCE DESCRIPTION: SEQ ID NO: 1141:  
US-09-107-532A-1141  
Alignment Scores:  
Pred. No.: 80.3 Length: 765  
Score: 7.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.86% Indels: 0  
DB: 4 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-107-532A-1141 (1-765)  
QY 46 LysArgLysLeuProPheLeu 52  
DB 97 AAAAGAAAATTACCTTCTTG 117  
RESULT 7  
US-09-252-991A-9431  
Sequence 9431, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 9431  
LENGTH: 774  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9431  
Alignment Scores:  
Pred. No.: 81.2 Length: 774  
Score: 7.00 Matches: 7  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.86% Indels: 0  
DB: 4 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-252-991A-9431 (1-774)  
QY 60 LeuLysGlyLeuArgSerAla 66  
|||||



Db 739 CTCAGGCGCTGCGTAGCGCT 759

## RESULT 8

US-09-221-017B-272/C

Sequence 272, Application US/09221017B

Patent No. 6444799

GENERAL INFORMATION:

APPLICANT: Ross, Bruce C.

TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF

NUMBER OF SEQUENCES: 1120

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/221,017B

FILING DATE: 23-DEC-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: P1182

FILING DATE: 31-DEC-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: P1546

FILING DATE: 30-JAN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: P2911

FILING DATE: 09-APR-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/AU98/01023

FILING DATE: 10-DEC-1998

ATTORNEY/AGENT INFORMATION:

NAME: MONROY, Gladys H

REGISTRATION NUMBER: 32,430

REFERENCE/DOCKET NUMBER: 27340-20021.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-813-5600

TELEFAX: 650-494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 272:

SEQUENCE CHARACTERISTICS:

LENGTH: 2397 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: UNKNOWN

ORIGINAL SOURCE:

ORGANISM: PORPHYROMONAS GINGIVALIS

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1...2397

US-09-221-017B-272

Alignment Scores:

Pred. No.: 244

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 9.86%

Db 647 TTCCTAAATAGATTAATTA 627

## RESULT 9

US-09-620-312D-128

Sequence 128, Application US/09620312D

Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyan

APPLICANT: Chen, Rui-hong

APPLICANT: Zhao, Qing A.

APPLICANT: Wehrman, Tom

APPLICANT: Xue, Aidong J.

APPLICANT: Yang, Yongshong

APPLICANT: Wang, Jian-Rui

APPLICANT: Zhou, Ping

APPLICANT: Ma, Yundong

APPLICANT: Wang, Dunrui

APPLICANT: Wang, Zhiwei

APPLICANT: John Tillinghast

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. 6569662el Nucleic Acids and

FILE REFERENCE: Polypeptides

CURRENT APPLICATION NUMBER: US/09/620,312D

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1105

SOFTWARE: pt\_FL\_genes Version 1.0

SEQ ID NO 128

LENGTH: 3964

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (174)..(2540)

US-09-620-312D-128

Alignment Scores:

Pred. No.: 399

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 9.86%

DB: 4

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-620-312D-128 (1-3964)

QY 10 A1aseArgProGluAlaPhe 16

Db 2273 GCTTCAGGCGCAGAGCCTT 2293

RESULT 10

US-09-369-364A-12

Sequence 12, Application US/09369364A

Patent No. 6391610

GENERAL INFORMATION:

APPLICANT: Apte, Suneel

APPLICANT: Hurekainen, Tiina L.

APPLICANT: Hirahata, Satoshi

TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases

FILE REFERENCE: 26473/4007/10-30-00

CURRENT APPLICATION NUMBER: US/09/369,364A

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin Ver. 2.1

```

; SEQ ID NO 12
; LENGTH: 5804
; TYPE: DNA
; ORGANISM: Homo sapiens ADAMTS-9
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(5648)
; NAME/KEY: misc_feature
; LOCATION: (1406)
; OTHER INFORMATION: n=T
; NAME/KEY: misc_feature
; LOCATION: (1563)
; OTHER INFORMATION: n=T
US-09-369-364A-12

Alignment Scores:
Pred. No.: 578 Length: 5804
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.86% Indels: 0
Gaps: 0

US-10-059-395-142_COPY_29_99 (1-71) x US-09-369-364A-12 (1-5804)

Cy 45 |||LySArGLySLeuProPhe 51
Db 2959 ATCAAGAGAAAGTTACCAATTC 2979

RESULT 11
US-09-852-067-3
; Sequence 3, Application US/09852067
; Patent No. 6531297
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1600897-CIP
; CURRENT APPLICATION NUMBER: US/09/852,067
; CURRENT FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 31208
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(31208)
; OTHER INFORMATION: n = A,T,C or G
US-09-852-067-3

Alignment Scores:
Pred. No.: 2.97e+03 Length: 31208
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.86% Indels: 0
Gaps: 0

US-10-059-395-142_COPY_29_99 (1-71) x US-09-852-067-3 (1-31208)

Cy 46 |||LySArGLySLeuProPheLeu 52
Db 24241 AAGAGAAAGTCCCTTCTTG 24261

RESULT 12
US-09-103-330-35
; Sequence 35, Application US/09103330A
; Patent No. 6319716
; GENERAL INFORMATION:

; APPLICANT: TIKOO, SURESH K.
; APPLICANT: BABIUX, LORNE A.
; APPLICANT: REDDY, POLICE S.
; TITLE OF INVENTION: ISOLATION OF MUTANTS IN THE E3 REGION OF THE
; TITLE OF INVENTION: BOVINE ADENOVIRUS GENOME AND THEIR USE IN VACCINES
; FILE REFERENCE: 293102002121
; CURRENT APPLICATION NUMBER: US/09/103,330A
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 08/880,234
; EARLIER FILING DATE: 1997-06-23
; EARLIER APPLICATION NUMBER: 08/164,292
; EARLIER FILING DATE: 1993-12-09
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 34446
; TYPE: DNA
; ORGANISM: Bovine adenovirus type 3
US-09-103-330-35

Alignment Scores:
Pred. No.: 3.28e+03 Length: 34446
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.86% Indels: 0
Gaps: 0

US-10-059-395-142_COPY_29_99 (1-71) x US-09-103-330-35 (1-34446)

Cy 62 |||LyLeuArgSerAlaThrPro 68
Db 14923 GGCCTACGTCAGCAACACCG 14943

RESULT 13
US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(15000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (15001)..(30000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (30001)..(45000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (45001)..(60000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (60001)..(75000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (75001)..(90000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (90001)..(105000)
; OTHER INFORMATION: n=a or c or g or t
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|--------------------|---------------------|
| LOCATION:          | (465001)..(480000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (480001)..(495000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (495001)..(510000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (510001)..(525000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (525001)..(540000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (540001)..(555000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (555001)..(570000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (570001)..(585000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (585001)..(600000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (600001)..(615000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (615001)..(630000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (630001)..(645000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (645001)..(660000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (660001)..(675000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (675001)..(690000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (690001)..(705000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (705001)..(720000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (720001)..(735000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (735001)..(750000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (750001)..(765000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (765001)..(780000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (780001)..(795000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (795001)..(810000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (810001)..(825000)  |
| OTHER INFORMATION: | -n=a or c or g or t |
| NAME/KEY:          | misc_feature        |
| LOCATION:          | (825001)..(840000)  |

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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (840001)..(855000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (855001)..(870000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (870001)..(885000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (885001)..(900000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature

Alignment Scores:
Pred. No.: 1.02e+05 Length: 1230025
Score: 7.00 Matches: 7
Percent: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.86% Indels: 0
DB: 4 Gaps: 0

US-10-059-395-142_COPY_29_99 (1-71) x US-09-198-452A-1 (1-1230025)

Qy 16 PheanThProPheteusn 22
Db 391689 TTCACACACATTTTGAAAT 391669

RESULT 14
US-08-916-421B-1/c
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Built et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco
Patent No. 6503729
TITLE OF INVENTION: jannaechi
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaechi
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t, c, or g
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (657203)..(657203)
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NAME/KEY: misc_feature
LOCATION: (674435)..(674435)
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NAME/KEY: misc feature  
LOCATION: (682442) .. (682442)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (713652) .. (713652)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (741684) .. (741684)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (779455) .. (779455)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (779676) .. (779676)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (855539) .. (855539)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (871619) .. (871619)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1084830) .. (1084830)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1096846) .. (1096846)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
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OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1130881) .. (1130881)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1310988) .. (1310988)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1313224) .. (1313224)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1349473) .. (1349473)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1349491) .. (1349491)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1470091) .. (1470091)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1569020) .. (1569020)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1602912) .. (1602912)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1603734) .. (1603734)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1637998) .. (1637998)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (1664854) .. (1664854)  
OTHER INFORMATION: n equals a, t, c, or g  
US-08-916-421B-1

Alignment Scores:  
Pred. No.: 1.34e+05  
Score: 7.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 9.86%  
DB: 4

Length: 1664976  
Matches: 7  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-08-916-421B-1 (1-1664976)  
QY 44 Ser1eLya9rgLysLeuPro 50  
DB 1134223 AGCATTAAGAGCAATTACT 1134203

RESULT 15  
US-08-335-583C-20  
Sequence 20, Application US/08335583C  
Patent No. 5693779  
GENERAL INFORMATION:  
APPLICANT: Moos Jr., Malcolm  
APPLICANT: Wang, Shouwan  
APPLICANT: Krinks, Marie  
TITLE OF INVENTION: PRODUCTION AND USE OF  
TITLE OF INVENTION: ANTI-DORSALIZING MORPHOGENETIC PROTEIN  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson and Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: USA  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,583C  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
IMMEDIATE SOURCE:  
LIBRARY: GENWORKS, X57234  
US-08-335-583C-20

Alignment Scores:  
Pred. No.: 27.1  
Score: 6.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 8.45%  
DB: 1

Length: 20  
Matches: 6  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-08-335-583C-20 (1-20)  
QY 62 GlyLeuA9gSer1aThr 67  
DB 3 GGACTTCGAAAGTCAACC 20

Sat Nov 29 17:52:39 2003

us-10-059-395-142\_copy\_29\_99.olt\_1.rmt

Page 10

Search completed: November 28, 2003, 12:18:00  
Job time : 309 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: November 28, 2003, 10:52:35 / Search time 1606 Seconds

(without alignments)  
1074.482 Million cell updates/sec

## SUMMARIES

29: gb\_gsa2:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Title: US-10-059-395-142\_COPY\_29\_99  
Perfect score: 71  
Sequence: 1 BEESTENYASRPEAFNTPF.....LNMDAPKXGHSATPDAQ 71

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Word size: 1

Total number of hits satisfying chosen parameters: 45562437

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Listing first 45 summaries

Command line parameters:

-MODBL=frame+ p2n model -DBV=xlh  
-O/cgpn2.1/USFTO.spool/US10059395/runat.25112003\_140844.7677/app\_query.fasta\_1.263  
-DB=EST -QFMT=fastap -SUFPTX=0.1 -rst -MTNMTCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=b1ts -STMT=1 -END=1 -MATRIX=oligo -TRANS=human40.cci -LIST=45  
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcio  
-NORM=ext -HSPSIZE=500 -MTLEN=0 -MAXLEN=200000000  
-USER=US10059395 @CGN 1.1 2810 @runat.25112003\_140844.7677 -NCPU=6 -ICPU=3  
-NO MAP -LANG=OTHER -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOC  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estlin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gsa\_hum:\*
- 18: em\_gsa\_inv:\*
- 19: em\_gsa\_pln:\*
- 20: em\_gsa\_vit:\*
- 21: em\_gsa\_fun:\*
- 22: em\_gsa\_mam:\*
- 23: em\_gsa\_mus:\*
- 24: em\_gsa\_pro:\*
- 25: em\_gsa\_rnd:\*
- 26: em\_gsa\_png:\*
- 27: em\_gsa\_vil:\*
- 28: gb\_gsa1:\*

| Result No. | Score | Match | Length | DB | ID       | Description         |
|------------|-------|-------|--------|----|----------|---------------------|
| 1          | 71    | 100.0 | 318    | 9  | AA586846 | AA586846 nm67e11.s  |
| 2          | 71    | 100.0 | 334    | 9  | AA297512 | AA297512 EST113061  |
| 3          | 71    | 100.0 | 339    | 9  | AA778414 | AA778414 zfi9e05.s  |
| 4          | 71    | 100.0 | 348    | 9  | AM238758 | AM238758 xp03e08.x  |
| 5          | 71    | 100.0 | 359    | 10 | BE466728 | BE466728 h224g06.x  |
| 6          | 71    | 100.0 | 362    | 9  | AI140605 | AI140605 qe05f03.x  |
| 7          | 71    | 100.0 | 373    | 9  | AA722694 | AA722694 z982b06.s  |
| 8          | 71    | 100.0 | 381    | 14 | W69108   | W69108 z444c04.s1   |
| 9          | 71    | 100.0 | 394    | 14 | W60320   | W60320 z429g01.s1   |
| 10         | 71    | 100.0 | 412    | 14 | W60268   | W60268 z429g01.s1   |
| 11         | 71    | 100.0 | 424    | 14 | W69083   | W69083 z444b06.s1   |
| 12         | 71    | 100.0 | 432    | 13 | EX112106 | EX112106 BX112106   |
| 13         | 71    | 100.0 | 432    | 13 | W69233   | W69233 z444c04.r1   |
| 14         | 59    | 83.1  | 431    | 14 | W69227   | W69227 z444b06.r1   |
| 15         | 58    | 81.7  | 413    | 9  | AA393296 | AA393296 zt74f05.x  |
| 16         | 57    | 80.3  | 345    | 9  | AI217565 | AI217565 qd43d02.x  |
| 17         | 56    | 78.9  | 241    | 9  | AA59589  | AA59589 nm64g08.s   |
| 18         | 53    | 74.6  | 359    | 10 | BG150312 | BG150312 7j98g03.x  |
| 19         | 51    | 71.8  | 334    | 9  | AI217587 | AI217587 qd43f04.x  |
| 20         | 43    | 60.6  | 345    | 9  | AA583942 | AA583942 nm64f07.s  |
| 21         | 43    | 60.6  | 376    | 14 | W95920   | W95920 ze08d01.r1   |
| 22         | 39    | 54.9  | 221    | 9  | AA584333 | AA584333 nm73a09.s  |
| 23         | 39    | 54.9  | 326    | 9  | AA297513 | AA297513 EST113062  |
| 24         | 37    | 52.1  | 358    | 9  | AM003825 | AM003825 wq83f12.x  |
| 25         | 37    | 52.1  | 377    | 9  | AA582988 | AA582988 nm72h02.s  |
| 26         | 35    | 49.3  | 330    | 14 | W95883   | W95883 ze08d01.s1   |
| 27         | 33    | 46.5  | 218    | 9  | AA398638 | AA398638 zt74f05.s  |
| 28         | 33    | 46.5  | 239    | 9  | AA595930 | AA595930 nm66a07.s  |
| 29         | 27    | 38.0  | 339    | 14 | W52030   | W52030 z413b01.s1   |
| 30         | 27    | 38.0  | 378    | 9  | AI184682 | AI184682 qd68b02.x  |
| 31         | 24    | 33.8  | 436    | 9  | AA260965 | AA260965 EOUK0243   |
| 32         | 24    | 33.8  | 436    | 9  | AV597545 | AV597545 AV597545   |
| 33         | 18    | 25.4  | 163    | 9  | AA776980 | AA776980 zfi23d05.s |
| 34         | 15    | 21.1  | 377    | 9  | AA260982 | AA260982 EOUK0196   |
| 35         | 14    | 19.7  | 421    | 9  | AV618771 | AV618771 AV618771   |
| 36         | 12    | 16.9  | 323    | 10 | BE715771 | BE715771 MR2-HT075  |
| 37         | 8     | 11.3  | 271    | 10 | BE701465 | BE701465 PM2-NN017  |
| 38         | 8     | 11.3  | 304    | 9  | AI894297 | AI894297 ms66b04.x  |
| 39         | 8     | 11.3  | 310    | 14 | CD036743 | CD036743 mgsu011xd  |
| 40         | 8     | 11.3  | 353    | 10 | BP366304 | BP366304 CM1-NT008  |
| 41         | 8     | 11.3  | 365    | 10 | BF735391 | BF735391 CM1-AN008  |
| 42         | 8     | 11.3  | 378    | 10 | BF522420 | BF522420 UI-R-C3-C  |
| 43         | 8     | 11.3  | 382    | 12 | BI881645 | BI881645 fm88g05.y  |
| 44         | 8     | 11.3  | 399    | 12 | BI881568 | BI881568 fm87c01.y  |
| 45         | 8     | 11.3  | 404    | 14 | R80137   | R80137 y195c09.r1   |

## ALIGNMENTS

RESULT 1  
AA586846/c 318 bp mRNA linear EST 26-SEP-1997  
LOCUS nm67e11.81 NCI\_CGAP\_Lar1 Homo sapiens cDNA clone IMAGE:1088972 3'  
DEFINITION mRNA sequence.  
AA586846  
ACCESSION AA586846  
VERSION AA586846.1 GI:2397660  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 318)

**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
**JOURNAL** Unpublished  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgaaps-remail.nih.gov  
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: Stratagene, Inc.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLW at:  
[www-bio.lnl.gov/bbrip/image/image.html](http://www-bio.lnl.gov/bbrip/image/image.html)  
 Insert Length: 465 Std Error: 0.00  
 Seq primer: -40m3 fwd. RT from Amersham.

**FEATURES**  
 source  
 1. 318  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1088972"  
 /tissue\_type="larynx"  
 /lab\_host="RSOR (kanamycin resistant)"  
 /clone\_lib="NCI-CGAP\_Lar1"  
 /note="Organ: larynx; Vector: Bluescript SK-; Site: 1:  
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:  
 3' 3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'  
 Average insert size: 0.9 kb."

**BASE COUNT** 76 a 67 c 90 g 85 t

**ORIGIN**

**Alignment Scores:**

| Pred. No.:             | Length:  | Matches:      | 318 |
|------------------------|----------|---------------|-----|
| Score:                 | 5.07e-68 | 71.00         | 71  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 9        | Gaps:         | 0   |

US-10-059-395-142\_COPY\_29\_99 (1-71) x AA586846 (1-318)

**Qy** 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20

**Db** 316 GAGGAGAAAGACACCATTCGATGATATGCTCAGACCGAGCGCTTAAACACCCCGTTC 257

**Qy** 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnThrPheAla 40

**Db** 256 CTGAACATCGACCAATTGCGATCGCTTAAAGGCTGATGAGTTCCTGAACCTGGACACGCC 197

**Qy** 41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnTyrPheAlaPheProIysLeu 60

**Db** 196 CTCCTTAGCTATCAAAAGAAAGAACTTCCTTCCCACTGGATGCTTCCTTAAGCTG 137

**Qy** 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71

**Db** 136 AAAGAGCTGAGAGCGCACTCGATGCCAG 104

**RESULT 2**

**AA297512** LOCUS AA297512 334 bp mRNA linear EST 18-APR-1997

**DEFINITION** EST113061 Fetal skin Homo sapiens cDNA 5' end, mRNA sequence.

**ACCESSION** AA297512

**VERSION** AA297512.1 GI:1949866

**KEYWORDS** EST.

**SOURCE** Homo sapiens (human)

**ORGANISM** Homo sapiens

**REFERENCE** 1 (bases 1 to 334)

**AUTHORS** Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulmer, R.A., Bult,  
 C.J., Lee, N.H., Kinkness, E.F., Weinstein, K.G., Gocayne, J.D., White

**TITLE** Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (6547 Suppl), 3-174 (1995)

**JOURNAL** MEDLINE 96026280

**PUBMED** 7566098

**COMMENT** Other ESTs: TH0151622  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.

**FEATURES**  
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 1. 334  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /db\_xref="tacc:141532"  
 /db\_xref="taxon:9606"  
 /tissue\_type="epithelium"  
 /cell\_type="epithelial cell"  
 /dev\_stage="fetus"  
 /clone\_lib="Fetal skin"  
 /note="Organ: skin; Vector: pBluescript SK-; Site: 1:  
 EcoRI; Site 2: XhoI"

**BASE COUNT** 77 a 100 c 78 g 78 t 1 others

**ORIGIN**

**Alignment Scores:**

| Pred. No.:             | Length:  | Matches:      | 334 |
|------------------------|----------|---------------|-----|
| Score:                 | 5.35e-68 | 71.00         | 71  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 9        | Gaps:         | 0   |

US-10-059-395-142\_COPY\_29\_99 (1-71) x AA297512 (1-334)

**Qy** 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20

**Db** 98 GAGGAGAAAGACACCATTCGATGATATGCTCAGACCGAGCGCTTAAACACCCCGTTC 157

**Qy** 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnThrPheAla 40

**Db** 158 CTGAACATCGACCAATTGCGATCGCTTAAAGGCTGATGAGTTCCTGAACCTGGACACGCC 217

**Qy** 41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnTyrPheAlaPheProIysLeu 60

**Db** 218 CTCCTTAGCTATCAAAAGAAAGAACTTCCTTCCCACTGGATGCTTCCTTAAGCTG 277

**Qy** 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71

**Db** 278 AAAGAGCTGAGAGCGCACTCGATGCCAG 310



RESULT 3  
AA778414/c 339 bp mRNA linear EST 05-FEB-1998  
LOCUS AA778414  
DEFINITION z139605.b1 Soares fetal heart\_NBHL19W Homo sapiens cDNA clone  
IMAGE:379328 3', mRNA sequence.  
ACCESSION AA778414  
VERSION AA778414  
KEYWORDS GI:2837745  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Hillier, L., Allen, M., Bowles, J., Dubuque, T., Geisel, G., Joet, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Scheinberg, R., Steptoe, M., Tan, F., Theisling, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.  
TITLE WashU-NCI human EST Project  
JOURNAL Unpublished  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -40ml3 fwd. 5T from AmerSham.  
Location/Qualifiers  
1. .339  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1287584"  
/db\_xref="taxon:9606"  
/clone="IMAGE:379328"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_idb="Soares\_fetal\_heart\_NBHL19W"  
/note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTACCAATCGAAGTGGAGCGGCGCATCTTTTCTTTTCTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Patima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."

BASE COUNT 79 a 77 c 96 g 87 t  
ORIGIN

Alignment Scores:  
Pred. No.: 5.44e-68 Length: 339  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AA778414 (1-339)

QY 1 GUGUGUGUSeThrllGUAenTYrAlaSerArGProGUAlaPhaenAnThrPrope 20  
Db 316 GAGGAAGAAAGCAACATTGAGATTATGCTCAGACCCGAGCCCTTTAACAACCCGCTTC 257  
QY 21 LeuAenllleAspLySleuArGSerAlaPhelyAlaAAspGUlPheluAnThrPhisAla 40  
Db 256 CTGAACATCAACAATTCATCTGCGTTTAAAGCTGATAGTCCCGAAGCTGACGCGC 197  
QY 41 LeuPhelGluSerllelySArgLySleuProPheluAnThrPhaSpAlaPhepPolySleu 60

RESULT 4  
AW238758 348 bp mRNA linear EST 13-DEC-1999  
LOCUS AW238758  
DEFINITION xp03e08.x1 NCI\_CGAP\_HN8 Homo sapiens cDNA clone IMAGE:2739302 3', mRNA sequence.  
ACCESSION AW238758  
VERSION AW238758.1 GI:6571147  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 348)  
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb-r@mail.nih.gov  
Tissue Procurement: Edward Shillitoe Ph.D., Silvio Gutkind Ph.D., Chidcharok Leethanakul D.D.S., Michael Emmerit-Buck M.D. Ph.D.  
cDNA Library Preparation: David B. Krizman, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html  
Possible reversed clone: polyT not found  
Seq primer: -40UP from Gibco  
High quality sequence stop: 331.  
Location/Qualifiers  
1. .348  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2739302"  
/tissue\_type="well-differentiated invasive carcinoma, floor of mouth"  
/lab\_host="DH10B"  
/clone\_idb="NCI CGAP HN8"  
/note="Vector: pAMP10; cDNA made by oligo-dT priming. Non-directionally cloned into the UDG sites of pAMP10. Size-selected on agarose gel, average insert size 500 bp. Primary library; non-amplified. cDNA library Preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 82 a 104 c 84 g 78 t  
ORIGIN

Alignment Scores:  
Pred. No.: 5.6e-68 Length: 348  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AW238758 (1-348)

QY 1 GUGUGUGUSeThrllGUAenTYrAlaSerArGProGUAlaPhaenAnThrPrope 20  
Db 81 GAGGAAGAAAGCAACATTGAGATTATGCTCAGACCCGAGCCCTTTAACAACCCGCTTC 140  
QY 21 LeuAenllleAspLySleuArGSerAlaPhelyAlaAAspGUlPheluAnThrPhisAla 40

Db 141 CTGAACATCGACAAATTGGATCGCTTTAGAGCTGATGAGTTCCTGAACTGACGCC 200  
Qy Leuphegiuseri1eysarglyseupropheleuantiPaspAlaPheProlyseu 60  
Db 201 CTCCTTGAGTCTATCAAAAGAACTTCTTCTTCACTGGAGTCCCTTCTTAAGCTG 260  
Qy 61 LysGlyLeuAysSerAlaThrProAspAlaGln 71  
Db 261 AAAGACTGAGAGCGCAACTCTGATGCCAG 293

RESULT 5  
BE466728/c 359 bp mRNA linear EST 27-JUL-2000  
LOCUS h224906.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:3208954.3',  
DEFINITION mRNA sequence.  
ACCESSION BE466728  
VERSION BE466728.1 GI:9512503  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
1 (bases 1 to 359)  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher A. Meskalk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov  
Seq primer: -40UP from Gibco.  
Location/Qualifiers  
FEATURES  
source 1..359  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3208954"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_GC6"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA  
from the normalized library NCI\_CGAP GC4 was prepared, and  
as circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (clone1b  
1257096-1258631, 1469064-1470983, and 1475592-1476743).  
Subtraction by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 77 a 80 c 96 g 106 t  
ORIGIN

Alignment Scores:  
Pred. No.: 5,79e-68 Length: 359  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x BE466728 (1-359)

Qy 1 GtuglugluserThrilleglulantYralaserArgProglualaPheanthrPrope 20  
Db 332 GAGGAGAAAGCACTTGAATTAATGCGTCAAGACCGAGGCTTTAAACCCCGTTC 273

Qy 21 Leuan11eApy1eAysSerAlaPheYsAlaSpGluPheLeuAenTriPhisAla 40  
Db 272 CTGAACATCGACAAATTGGATCGCTTTAGAGCTGATGAGTTCCTGAACTGACGCC 213  
Qy 41 Leuphegiuseri1eysarglyseupropheleuantiPaspAlaPheProlyseu 60  
Db 212 CTCCTTGAGTCTATCAAAAGAACTTCTTCTTCACTGGAGTCCCTTCTTAAGCTG 153  
Qy 61 LysGlyLeuAysSerAlaThrProAspAlaGln 71  
Db 152 AAAGACTGAGAGCGCAACTCTGATGCCAG 120

RESULT 6  
A1140605/c 362 bp mRNA linear EST 29-OCT-1998  
LOCUS qe05f03.x1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1738109  
DEFINITION 3', mRNA sequence.  
ACCESSION A1140605  
VERSION A1140605.1 GI:3648062  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
1 (bases 1 to 362)  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert length: 425 Std Error: 0.00  
Seq primer: -40m13 fwd, RT from Amersham.  
Location/Qualifiers  
FEATURES  
source 1..362  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1738109"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares testis NHT"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech Laboratories  
, Inc., and primed with a Not I oligo(dT) primer [5'  
TGTTACCAATGTAAGTGGAGCGCGCCCAATTTTCTTTTCTTTT  
3']  
Double-stranded cDNA was ligated to Eco RI adaptor  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 77 a 81 c 99 g 105 t  
ORIGIN

Alignment Scores:  
Pred. No.: 5,84e-68 Length: 362  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x A1140605 (1-362)

QY 1 GluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
 DB 331 GAGGAGAAAGCACCATTGATGATTCACGACCCGACCTTTAAACCCCGTTC 272  
 QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPhe 40  
 DB 271 CTGAAATGACAAATGTCATCGCGTTTAAGCTGATGATGATTCCTGAACCTGACGCGC 212  
 QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrAspAlaPheProLysLeu 60  
 DB 211 CTTTGAAGCTATCAAAAGAAACCTTCCTTCTCAACCTGATGATGATTCCTTAAGCTG 152  
 QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
 DB 151 AAAGACTGAGGAGCGCACTCTGATGCCAG 119

RESULT 7  
 AA722694 373 bp mRNA linear EST 02-JAN-1998  
 LOCUS ZG82B06.s1 Soares fetal heart\_NbH19W Homo sapiens cDNA clone  
 DEFINITION IMAGE:399827.3, mRNA sequence.  
 ACCESSION AA722694  
 VERSION AA722694.1 GI:2740401  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,  
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
 White, Y., Mytle, T., Waterston, R., and Wilson, R.  
 WashU-NCI human EST Project  
 Unpublished  
 CONTACT: Wilson RK  
 WASHINGTON UNIVERSITY School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seg primer: -40m3 fwd. RT from Amersham.  
 Location/Qualifiers  
 1..373  
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 /mol\_type="mRNA"  
 /db\_xref="GDB:1307650"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:399827"  
 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_1lb="Soares fetal heart\_NbH19W"  
 /note="Organ: heart; Vector: pFRT3D (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo (dT) primer [5'  
 TGTTCACATCTGAGAGTGAGCGGCGCATCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pFRT3 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed from the  
 same fetus as the fetal lung library, Soares fetal lung  
 NbH19W."\*

BASE COUNT 89 a 81 c 113 g 90 t  
 ORIGIN

Alignment Scores: 6.04e-68 Length: 373  
 Pred. No.: 71.00 Matches: 71  
 Score:

Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AA722694 (1-373)

QY 1 GluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
 DB 319 GAGGAGAAAGCACCATTGATGATTCACGACCCGACCTTTAAACCCCGTTC 260  
 QY 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPhe 40  
 DB 259 CTGAAATGACAAATGTCATCGCGTTTAAGCTGATGATGATTCCTGAACCTGACGCGC 200  
 QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrAspAlaPheProLysLeu 60  
 DB 199 CTTTGAAGCTATCAAAAGAAACCTTCCTTCTCAACCTGATGATGATTCCTTAAGCTG 140  
 QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
 DB 139 AAAGACTGAGGAGCGCACTCTGATGCCAG 107

RESULT 8  
 W69108 381 bp mRNA linear EST 16-OCT-1996  
 LOCUS ZD44C04.s1 Soares fetal heart\_NbH19W Homo sapiens cDNA clone  
 DEFINITION IMAGE:343494.3, mRNA sequence.  
 ACCESSION W69108  
 VERSION W69108.1 GI:1378389  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Hillier, L., Clark, N., Dubuque, T., Ellstrom, K., Hawkins, M., Holman  
 W., Hultman, M., Kucaba, T., Le, N., Lennon, G., Marra, M., Parsons, J.,  
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, R., Waterston  
 R., Williamson, A., Wohlmann, P. and Wilson, R.  
 The WashU-Merck EST Project  
 Unpublished  
 CONTACT: Wilson RK  
 WASHINGTON UNIVERSITY School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert length: 442 Std Error: 0.00  
 Seg primer: mob. REGA+ET  
 High quality sequence strop: 347.  
 Location/Qualifiers  
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 /sex="unknown"  
 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_1lb="Soares fetal heart\_NbH19W"  
 /note="Organ: heart; Vector: pFRT3D (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo (dT) primer [5'  
 TGTTCACATCTGAGAGTGAGCGGCGCATCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pFRT3 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by

M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbH19W."
 

| BASE COUNT | 91 a | 86 c | 114 g | 89 t | 1 others |
|------------|------|------|-------|------|----------|
|------------|------|------|-------|------|----------|

Alignment Scores:

| Pred. No.:             | 6,18e-68 | Length:       | 381 |
|------------------------|----------|---------------|-----|
| Score:                 | 71.00    | Matches:      | 71  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 14       | Gaps:         | 0   |

US-10-059-395-142\_COPY\_29\_99 (1-71) x W69108 (1-381)

QY 1 GUGUGUGUSeThrlleGIUasntYrAlaseraPrGloUalAphaeantThrProPhe 20  
 Db 317 GAGGAGAAAGCACCATTGAGATTATGCGTCACACCGAGCCCTTTAACACCCCGTTC 258  
 QY 21 LeuAnilleaApLyLeuAryGserAlaPheLySaLaapGluPheLeuAnTrPHisAla 40  
 Db 257 CTGAACATCGACCAATTGCGATCTCGTTTAAGCTGATGACTCTGTAACCTGACAGCC 198  
 QY 41 LeuphegiuSerilleYsaryGlyLeuProPheLeuAnTrpAspAlaPheProLySleu 60  
 Db 197 CTCTTGAGTCTATCAAAAGAACTCTCTTCTCACTGGAGGAGCCCTTCTTAAGCTG 138  
 QY 61 LySGlyLeuAryGserAlaThrProAspAlaGln 71  
 Db 137 AAAGAGCTGAGAGCGCAACTCTGATGCCAG 105

RESULT 9  
 W60320 394 bp mRNA linear EST 15-OCT-1996  
 LOCUS zd29g01.81 Soares fetal heart NbH19W Homo sapiens cDNA clone  
 DEFINITION IMAGE:342096 3', mRNA sequence.  
 W60320  
 VERSION W60320.1 GI:1367079  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
 The WashU-Merck EST Project  
 Unpublished

TITLE  
 JOURNAL  
 COMMENT  
 CONTACT: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 476 Std Error: 0.00  
 Seq primer: mob.REGA+RT.  
 Location/Qualifiers

FEATURES  
 source

1..394  
 /organism="Homo sapiens"  
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 /clone="IMAGE:342096"  
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 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
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 /note="Organ: heart; Vector: pT73D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTACCAATCTGAGGAGCGGCGGCGATCTTTTCTTTTCTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbH19W."
 

| BASE COUNT | 94 a | 88 c | 119 g | 91 t | 2 others |
|------------|------|------|-------|------|----------|
|------------|------|------|-------|------|----------|

Alignment Scores:

| Pred. No.:             | 6.41e-68 | Length:       | 394 |
|------------------------|----------|---------------|-----|
| Score:                 | 71.00    | Matches:      | 71  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 14       | Gaps:         | 0   |

US-10-059-395-142\_COPY\_29\_99 (1-71) x W60320 (1-394)

QY 1 GUGUGUGUSeThrlleGIUasntYrAlaseraPrGloUalAphaeantThrProPhe 20  
 Db 320 GAGGAGAAAGCACCATTGAGATTATGCGTCACACCGAGCCCTTTAACACCCCGTTC 261  
 QY 21 LeuAnilleaApLyLeuAryGserAlaPheLySaLaapGluPheLeuAnTrPHisAla 40  
 Db 260 CTGAACATCGACCAATTGCGATCTCGTTTAAGCTGATGACTCTGTAACCTGACAGCC 201  
 QY 41 LeuphegiuSerilleYsaryGlyLeuProPheLeuAnTrpAspAlaPheProLySleu 60  
 Db 200 CTCTTGAGTCTATCAAAAGAACTCTCTTCTCACTGGAGGAGCCCTTCTTAAGCTG 141  
 QY 61 LySGlyLeuAryGserAlaThrProAspAlaGln 71  
 Db 140 AAAGAGCTGAGAGCGCAACTCTGATGCCAG 108

RESULT 10  
 W60268 412 bp mRNA linear EST 15-OCT-1996  
 LOCUS zd29g01.r1 Soares fetal heart NbH19W Homo sapiens cDNA clone  
 DEFINITION IMAGE:342096 5', mRNA sequence.  
 W60268  
 VERSION W60268.1 GI:1367169  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
 The WashU-Merck EST Project  
 Unpublished  
 CONTACT: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 476 Std Error: 0.00  
 Seq primer: mob.REGA+RT  
 High quality sequence stop: 385.  
 Location/Qualifiers

FEATURES  
 source

1..412

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/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_1ib="Soares fetal heart NbH19w"
/note="Organ: heart; Vector: pT7T3 (pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (dT) primer (5' GTTATCCATCATCATGAGGAGACGGCCGACATCTTTTCTTTTCTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapter (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbH19w."

```

TITLE  
Journal  
COMMENT

Radelof, U., Schneider, D. and Korn, B.  
Human Unigeneset - RZPD3  
Unpublished  
Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGp998D01781.  
RZPDlib; I.M.A.G.E. CDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDlib No. 972)  
http://www.rzpd.de/cloneCards/cgi-bin/showlib.pl.cgi/response=libNo=972 Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heidenweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de

This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r, Primer sequence: TTTCCACAGAGAAACGCTATGAC.  
Location/Qualifiers

## FEATURES

source

1. 432  
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/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal heart NBH19W"  
/note="Organ: heart; Vector: pTR73D (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCATCTGAGTGGAGCGCGCGCATCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pTR73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library was constructed from the  
M. Fatima Bonaldo. This library was constructed from the  
same fetus as the fetal lung library, Soares fetal lung  
NBH19W."

BASE COUNT 113 a 129 c 92 g 98 t  
ORIGIN

## Alignment Scores:

Pred. No.: 7,08e-68 Length: 432  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x BX112106 (1-432)

QY 1 GUGUGUGUSeThrTlEGUaSnTYrAlaSeArpProGUAlaPheAsnThrProPhe 20  
DB 99 GAGGAGAGAAAGCACCTTGAATTATGCGTCACGACCGGAGCCCTTTAAACCCCGTTC 158  
QY 21 LeuAniIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAniTrpHisAla 40  
DB 159 CTGAACATCGACAAATTGCGATCTGCGTTTAAGCTGAGTAGAGTCTCTGAACGCGACGCC 218  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAniTrpAspAlaPheProLysLeu 60  
DB 219 CTCCTTGAGTCATCAAAAGAAATCTTCCTTCTCACTGGGATGCCCTTTCTTAAGCG 278  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 279 AAAGGACTGAGGAGCGCAACTCTGATGCCAG 311

RESULT 13  
W69233  
LOCUS W69233 432 bp mRNA linear EST 16-OCT-1996

DEFINITION z44c04.i1 Soares fetal heart NBH19W Homo sapiens CDNA clone  
IMAGE:343494 5', mRNA sequence.  
ACCESSION W69233  
VERSION W69233.1 GI:1378493  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 432)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, R., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

The Washu-Merc EST Project

Unpublished

JOURNAL

TITLE

COMMENT

source

Contact: Wilson R.  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert Length: 442 Std Error: 0.00  
Seq primer: mob. REGA+ET  
High quality sequence stop: 341.  
Location/Qualifiers

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/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal heart NBH19W"  
/note="Organ: heart; Vector: pTR73D (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCATCTGAGTGGAGCGCGCGCATCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pTR73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library was constructed by  
M. Fatima Bonaldo. This library was constructed from the  
same fetus as the fetal lung library, Soares fetal lung  
NBH19W."

BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN

## Alignment Scores:

Pred. No.: 7,08e-68 Length: 432  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x W69233 (1-432)

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DB 96 GAGGAGAGAAAGCACCTTGAATTATGCGTCACGACCGGAGCCCTTTAAACCCCGTTC 155  
QY 21 LeuAniIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAniTrpHisAla 40  
DB 156 CTGAACATCGACAAATTGCGATCTGCGTTTAAGCTGAGTAGAGTCTCTGAACGCGACGCC 215  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAniTrpAspAlaPheProLysLeu 60

Db 216 CTCTTGAGTCTATCAAAAGAACTTCTTCTCAACTGGATGCTTCTTAAGCTG 275  
Qy 61 LYGGLYLEUARGSERIATHRPROASPALAGIN 71  
Db 276 AAAGACTGAGAGCCGCACTCTGATGCCCA 308

RESULT 14  
LOCUS M69227 431 bp mRNA linear EST 16-OCT-1996  
DEFINITION Z44D06.r1 Soares fetal heart\_NDH19W Homo sapiens CDNA clone  
IMAGE:343475 5', mRNA sequence.  
M69227  
W69227.1 GI:1378487  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 431)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman  
M., Hultman, M., Kucada, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston  
R., Williamson, A., Wohlmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LML; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
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Seq primer: mob.RGGA+ET  
High quality sequence stop: 410.

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/db\_xref="taxon:9606"  
/clone="IMAGE:343475"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo (dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCCATCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by  
M. Fatima Bonaldo. This library was constructed from the  
same fetus as the fetal lung library, Soares fetal lung  
NH19W."

BASE COUNT 106 a 127 c 94 g 102 t 2 others  
ORIGIN

Alignment Scores:  
Pred. No.: 1.07e-54 Length: 431  
Score: 59.00 Matches: 59  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 83.10% Indels: 0  
DB: 14 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x W69227 (1-431)  
Qy 13 Proglu1alphaenThrProPheLeuAsn1LeAspLyLeuArgSerAlaPheLyAla 32

Db 134 CCCAGGCCCTTTACACCCCGTTCTGAAACATGCAAAATTCGATCTCGTTAAGGCT 193  
Qy 33 ASPLGLPHELEUANTPRPHISALALEUPHGLUSERILEYARGLYSEUPROPELEU 52  
Db 194 GATGAGTCTCTGACACGACGCGCCCTTTGAGTCTATCAAAAGAAACTCTTCTTC 253

Qy 53 AERTTPASPALAPHEROLYSEULYGLYLEUARGSERIATHRPROASPALAGIN 71  
Db 254 AACTGGATGCCCTTCTTAAGCTGAAGAAGACTGAGAGCGCAACTCTGATGCCAG 310

RESULT 15  
LOCUS AA393296 413 bp mRNA linear EST 16-MAY-1997  
DEFINITION Z474F05.r1 Soares testis\_NHT Homo sapiens CDNA clone IMAGE:728097  
5', mRNA sequence.  
AA393296  
AA393296.1 GI:2046264  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 413)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Kucada, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,  
Schellenberg, K., Stepec, M., Tan, F., Theising, B., White, Y., Wylie  
T., Waterston, R. and Wilson, R.  
WashU-Merck EST Project 1997  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LML; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -28m13 rev2 ET from Amersham  
High quality sequence stop: 386.

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/sex="male"  
/lab\_host="DH10B"  
/note="Organ: testis\_NHT"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech Laboratories  
, Inc. and primed with a Not I - oligo (dT) primer [5'  
TGTTCAATCTGAAGTGGAGCGCGCCCAATCTTTTCTTTTCTTTT 3']  
Double-stranded cDNA was ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bonto Soares and M. Fatima Bonaldo."

BASE COUNT 96 a 113 c 125 g 79 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1.28e-53 Length: 413  
Score: 58.00 Matches: 71  
Percent Similarity: 98.61% Conservative: 0  
Best Local Similarity: 98.61% Mismatches: 0  
Query Match: 81.69% Indels: 1  
DB: 9 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AA393296 (1-413)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrPro-PH 20  
Db 164 GAGGAAAGAAAGCACCATTGAGATTATGCTCAGACCCGAGGCTTTAACACCCCGATT 223  
QY 20 eleuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnThrPheAl 40  
Db 224 CCTGACATCGACAAATTGCGATTGCGTTAAGGCTGATGAGTTCCTGAACCTGGCACGC 283  
QY 40 aleuPheGluSerIleIysArgIysLeuProPheLeuAsnThrAspAlaPheProIysLe 60  
Db 284 CCTCTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGGATGCCCTTCTTAAGCT 343  
QY 60 uIysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 344 GAAAGACTGAGAGCGCACTCTGATGCCAG 377

Search completed: November 28, 2003, 12:12:46  
Job time : 1608 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:38:12, Search time 21 Seconds  
(without alignments)  
143.051 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 375  
Sequence: 1 EEESTIENYASRPEAFNTF.....LNWDAFPKLGKRSATPPAQ 71

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:\*

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2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
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4: /cgn2\_6/prodata/2/1aa/6B\_COMB.pep:\*  
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6: /cgn2\_6/prodata/2/1aa/backfillseq.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                             |
|------------|-------|-------------|--------|-------|---|
| 1          | 375   | 100.0       | 99     | 4     | US-09-996-243-201 Sequence 201, App     |
| 2          | 59.5  | 15.9        | 233    | 4     | US-09-328-352-6059 Sequence 6059, Ap    |
| 3          | 59    | 15.7        | 324    | 4     | US-08-311-731A-252 Sequence 262, App    |
| 4          | 56.5  | 15.1        | 518    | 3     | US-08-399-723-2 Sequence 2, Appl1       |
| 5          | 56.5  | 15.1        | 518    | 3     | US-09-434-427-2 Sequence 2, Appl1       |
| 6          | 56.5  | 15.1        | 518    | 4     | US-09-548-372D-2 Sequence 2, Appl1      |
| 7          | 56.5  | 15.1        | 518    | 4     | US-09-548-367D-2 Sequence 2, Appl1      |
| 8          | 56.5  | 15.1        | 518    | 4     | US-09-551-853D-2 Sequence 2, Appl1      |
| 9          | 56    | 14.9        | 400    | 4     | US-09-150-347-1 Sequence 1, Appl1       |
| 10         | 56    | 14.9        | 400    | 4     | US-09-665-313-1 Sequence 1, Appl1       |
| 11         | 55    | 14.7        | 513    | 4     | US-09-595-857B-30 Sequence 30, Appl1    |
| 12         | 54.5  | 14.5        | 186    | 1     | US-08-117-083-22 Sequence 6996, Ap      |
| 13         | 54    | 14.4        | 285    | 4     | US-08-290-301-82 Sequence 82, Appl      |
| 14         | 54    | 14.4        | 1098   | 1     | US-08-290-301-82 Sequence 82, Appl      |
| 15         | 54    | 14.4        | 1098   | 4     | US-09-013-598-82 Sequence 82, Appl      |
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| 17         | 53.5  | 14.3        | 634    | 4     | US-09-134-001C-3891 Sequence 2, Appl1   |
| 18         | 53.5  | 14.3        | 853    | 5     | PCT-US92-09326-2 Sequence 46, Appl1     |
| 19         | 53    | 14.1        | 187    | 3     | US-08-981-392-46 Sequence 5386, Ap      |
| 20         | 53    | 14.1        | 192    | 4     | US-09-134-001C-5386 Sequence 7009, Ap   |
| 21         | 53    | 14.1        | 373    | 4     | US-09-328-352-7009 Sequence 19274, A    |
| 22         | 53    | 14.1        | 401    | 4     | US-09-352-991A-19274 Sequence 101, Appl |
| 23         | 53    | 14.1        | 693    | 4     | US-08-705-477E-101 Sequence 18, Appl1   |
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| 25         | 53    | 14.1        | 707    | 5     | PCT-US95-11720-18 Sequence 2, Appl1     |
| 26         | 53    | 14.1        | 750    | 1     | US-08-325-553-2 Sequence 2, Appl1       |
| 27         | 53    | 14.1        | 750    | 2     | US-08-394-152A-2 Sequence 2, Appl1      |

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| 29 | 53   | 14.1 | 750  | 4 | US-08-705-477E-2 Sequence 2, Appl1     |
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| 32 | 53   | 14.1 | 2206 | 1 | US-07-852-260-2 Sequence 2, Appl1      |
| 33 | 53   | 14.1 | 2206 | 2 | US-08-461-503-2 Sequence 2, Appl1      |
| 34 | 53   | 14.1 | 2206 | 3 | US-08-465-250-2 Sequence 32165, A      |
| 35 | 52.5 | 14.0 | 382  | 4 | US-09-252-991A-32165 Sequence 4516, Ap |
| 36 | 52.5 | 14.0 | 825  | 4 | US-08-451-946B-6 Sequence 6, Appl1     |
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| 39 | 52.5 | 14.0 | 853  | 3 | US-08-311-703A-6 Sequence 6, Appl1     |
| 40 | 52.5 | 14.0 | 853  | 3 | US-08-446-938B-6 Sequence 6, Appl1     |
| 41 | 52.5 | 14.0 | 853  | 3 | US-08-183-543-6 Sequence 6, Appl1      |
| 42 | 52.5 | 14.0 | 853  | 3 | US-08-446-936A-6 Sequence 6, Appl1     |
| 43 | 52   | 13.9 | 235  | 3 | US-09-066-408-12 Sequence 12, Appl1    |
| 44 | 51.5 | 13.7 | 396  | 3 | US-08-961-083-16 Sequence 16, Appl1    |
| 45 | 51.5 | 13.7 | 396  | 4 | US-09-536-784-16 Sequence 16, Appl1    |

#### ALIGNMENTS

RESULT 1  
US-09-996-243-201  
Sequence 201, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavits, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P13  
CURRENT APPLICATION NUMBER: US/09/996,243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
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PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28

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| PRIOR APPLICATION NUMBER: | 60/090862  |
| PRIOR FILING DATE:        | 1998-06-26 |
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| PRIOR APPLICATION NUMBER: | 60/091360  |
| PRIOR FILING DATE:        | 1998-07-01 |
| PRIOR APPLICATION NUMBER: | 60/091478  |
| PRIOR FILING DATE:        | 1998-07-02 |
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| PRIOR FILING DATE:        | 1998-07-02 |
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| PRIOR FILING DATE:        | 1998-07-02 |
| PRIOR APPLICATION NUMBER: | 60/091633  |
| PRIOR FILING DATE:        | 1998-07-02 |

;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09  
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Best Local Similarity 100.0%; Pred. No. 2e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 60  
DB 29 EESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 88  
QY 61 KGLRSATPDQA 71  
DB 89 KGLRSATPDQA 99  
RESULT 2  
US-09-328-352-6059  
; Sequence 6059, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 6059  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-6059  
Query Match 15.9%; Score 59.5; DB 4; Length 233;  
Best Local Similarity 31.0%; Pred. No. 5.6;  
Matches 18; Conservative 12; Mismatches 21; Indels 7; Gaps 3;  
QY 3 EESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 56  
DB 166 QMWIDYAG--EEFTAVNVIVATVDKVARCDLTLEKHAAY-TMGAKLEWLPDS 220  
RESULT 3  
US-08-311-731A-262  
; Sequence 262, Application US/08311731A  
; Patent No. 6583266  
; GENERAL INFORMATION:  
; APPLICANT: SMITH, DOUGLAS  
; APPLICANT: MAO, JEN-1  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
; NUMBER OF SEQUENCES: 411  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
; STREET: 600 ATLANTIC AVENUE  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Releasee #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/311,731A  
; FILING DATE:

;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: GATES, EDWARD R.  
;; REGISTRATION NUMBER: 31,616  
;; REFERENCE/DOCKET NUMBER: C0044/7125  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617/720-3500  
;; TELEFAX: 617/720-2441  
;; INFORMATION FOR SEQ ID NO: 262:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 324 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: YES  
;; ORIGINAL SOURCE:  
;; ORGANISM: Mycobacterium leprae  
US-08-311-731A-262  
Query Match 15.7%; Score 59; DB 4; Length 324;  
Best Local Similarity 30.8%; Pred. No. 9.7;  
Matches 20; Conservative 11; Mismatches 26; Indels 8; Gaps 3;  
QY 11 SRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 64  
DB 62 SNLDSANIVFVDEDTSTYDGHIAIKLMDRADLQPIKR--DFIDTQGFSKLGR 119  
QY 65 SATPD 69  
DB 120 GISND 124  
RESULT 4  
US-08-999-723-2  
; Sequence 2, Application US/08999723A  
; Patent No. 6025180  
; GENERAL INFORMATION:  
; APPLICANT: Powell, David J.  
; APPLICANT: Southan, Christopher  
; APPLICANT: Chapman, Conrad G.  
; APPLICANT: Evans, Joanne R.  
; TITLE OF INVENTION: ASP1  
; FILE REFERENCE: GH70262  
; CURRENT APPLICATION NUMBER: US/08/999,723A  
; CURRENT FILING DATE: 1997-10-06  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-999-723-2  
Query Match 15.1%; Score 56.5; DB 3; Length 518;  
Best Local Similarity 29.5%; Pred. No. 37;  
Matches 18; Conservative 8; Mismatches 18; Indels 17; Gaps 2;  
QY 7 ENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPFKL 66  
DB 160 EDLVITPKGFNTSFL-----VNATIFESGNFPLPGIKKNG---ILGLAVA 202  
QY 67 T 67  
DB 203 T 203  
RESULT 5  
US-09-434-427-2  
; Sequence 2, Application US/09434427  
; Patent No. 6162630  
; GENERAL INFORMATION:  
; APPLICANT: POWELL, DAVID J.  
; APPLICANT: SOUTHAN, CHRISTOPHER

```

; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: EVANS, JOANNE R.
; TITLE OF INVENTION: ASP1
; FILE REFERENCE: GH-70262-D1
; CURRENT APPLICATION NUMBER: US/09/434,427
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 08/999,723
; EARLIER FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: US 06/999,723
; EARLIER FILING DATE: 1996-12-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-434-427-2

Query Match
Best Local Similarity 15.1%; Score 56.5; DB 3; Length 518;
Best Local Similarity 29.5%; Pred. No. 37;
Matches 18; Conservative 8; Mismatches 18; Indels 17; Gaps 2;

QY 7 ENVASRPEAFNTPTPLNDKLSAFKADFLNMHALFESIKRKLPLNDAPPKLGKLSA 66
DB 160 EDLVITPKGFNTSFL-----VNATTFESENFPLPKIKWG---ILGLAYA 202

QY 67 T 67
DB 203 T 203

RESULT 6
US-09-548-372D-2
; Sequence 2, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-2

Query Match
Best Local Similarity 15.1%; Score 56.5; DB 4; Length 518;
Best Local Similarity 29.5%; Pred. No. 37;
Matches 18; Conservative 8; Mismatches 18; Indels 17; Gaps 2;

QY 7 ENVASRPEAFNTPTPLNDKLSAFKADFLNMHALFESIKRKLPLNDAPPKLGKLSA 66
DB 160 EDLVITPKGFNTSFL-----VNATTFESENFPLPKIKWG---ILGLAYA 202

QY 67 T 67
DB 203 T 203

RESULT 7
US-09-548-367D-2
; Sequence 2, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-2

Query Match
Best Local Similarity 15.1%; Score 56.5; DB 4; Length 518;
Best Local Similarity 29.5%; Pred. No. 37;
Matches 18; Conservative 8; Mismatches 18; Indels 17; Gaps 2;

QY 7 ENVASRPEAFNTPTPLNDKLSAFKADFLNMHALFESIKRKLPLNDAPPKLGKLSA 66
DB 160 EDLVITPKGFNTSFL-----VNATTFESENFPLPKIKWG---ILGLAYA 202

QY 67 T 67
DB 203 T 203

RESULT 8
US-09-551-853D-2
; Sequence 2, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-2

Query Match
Best Local Similarity 15.1%; Score 56.5; DB 4; Length 518;
Best Local Similarity 29.5%; Pred. No. 37;
Matches 18; Conservative 8; Mismatches 18; Indels 17; Gaps 2;

QY 7 ENVASRPEAFNTPTPLNDKLSAFKADFLNMHALFESIKRKLPLNDAPPKLGKLSA 66
DB 160 EDLVITPKGFNTSFL-----VNATTFESENFPLPKIKWG---ILGLAYA 202

QY 67 T 67
DB 203 T 203
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QY 67 T 67  
Db 203 T 203

## RESULT 9

US-09-150-347-1  
; Sequence 1, Application US/09150347  
; Patent No. 6372269  
; GENERAL INFORMATION:  
; APPLICANT: Rangel-Aldao, Rafael  
; APPLICANT: Bravo, Adriana  
; APPLICANT: Sanchez, Beatriz  
; APPLICANT: Galindo-Castro, Ivan  
; TITLE OF INVENTION: Malt Beverage Having Stabilized Flavor and Methods of Production  
; TITLE OF INVENTION: Thereof  
; FILE REFERENCE: 1390.0070004  
; CURRENT APPLICATION NUMBER: US/09/150,347  
; CURRENT FILING DATE: 1998-09-09  
; EARLIER APPLICATION NUMBER: 60/058,398  
; EARLIER FILING DATE: 1997-09-09  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 400  
; TYPE: PRT  
; ORGANISM: Saccharomyces carlsbergensis  
US-09-150-347-1

Query Match 14.3%; Score 56; DB 4; Length 400;  
Best Local Similarity 23.9%; Pred. No. 31;  
Matches 17; Conservative 9; Mismatches 27; Indels 18; Gaps 3;

QY 6 IENYARPE-----AFNTPL-NIDKLSAFKADFLNWHALFESIKRKLPP---51  
Db 55 VEYTORAPRGMTITTEGAFISPOAGYDNAPGVSEQWVMTXIFNAIHEKKSFWVW 114  
QY 52 ----LNMWDAFP 58  
Db 115 QLMVLGMMAFP 125

## RESULT 10

US-09-665-313-1  
; Sequence 1, Application US/09665313  
; Patent No. 6468567  
; GENERAL INFORMATION:  
; APPLICANT: Rangel-Aldao, Rafael  
; APPLICANT: Bravo, Adriana  
; APPLICANT: Sanchez, Beatriz  
; APPLICANT: Galindo-Castro, Ivan  
; TITLE OF INVENTION: Malt Beverage Having Stabilized Flavor and Methods of Production  
; TITLE OF INVENTION: Thereof  
; FILE REFERENCE: 1390.0070004  
; CURRENT APPLICATION NUMBER: US/09/665,313  
; CURRENT FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 09/150,347  
; PRIOR FILING DATE: 1998-09-09  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 400  
; TYPE: PRT  
; ORGANISM: Saccharomyces carlsbergensis  
US-09-665-313-1

Query Match 14.3%; Score 56; DB 4; Length 400;  
Best Local Similarity 23.9%; Pred. No. 31;  
Matches 17; Conservative 9; Mismatches 27; Indels 18; Gaps 3;

QY 6 IENYARPE-----AFNTPL-NIDKLSAFKADFLNWHALFESIKRKLPP---51  
Db 55 VEYTORAPRGMTITTEGAFISPOAGYDNAPGVSEQWVMTXIFNAIHEKKSFWVW 114

QY 52 ----LNMWDAFP 58  
Db 115 QLMVLGMMAFP 125

## RESULT 11

US-09-595-857B-30  
; Sequence 30, Application US/09595857B  
; Patent No. 6495743  
; GENERAL INFORMATION:  
; APPLICANT: Pauli, Robert E.  
; APPLICANT: Chen, Nancy J.  
; TITLE OF INVENTION: PLANT XYLANASES  
; FILE REFERENCE: 234612001800  
; CURRENT APPLICATION NUMBER: US/09/595,857B  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/141,543  
; PRIOR FILING DATE: 1999-06-28  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-595-857B-30

Query Match 14.7%; Score 55; DB 4; Length 513;  
Best Local Similarity 21.2%; Pred. No. 57;  
Matches 14; Conservative 14; Mismatches 30; Indels 8; Gaps 2;

QY 2 EESTIENYSREAREPTPLNIDKLSAFKADFLNWHALFESIKRKLPPFLNMWDAFPK 61  
Db 268 QPSWKNIDPNDVNVVTLNRINSVWKRYKG-KLTGMDVNVN-----LHMDYFEKXVL 319  
QY 62 GLRSAT 67  
Db 320 GANAST 325

## RESULT 12

US-08-117-083-22  
; Sequence 22, Application US/08117083  
; Patent No. 5719054  
; GENERAL INFORMATION:  
; APPLICANT: Bourisnell, Michael E.  
; APPLICANT: Ingile, Stephen C.  
; APPLICANT: Munro, Alan J.  
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human  
; NUMBER OF SEQUENCES: 70  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Walter H. Dreger  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/117,083  
; FILING DATE: 10-SEP-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-58783  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989

```

; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 186 amino acids
; TYPE: amino acid
; STRANDEDNESS: double...
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-117-083-22

Query Match          14.5%; Score 54.5; DB 1; Length 186;
Best Local Similarity 24.5%; Pred. No. 19;
Matches 12; Conservative 10; Mismatches 8; Indels 19; Gaps 2;

QY 9 YASRPFA-----NTP-----FLINDLRSAFRADEFLNW 38
DB 22 FAEYPSFGFSVSTRTRRAGVNGKDYNFVSVDEFKSMIXNEFIEM 70

RESULT 13
US-09-328-352-6996
; Sequence 6996, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6996
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6996

Query Match          14.4%; Score 54; DB 4; Length 285;
Best Local Similarity 27.6%; Pred. No. 37;
Matches 16; Conservative 10; Mismatches 26; Indels 6; Gaps 1;

QY 16 FNTPTINTKLSAF-----KADEFLNHALFESIKRKLPLINDAFPKLQKLSAT 67
DB 4 FNNDYVVICMNSAFIKNGILKSLFPASTLSLTPVMAQATFLIPIYKIEANERAT 61

RESULT 14
US-08-290-301-82
; Sequence 82, Application US/08290301
; Patent No. 5792921
; GENERAL INFORMATION:
; APPLICANT: Londeborough, John
; APPLICANT: Tunnela, Outi
; APPLICANT: Palva, Tupio
; APPLICANT: Holmstrom, Kjell-Ove
; APPLICANT: Mandel, Bjorn
; APPLICANT: Mandel, Abul
; TITLE OF INVENTION: Increasing the trehalose content
; TITLE OF INVENTION: of organisms by transforming them with combinations of
; TITLE OF INVENTION: the structural genes for trehalose synthase.
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alko Ltd.
; STREET: PO Box 350
; CITY: Helsinki
; STATE:
; COUNTRY: Finland
; ZIP: SF-00101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 KB
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: PC-DOS

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; SOFTWARE: WP5.1 file exported as DOS text file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,301
; FILING DATE: 15 August 1994
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: FI 943133
; FILING DATE: 29 June 1994
; APPLICATION NUMBER: PCT/FI93/00049
; FILING DATE: 15 February 1993
; APPLICATION NUMBER: 07/841,997
; FILING DATE: 28 February 1992
; APPLICATION NUMBER: 07/836,021
; FILING DATE: 14 February 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubovcik, Ronald J.
; NAME: Lydon, James C.
; REGISTRATION NUMBER: 25,401
; REFERENCE/DOCKET NUMBER: 30,082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 467-6300
; TELEFAX: (202) 466-2006
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1098 amino acids
; TYPE: Amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Polypeptide
; HYPOTHEICAL: Yes
US-08-290-301-82

Query Match          14.4%; Score 54; DB 1; Length 1098;
Best Local Similarity 23.5%; Pred. No. 26+02;
Matches 16; Conservative 11; Mismatches 33; Indels 8; Gaps 1;

QY 3 ESTIENVASRPFAFNTPLINTDKLSAFKADEF-----LNMHALFESIKRKLPLINW 54
DB 287 ESDPDLTTAPDEEVSDLEMDDAKQDYKVPKFGYSNKSLLKKYALRSSQELFSRLPW 346

QY 55 DAFPLKLG 62
DB 347 STVPSIKG 354

RESULT 15
US-09-013-598-82
; Sequence 82, Application US/09013598
; Patent No. 6323001
; GENERAL INFORMATION:
; APPLICANT: Londeborough, John
; APPLICANT: Tunnela, Outi
; APPLICANT: Palva, Tupio
; APPLICANT: Holmstrom, Kjell-Ove
; APPLICANT: Mandel, Bjorn
; APPLICANT: Mandel, Abul
; TITLE OF INVENTION: Increasing the trehalose content
; TITLE OF INVENTION: of organisms by transforming them with combinations of
; TITLE OF INVENTION: the structural genes for trehalose synthase.
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alko Ltd.
; STREET: PO Box 350
; CITY: Helsinki
; STATE:
; COUNTRY: Finland
; ZIP: SF-00101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 KB
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WP5.1 file exported as DOS text file
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/013,598  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/290,301  
FILING DATE:  
APPLICATION NUMBER: PCT/FI93/00049  
FILING DATE: 15 February 1993  
APPLICATION NUMBER: 07/841,997  
FILING DATE: 28 February 1992  
APPLICATION NUMBER: 07/836,021  
FILING DATE: 14 February 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubovcik, Ronald J.  
NAME: Lydon, James C.  
REGISTRATION NUMBER: 25,401  
REFERENCE/DOCKET NUMBER: 30,082  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 467-6300  
TELEFAX: (202) 466-2006  
INFORMATION FOR SEQ. ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1098 amino acids  
TYPE: Amino acid  
TOPOLOGY: Linear  
MOLECULE TYPE: Polypeptide  
HYPOTHETICAL: Yes  
US-09-013-598-82

Query Match 14.4%; Score 54; DB 4; Length 1098;  
Best Local Similarity 23.5%; Pred. No. 2e+02;  
Matches 16; Conservative 11; Mismatches 33; Indels 8; Gaps 1;

QY 3 ESTIENYASRPPAFNTFFINIDKLSAFAQDEF-----LWHAALFESIKRKLPLFW 54  
DB 287 ESDPDDLTTAPDEYVSDLEMDAKQDYKVPKFGYSNRSKLKYYALRRSQELFSRLPW 346  
QY 55 DAFPKLKG 62  
DB 347 SIYPSIKG 354

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Job time : 24 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: November 28, 2003, 13:43:24 / Search time 2638 Seconds

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Title: US-10-059-395-142\_COPY\_29\_99

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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2: gb\_hcg: \*  
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6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_seg: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_ph: \*  
24: em\_pat: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_seg: \*  
28: em\_un: \*

29: em\_vl: \*  
30: em\_hcg\_hum: \*  
31: em\_hcg\_inv: \*  
32: em\_hcg\_other: \*  
33: em\_hcg\_mus: \*  
34: em\_hcg\_pln: \*  
35: em\_hcg\_rod: \*  
36: em\_hcg\_mam: \*  
37: em\_hcg\_vrt: \*  
38: em\_sy: \*  
39: em\_hcgo\_hum: \*  
40: em\_hcgo\_mus: \*  
41: em\_hcgo\_other: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | *<br>Query Match | Length | DB ID        | Description          |
|------------|-------|------------------|--------|--------------|----------------------|
| 1          | 375   | 100.0            | 414    | 6 AX055438   | AX055438 Sequence    |
| 2          | 375   | 100.0            | 415    | 6 AR252517   | AR252517 Sequence    |
| 3          | 375   | 100.0            | 415    | 6 AX077031   | AX077031 Sequence    |
| 4          | 375   | 100.0            | 415    | 6 AX358892   | AX358892 Sequence    |
| 5          | 375   | 100.0            | 415    | 6 AX362385   | AX362385 Sequence    |
| 6          | 375   | 100.0            | 415    | 6 AX403313   | AX403313 Sequence    |
| 7          | 375   | 100.0            | 415    | 6 AX454546   | AX454546 Sequence    |
| 8          | 375   | 100.0            | 415    | 6 AX491024   | AX491024 Sequence    |
| 9          | 375   | 100.0            | 415    | 6 AX574494   | AX574494 Sequence    |
| 10         | 375   | 100.0            | 432    | 6 AX080815   | AX080815 Sequence    |
| 11         | 375   | 100.0            | 432    | 6 AX080818   | AX080818 Sequence    |
| 12         | 375   | 100.0            | 456    | 6 BD082389   | BD082389 87 human    |
| 13         | 375   | 100.0            | 456    | 6 AX080817   | AX080817 Sequence    |
| 14         | 368   | 98.1             | 529    | 9 HSA293408  | AJ293408 Homo sapi   |
| 15         | 362   | 96.5             | 435    | 6 AX080816   | AX080816 Sequence    |
| 16         | 308   | 82.1             | 278    | 6 AX041085   | AX041085 Sequence    |
| 17         | 219.5 | 58.5             | 449    | 10 AB011028  | AB011028 Rattus no   |
| 18         | 210.5 | 56.1             | 288    | 6 AR248775   | AR248775 Sequence    |
| 19         | 109   | 29.1             | 44679  | 9 CH19F21246 | AD001502 Homo sapi   |
| 20         | 82.5  | 22.0             | 590    | 6 BD025234   | BD025234 Sequence    |
| 21         | 80    | 21.3             | 244844 | 2 AC120613   | AC120613 Rattus no   |
| 22         | 80    | 21.3             | 263584 | 2 AC099301   | AC099301 Rattus no   |
| 23         | 78.5  | 20.9             | 700    | 6 AX135555   | AX135555 Sequence    |
| 24         | 78.5  | 20.9             | 1000   | 9 BC011886   | BC011886 Homo sapi   |
| 25         | 78.5  | 20.9             | 1579   | 9 AC096215   | AC096215 Homo sapi   |
| 26         | 78.5  | 20.9             | 1982   | 9 BC035311   | BC035311 Homo sapi   |
| 27         | 78    | 20.8             | 156508 | 3 AC007581   | AC007581 Drosophila  |
| 28         | 78    | 20.8             | 171151 | 3 AC007574   | AC007574 Drosophila  |
| 29         | 78    | 20.8             | 310958 | 3 AE003464   | AE003464 Drosophila  |
| 30         | 74    | 19.7             | 680    | 6 AX602111   | AX602111 Sequence    |
| 31         | 74    | 19.7             | 2667   | 8 HVS5YMR    | X658671 H. vulgare m |
| 32         | 74    | 19.7             | 167878 | 8 AC096645   | AC096645 Homo sapi   |
| 33         | 73.5  | 19.6             | 9216   | 1 AB012868   | AB012868 Chlorobiu   |
| 34         | 73    | 19.5             | 243387 | 2 AC097151   | AC097151 Rattus no   |
| 35         | 73    | 19.5             | 267104 | 2 AC111694   | AC111694 Rattus no   |
| 36         | 73    | 19.5             | 303894 | 2 AC105854   | AC105854 Rattus no   |
| 37         | 72.5  | 19.3             | 55568  | 2 AC105850_3 | Continuation (4 of   |
| 38         | 72.5  | 19.3             | 104869 | 2 AC087611   | AC087611 Homo sapi   |
| 39         | 72.5  | 19.3             | 110000 | 2 AC015850_2 | Continuation (3 of   |
| 40         | 72    | 19.2             | 11533  | 1 AE009124   | AE009124 Agrobacte   |
| 41         | 72    | 19.2             | 12074  | 1 AE008089   | AE008089 Agrobacte   |
| 42         | 72    | 19.2             | 140667 | 2 AC121065   | AC121065 Gallus ga   |
| 43         | 71    | 18.9             | 1155   | 6 AX607240   | AX607240 Sequence    |
| 44         | 71    | 18.9             | 97666  | 6 AX602209   | AX602209 Sequence    |
| 45         | 71    | 18.9             | 148801 | 9 AC100808   | AC100808 Homo sapi   |

RESULT 1

#### ALIGNMENTS



AX055438  
LOCUS AX055438 414 bp DNA linear PAT 13-JAN-2001  
DEFINITION Sequence 68 from Patent WO0073452.  
ACCESSION AX055438  
VERSION AX055438.1 GI:12228711  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS 1  
Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L.,  
Tumas, D., Watanabe, C.K. and Wood, W.I.  
TITLE Compositions and methods for the treatment of immune related  
diseases  
JOURNAL Patent: WO 0073452-A 68 07-DEC-2000;  
Genentech, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 98 a 126 c 92 g 98 t  
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Pred. No.: 8.02e-44 Length: 414  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
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QY 21 LeuAnTleApLyLeuArGSeRAlaPheLySaLaSpGIuPheLeuAnTTrpHisAla 40  
DB 157 CTGAACATCGACAATTCGATCGATTCGTTAAGGCTGAAGAGTTCTTAACCTGGACAGCC 216  
QY 41 LeupheGIuSeRILeYArGyLeuPheProPheLeuAnTTrpAspAlaPheProLyLeu 60  
DB 217 CTTTGAGTCTATCAAAAGAAACTTCCTTCCCTCACTGGAGTGCCTTCTTAAGCTG 276  
QY 61 LySGILeUArGSeRAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCAACTCTGATGCCAG 309  
RESULT 2  
AR252517 415 bp DNA linear PAT 20-DEC-2002  
LOCUS AR252517  
DEFINITION Sequence 200 from patent US 6478825.  
ACCESSION AR252517  
VERSION AR252517.1 GI:27300425  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS 1 (bases 1 to 415)  
Wineretotcom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.  
TITLE Implant, method of making same and use of the implant for the  
treatment of bone defects  
JOURNAL Patent: US 6478825-A 200 12-NOV-2002;  
FEATURES  
source Location/Qualifiers  
1..415  
/organism="unknown"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 8.05e-44 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
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QY 1 GUGUGUGUSeThrTILeGIUaSnTYrAlaSeArpProGIuaAlaPheAnThProPhe 20  
DB 97 GAGGAAGAAAGCACCATTGAGATTAATGCGTCACAGCCGAGCCCTTTAAACACCCCGTTC 156  
QY 21 LeuAnTleApLyLeuArGSeRAlaPheLySaLaSpGIuPheLeuAnTTrpHisAla 40  
DB 157 CTGAACATCGACAATTCGATCGATTCGTTAAGGCTGAAGAGTTCTTAACCTGGACAGCC 216  
QY 41 LeupheGIuSeRILeYArGyLeuPheProPheLeuAnTTrpAspAlaPheProLyLeu 60  
DB 277 AAAGACTGAGAGCGCAACTCTGATGCCAG 309  
RESULT 3  
AX077031 415 bp DNA linear PAT 22-FEB-2001  
LOCUS AX077031  
DEFINITION Sequence 19 from Patent WO0105972.  
ACCESSION AX077031  
VERSION AX077031.1 GI:13121661  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS 1  
Ashkenazi, A.J., Baker, K.P., Fong, S., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Hillan, K.J., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
Tumas, D., Watanabe, C.K. and Wood, W.I.  
TITLE Compositions and methods for the treatment of immune related  
diseases  
JOURNAL Patent: WO 0105972-A 19 25-JAN-2001;  
Genentech, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 8.05e-44 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AX077031 (1-415)  
QY 1 GUGUGUGUSeThrTILeGIUaSnTYrAlaSeArpProGIuaAlaPheAnThProPhe 20  
DB 97 GAGGAAGAAAGCACCATTGAGATTAATGCGTCACAGCCGAGCCCTTTAAACACCCCGTTC 156  
QY 21 LeuAnTleApLyLeuArGSeRAlaPheLySaLaSpGIuPheLeuAnTTrpHisAla 40  
DB 157 CTGAACATCGACAATTCGATCGATTCGTTAAGGCTGAAGAGTTCTTAACCTGGACAGCC 216  
QY 41 LeupheGIuSeRILeYArGyLeuPheProPheLeuAnTTrpAspAlaPheProLyLeu 60

Db 217 CTCCTTGAGTCTATCAAAAGAACTTCCTTCCTCACTGGATGCTTCTTAAGCTG 276  
Qy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGAGCGCACTCTGATGCCAG 309

RESULT 4  
AX358892  
LOCUS AX358892 415 bp DNA linear PAT 13-FEB-2002  
DEFINITION Sequence 145 from Patent WO0193983.  
ACCESSION AX358892  
VERSION AX358892.1 GI:18675347  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Baker, K.P., Deenoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: WO 0193983-A 145 13-DEC-2001;  
FEATURES  
source location/Qualifiers  
1..415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 8.05e-44 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX358892 (1-415)

Qy 1 GluGluGluSerThrIleGluAsnTYRAlaSerArgProGluAlaPheAsnThrPrope 20  
Db 97 GAGGAAAGAAAGCAACATTGAAATTAAGCTGCAAGACCCGACTTAAACCCGCTTC 156  
Qy 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPHisAla 40  
Db 157 CTGAACATCGACAAATTGGCATCTGCTTTAAGGCTGATGAGTTCTGAACCTGGCAGCC 216  
Qy 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrAspAlaPheProLysLeu 60  
Db 217 CTCCTTGAGTCTATCAAAAGAACTTCCTTCCTCACTGGATGCTTCTTAAGCTG 276  
Qy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGAGCGCACTCTGATGCCAG 309

RESULT 5  
AX362385  
LOCUS AX362385 415 bp DNA linear PAT 15-FEB-2002  
DEFINITION Sequence 145 from Patent WO0208288.  
ACCESSION AX362385  
VERSION AX362385.1 GI:18694650  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Baker, K.P., Deenoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,

Watanabe, C.K. and Wood, W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: WO 0208288-A 145 31-JAN-2002;  
FEATURES  
source location/Qualifiers  
1..415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 8.05e-44 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX362385 (1-415)

Qy 1 GluGluGluSerThrIleGluAsnTYRAlaSerArgProGluAlaPheAsnThrPrope 20  
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Qy 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPHisAla 40  
Db 157 CTGAACATCGACAAATTGGCATCTGCTTTAAGGCTGATGAGTTCTGAACCTGGCAGCC 216  
Qy 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrAspAlaPheProLysLeu 60  
Db 217 CTCCTTGAGTCTATCAAAAGAACTTCCTTCCTCACTGGATGCTTCTTAAGCTG 276  
Qy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGAGCGCAACCTCTGATGCCAG 309

RESULT 6  
AX403313  
LOCUS AX403313 415 bp DNA linear PAT 14-JUN-2002  
DEFINITION Sequence 200 from Patent WO0073454.  
ACCESSION AX403313  
VERSION AX403313.1 GI:21436871  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Ashkenazi, A.J., Baker, K.P., Botstein, D., Deenoyers, L., Eaton, D., Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P., Grimaldi, J.C., Gurney, A.L., Kijavich, I., Napier, M.A., Pan, J., Paoni, N.F., Roy, M., Stewart, T.A., Tamas, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: WO 0073454-A 200 07-DEC-2000;  
FEATURES  
source location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
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Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

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Query Match:      100.00%      Index:      0
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US-10-059-395-142_COPY_29_99 (1-71) x AX40313 (1-415)

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 Db 157 CTGAACATCGACAAATTGCCGATCTGGCTTTAAGCTGATGAGTTCCCTGAACTGGCAGCC 216

41 LeuPegInserIIeYsBaIySleIProLeuSnTpaSpaApheProIySleu 60  
217 CTCTTGAGICTATCAAAAGAACTTCCTTCCTCAACTGGGATGCCTTCTTAAGCTG 276

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Db      277 AAAGACTGAGGAGCGCACTTCTGTGCCAG 309

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|            |                                     |        |     |        |                 |
|------------|-------------------------------------|--------|-----|--------|-----------------|
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| LOCUS      | AX454546                            |        |     |        |                 |
| DEFINITION | Sequence 131 from Patent WO0208284. | 415 bp | DNA | linear | PAT 06-JUL-2002 |
| ACCESSION  | AX454546                            |        |     |        |                 |
| VERSION    | AX454546.1                          |        |     |        |                 |
| KEYWORDS   | GI:21713897                         |        |     |        |                 |
| SOURCE     | .                                   |        |     |        |                 |
| ORGANISM   | Homo sapiens (human)                |        |     |        |                 |
|            | Homo sapiens                        |        |     |        |                 |

1  
Baker, K. P., Ferrara, N., Gerber, H., Gerritsen, M. E., Goddard, A.,  
Godowski, P. J., Guney, A. L., Hillan, K. J., Marsters, S. A., Pan, J.,  
Poon, N. F., Stephan, J. P., Matanabe, C. K., Williams, P. M., Wood, W. I.  
and Ye, W.

**TITLE** Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis  
**JOURNAL** Patent: WO 0208284-A 131 31-JAN-2002:  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrante, Napoleone (US) ; Garber, Hanspeter (US) ; Gertlisen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Guirney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Mersereau, Scott A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)

| FEATURES   | Location/Qualifiers      |
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|            | /organism="Homo sapiens" |
|            | /mol_type="genomic DNA"  |
|            | /db_xref="taxon:9606"    |
| BASE COUNT | 99 a 126 c 92 g 98 t     |
| ORIGIN     |                          |

|                        |          |
|------------------------|----------|
| Alignment Scores:      |          |
| Pred. No.:             | 8.05e-44 |
| Score:                 | 375.00   |
| Percent Similarity:    | 100.00%  |
| Best Local Similarity: | 100.00%  |
| Query Match:           | 100.00%  |
| DB:                    | 6        |
|                        |          |
| Length:                | 415      |
| Matches:               | 71       |
| Conservative:          | 0        |
| Mismatches:            | 0        |
| Indels:                | 0        |
| Gaps:                  | 0        |

US-10-059-395-142\_COPY\_29\_99 (1-71) X AX454546 (1-415)

QY 1 GIUGIUGIuserThriIeGIUasNTyrrAlasErargProGIUAlaPheasnthrProphe 20

DB 9 / GAGGAGAAACACCAATGAGAAATATGCGTACCGACCCGAGGCGCTTTACACCCCCGTTT 156

Qy 21 LeuAsnIleAspIysLeuAsgSerAlaPheIysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACCAATTGCATCTGCCTTTAAGCGCTGATGAGTTCTGCACTGGCAGCC 216

Qy 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Dp 217 CTCTTGAGTCATCAAGGAACTTCTTCTCACTGGAGTCCCTTCTTAAGCTG 276

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      | 6LLYSGLYLEUATGSEIAlatInFRIOABPAGAGIn /1
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Db    277 AAAGACTGAGGAGCGCACTCCTGATGCCACG 309

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|            |                                     |             |     |        |                 |
|------------|-------------------------------------|-------------|-----|--------|-----------------|
| RESULT 8   | AX491024                            | 415 bp      | DNA | linear | PAT 16-AUG-2002 |
| LOCUS      | AX491024                            |             |     |        |                 |
| DEFINITION | Sequence 131 from Patent WO0200690. |             |     |        |                 |
| ACCESSION  | AX491024                            |             |     |        |                 |
| VERSION    | AX491024.1                          | GI:22323849 |     |        |                 |
| KEYWORDS   |                                     |             |     |        |                 |
| SOURCE     | Homo sapiens                        |             |     |        |                 |
| ORGANISM   | Homo sapiens (human)                |             |     |        |                 |

| REFERENCE | AUTHORS  | TITLE  | JOURNAL  |
|-----------|--|--|--|
| 1         | Baker, K. P., Ferrara, N., Gerber, H., Gertlsen, M. B., Goddard, A., Gonsky, R. J., Guiney, A. L., Hillan, K. J., Maresets, S. A., Pan, D., Peoni, N. F., Stephan, J. P., Watanabe, C. K., Williams, P. M., Wood, W. I. and Ye, W. | Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis | Patent: WO 0200690-A 131 03-JAN-2002; Genentech, Inc. (US) |

| FEATURES   | Location/Qualifiers      |
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|            | /organism="Homo sapiens" |
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|            | /db_xref="taxon:9606"    |
| BASE COUNT | 99 a 126 c 92 g 98 t     |
| ORIGIN     |                          |

|                        |          |
|------------------------|----------|
| Alignment Scores:      |          |
| Pred. No.:             | 8.05e-44 |
| Score:                 | 375.00   |
| Percent Similarity:    | 100.00%  |
| Best Local Similarity: | 100.00%  |
| Query Match:           | 100.00%  |
| DB:                    | 6        |
|                        |          |
| Length:                | 415      |
| Matches:               | 71       |
| Conservative:          | 0        |
| Mismatches:            | 0        |
| Indels:                | 0        |
| Gaps:                  | 0        |

US-10-059-395-142\_COPY\_29\_99 (1-71) X AX491024 (1-415

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Db 97 GAGGAGAAAGCACCCATTGAGATTATGCGTCACGACCCGAGGCCCTTTAACACCCCCGTTT 15

Db 157 CTGACATGACAAATTGCGATCTGCTTTAAGGCTGATGACTTCTGAAC TGGAACGCC 211

217 CTCTTGA GTCTATCAAAAGGAAC TCTCTCTCTCAACTGGATGCCCTTCTCTAAGCTG 277

277 AAGGACTGAGGCGCACTCTGTATGCCAG 309

|            |                         |             |     |        |                 |
|------------|-------------------------|-------------|-----|--------|-----------------|
| RESULT 9   |                         |             |     |        |                 |
| AX574494   |                         |             |     |        |                 |
| LOCUS      | AX574494                | 415 bp      | DNA | linear | PAT 07-JAN-2003 |
| DEFINITION | Sequence 21 from Patent | MO0224888.  |     |        |                 |
| ACCESSION  | AX574494                |             |     |        |                 |
| VERSION    | AX574494.1              | GI:27551800 |     |        |                 |
| KEYWORDS   |                         |             |     |        |                 |

REFERENCE 1  
AUTHORS Baker, K.P., Bacon, D.L., Pilvaroff, E., Goddard, A., Grimaldi, J.C.,  
Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., Wood, W.I.,  
Zhang, Z. and Pong, S.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0224888-A 21 28-MAR-2002;  
GENENTECH, INC. (US)  
FEATURES  
source location/Qualifiers  
1. .415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 8.05e-44 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservat: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
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QY 1 GUGUGUGUSeThrllegUAenTYrAlaSerArProGluAlaPheAenThrProPhe 20  
DB 97 GAGGAAGAAAGCACATTGGAATTAATGCGTCAGACCGCGGCTTTAAACCCCGCTTC 156  
QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnTPH:Ala 40  
DB 157 CTGAACATCGACAATTCGATCGCTTTAAGCTGATGAGTTCCTGAACCTGACGCC 216  
QY 41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnTPH:AspAlaPheProIysLeu 60  
DB 217 CTCCTTGAGCTATCAAAAGAAACTTCCTTCTCAACGAGGATGCTTTCCTTAAGCTG 276  
QY 61 LysGlyIysLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCAACTCCGATGCCGAG 309  
RESULT 10  
AX080815 432 bp DNA linear PAT 27-FEB-2001  
LOCUS AX080815  
DEFINITION Sequence 61 from Patent WO0109327.  
ACCESSION AX080815  
VERSION AX080815.1 GI:13169784  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Kijavini, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
Watanabe, C.K. and Wood, W.I.  
TITLE Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
JOURNAL Patent: WO 0109327-A 61 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES  
source location/Qualifiers  
1. .432  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Virtual DNA fragment used in the isolation of  
DNAS7694."  
BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN  
Alignment Scores:  
Pred. No.: 8.45e-44 Length: 432  
Score: 375.00 Matches: 71  
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DB: Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080815 (1-432)

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DB 96 GAGGAAGAAAGCACATTGGAATTAATGCGTCAGACCGCGGCTTTAAACCCCGCTTC 155  
QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnTPH:Ala 40  
DB 156 CTGAACATCGACAATTCGATCGCTTTAAGCTGATGAGTTCCTGAACCTGACGCC 215  
QY 41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnTPH:AspAlaPheProIysLeu 60  
DB 216 CTCCTTGAGCTATCAAAAGAAACTTCCTTCTCAACGAGGATGCTTTCCTTAAGCTG 275  
QY 61 LysGlyIysLeuArgSerAlaThrProAspAlaGln 71  
DB 276 AAAGACTGAGAGCGCAACTCCGATGCCCAA 308  
RESULT 11  
AX080818 432 bp DNA linear PAT 27-FEB-2001  
LOCUS AX080818  
DEFINITION Sequence 64 from Patent WO0109327.  
ACCESSION AX080818  
VERSION AX080818.1 GI:13169787  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Kijavini, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
Watanabe, C.K. and Wood, W.I.  
TITLE Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
JOURNAL Patent: WO 0109327-A 64 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES  
source location/Qualifiers  
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BASE COUNT 106 a 127 c 94 g 102 t 3 others  
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Alignment Scores:  
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Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservat: 0  
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DB 96 GAGGAAGAAAGCACATTGGAATTAATGCGTCAGACCGCGGCTTTAAACCCCGCTTC 155  
QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnTPH:Ala 40  
DB 156 CTGAACATCGACAATTCGATCGCTTTAAGCTGATGAGTTCCTGAACCTGACGCC 215  
QY 41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnTPH:AspAlaPheProIysLeu 60  
DB 216 CTCCTTGAGCTATCAAAAGAAACTTCCTTCTCAACGAGGATGCTTTCCTTAAGCTG 275  
QY 61 LysGlyIysLeuArgSerAlaThrProAspAlaGln 71

| Db  | 276  | AAAGACTGAGAGCCGACCTCTGATGCCCA                                  | 308                                    |
|---|--|--|--|
| RESULT 12   |  |  |  |
| LOCUS   | BD082389   | 456 bp   | DNA                                    |
| DEFINITION  | 87 human secreted. proteins.   |  | linear                                 |
| ACCESSION   | BD082389   |  |  |
| VERSION   | BD082389.1   |  |  |
| KEYWORDS  | UP 2001522239-A/31.  |  |  |
| SOURCE  | Maestadenovirus  |  |  |
| ORGANISM  | Viruses; dsDNA viruses, no RNA stage; Adenoviridae.  |  |  |
| REFERENCE   | 1 (bases 1 to 456)   |  |  |
| AUTHORS   | Young, P., Greene, J.M., Ferrie, A.M., Ruben, S.M., Rosen, C.A., Duane, R.D., Hu, J.S., Florence, K.A., Olsen, H.S., Ebner, K., Brewer, L.A., Moore, P.A., Shi, Y., Lafleur, D.W. and Ni, J. |  |  |
| TITLE   | 87 human secreted protein  |  |  |
| JOURNAL   | Patent: JP 2001522239-A 31 13-NOV-2001;  |  |  |
| COMMENT   | HUMAN GENOME SCIENCES INC SECRETARY OF THE DEPARTMENT OF HEALTH<br>HUMAN SERVICES  |  |  |
| PD  | 13-NOV-2001  | PN   | JP 2001522239-A/31                     |
| PF  | 19-MAR-1998  | JP   | 1998542119                             |
| PR  | 21-MAR-1997  | US   | 60/041281, 21-MAR-1997 US 60/041276 PR |
| 21-MAR-1997   | US   | 60/042344, 21-MAR-1997   | US 60/041277 PR                        |
| 30-MAY-1997   | US   | 60/048355, 30-MAY-1997   | US 60/048096 PR                        |
| 30-MAY-1997   | US   | 60/048351, 30-MAY-1997   | US 60/048154 PR                        |
| 30-MAY-1997   | US   | 60/048160, 30-MAY-1997   | US 60/048069 PR                        |
| 30-MAY-1997   | US   | 60/048131, 30-MAY-1997   | US 60/048186 PR                        |
| 30-MAY-1997   | US   | 60/048095, 30-MAY-1997   | US 60/048187 PR                        |
| 30-MAY-1997   | US   | 60/048099, 30-MAY-1997   | US 60/050937 PR                        |
| 30-MAY-1997   | US   | 60/048352, 30-MAY-1997   | US 60/048135 PR                        |
| 30-MAY-1997   | US   | 60/048188, 30-MAY-1997   | US 60/048094 PR                        |
| 30-MAY-1997   | US   | 60/048350, 05-AUG-1997   | US 60/054804 PR                        |
| 19-AUG-1997   | US   | 60/056370, 02-OCT-1997   | US 60/060862 PI                        |
| YOUNG, JOHN M GREENE, ANN M FERRIE, STEVEN M RUBEN, CRAIG A ROSEN, PI |  |  | PAUL                                   |
| PI  | ROXANNE D DUAN, JING SHAN HU, KIMBERLY A FLORENCE, HENRIK S OLSEN,   |  |  |
| PI  | REINHARD EBNER, LAURIE A BREWER, PAUL A MOORE, YANGSU SHI, DAVID W   |  |  |
| FEATURES  |  |  |  |
| SOURCE  | 1. 456   | Location/Qualifiers  |  |
|   | /organism="Maestadenovirus"  |  |  |
|   | /mol_type="Genomic DNA"  |  |  |
|   | /db_xref="taxon:10509"   |  |  |
| BASE COUNT  | 117 a 136 c 104 g 98 t   | 1 others   |  |
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| QY  | 1  | GluciguJuserThrllegluasntYrIaseraTgProgluaIaphesantRPrope      | 20                                     |
| DB  | 105  | GAGGAGAGAGACCATGATGAGATTATGGCTGACAGCCGAGCCCTTTAAGCCCGCTTC      | 164                                    |
| QY  | 21   | LeuauanlleaplyleuayrgSerAlaphelysAlaaspGluPheluauantRphIsala   | 40                                     |
| DB  | 165  | CTGAACATCGACCAATTGGATCGTCTGTTAAGGCTGATGAGATTCTCTGAACATCGACCGCC | 224                                    |

|  |  |                                    |  |                 |
|--|--|------------------------------------|--|-----------------|
| Oy   |  | 41                                 | LysGlyLeuArgSerAlaThrProAspAlaGln                            | 71              |
| Dd   |  | 225                                | CTCTTTAGGTCTATCAAAAGGAACCTTCCTTCTCACAACGGATGCCCTTCCTAAGCTG   | 284             |
| Oy   |  | 61                                 | LysGlyLeuArgSerAlaThrProAspAlaGln                            | 71              |
| Dd   |  | 285                                | AAAGGACTGAGAGCGCACTCCGTGATGCCAG                              | 317             |
| RESULT 13  |  |                                    |  |                 |
| AX080817   |  |                                    |  |                 |
| LOCUS  |  | AX080817                           | 490 bp   | DNA             |
| DEFINITION   |  | Sequence 63 from Patent WO0109327. |  | linear          |
| ACCSSION   |  | AX080817                           |  | PAT 27-FEB-2001 |
| VERSION  |  | AX080817.1                         | GI:13169786  |                 |
| KEYWORDS   |  |                                    |  |                 |
| SOURCE   |  |                                    |  |                 |
| ORGANISM   |  |                                    |  |                 |
| REFERENCE  |  |                                    |  |                 |
| AUTHORS  |  | 1                                  |  |                 |
| TITLE  |  |                                    |  |                 |
| JOURNAL  |  |                                    |  |                 |
| FEATURES   |  |                                    |  |                 |
| Source   |  |                                    |  |                 |
| Alignment Scores:                                      |  |                                    |  |                 |
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| Oy   |  | 1                                  | GlucIgluSerThrIleGluAsnTrpAlaSerArgProGluAlaPheAsnThrProPhe  | 20              |
| Dd   |  | 164                                | GAGGAGAAGAACCATTTGAGATTATGCGTCAGACGCCGAGGCGCTTTAACAACCCCGTTC | 223             |
| Oy   |  | 21                                 | LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrHisAla | 40              |
| Dd   |  | 224                                | CTGACACATGCACAATTGCGATGCGCTTTAAGCGTAGTGATGCTGAGACTGGCACGCC   | 283             |
| Oy   |  | 41                                 | LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu | 60              |
| Dd   |  | 284                                | CTCTTTAGGTCTATCAAAAGGAACCTTCCTTCTCACAACGGATGCCCTTCCTAAGCTG   | 343             |
| Oy   |  | 61                                 | LysGlyLeuArgSerAlaThrProAspAlaGln                            | 71              |
| Dd   |  | 344                                | AAAGGACTGAGAGCGCACTCCGTGATGCCAG                              | 376             |
| RESULT 14  |  |                                    |  |                 |
| HSA293408  |  |                                    |  |                 |
| LOCUS  |  | HSA293408                          | 529 bp   | mRNA            |
| DEFINITION   |  | clone NN 15.                       |  | linear          |
| ACCSSION   |  | AF293408                           |  | FRI 06-JAN-2003 |
| VERSION  |  | AF293408.1                         | GI:27526545  |                 |
| KEYWORDS   |  |                                    |  |                 |
| SOURCE   |  |                                    |  |                 |
| ORGANISM   |  |                                    |  |                 |
| Human sapiens  |  |                                    |  |                 |
| differentially expressed in malignant melanoma,        |  |                                    |  |                 |
| differential expression; malignant; melanoma.          |  |                                    |  |                 |
| Human sapiens (human)                                  |  |                                    |  |                 |



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 13:44:54 / Search time 53 Seconds

(Without alignments)  
591.287 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

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| Ygapop 10.0 | Ygapext 0.5 |
| Fgapop 6.0  | Fgapext 7.0 |
| Delop 6.0   | Delext 7.0  |

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTCUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/beckfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARYS

| Result No. | Score | Query | Length  | DB ID | Description         |
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| 1          | 375   | 100.0 | 415     | 4     | US-09-996-243-200   |
| 2          | 210.5 | 56.1  | 288     | 4     | US-09-313-294A-4134 |
| 3          | 78.5  | 20.6  | 686     | 3     | US-09-318-111-364   |
| 4          | 67.5  | 18.0  | 1830121 | 4     | US-09-557-884-1     |
| 5          | 62.5  | 16.7  | 1830121 | 4     | US-09-643-990A-1    |
| 6          | 62.5  | 16.7  | 4084    | 3     | US-08-866-340-1     |
| 7          | 62.5  | 16.7  | 4460    | 3     | US-09-103-875-4     |
| 8          | 62    | 16.5  | 1845    | 4     | US-09-328-352-1350  |
| 9          | 62    | 16.5  | 71989   | 4     | US-09-443-501A-2    |
| 10         | 60.5  | 16.1  | 1664976 | 4     | US-08-916-421B-1    |
| 11         | 60    | 16.0  | 1542    | 1     | US-08-328-962-1     |
| 12         | 59.5  | 15.9  | 702     | 4     | US-09-328-352-1933  |

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| 13 | 59.5 | 15.9 | 2253    | 4 | US-09-107-532A-2214 | Sequence 2214, Ap  |
| 14 | 59   | 15.7 | 40123   | 4 | US-08-311-731A-137  | Sequence 137, App  |
| 15 | 58   | 15.5 | 1062    | 4 | US-08-961-527-197   | Sequence 197, App  |
| 16 | 57   | 15.2 | 340     | 3 | US-08-836-075A-61   | Sequence 61, Appl  |
| 17 | 57   | 15.2 | 2095    | 1 | US-08-405-230-8     | Sequence 8, Appl1  |
| 18 | 57   | 15.2 | 2095    | 2 | US-08-910-990-8     | Sequence 8, Appl1  |
| 19 | 57   | 15.2 | 2564    | 3 | US-08-276-968A-19   | Sequence 19, Appl  |
| 20 | 57   | 15.2 | 4655    | 4 | US-09-643-597-151   | Sequence 151, Appl |
| 21 | 57   | 15.2 | 4655    | 4 | US-09-880-884A-151  | Sequence 151, App  |
| 22 | 57   | 15.2 | 4655    | 4 | US-09-542-615A-151  | Sequence 151, App  |
| 23 | 57   | 15.2 | 4655    | 4 | US-09-606-421B-151  | Sequence 151, App  |
| 24 | 57   | 15.2 | 4849    | 4 | US-09-643-597-335   | Sequence 335, App  |
| 25 | 57   | 15.2 | 4849    | 4 | US-09-542-615A-335  | Sequence 335, App  |
| 26 | 57   | 15.2 | 4849    | 4 | US-09-606-421B-335  | Sequence 335, App  |
| 27 | 57   | 15.2 | 1830121 | 4 | US-09-557-884-1     | Sequence 1, Appl1  |
| 28 | 57   | 15.2 | 1830121 | 4 | US-09-643-990A-1    | Sequence 1, Appl1  |
| 29 | 56.5 | 15.1 | 1021    | 4 | US-09-280-116-85    | Sequence 85, Appl1 |
| 30 | 56.5 | 15.1 | 1804    | 4 | US-09-548-372D-1    | Sequence 1, Appl1  |
| 31 | 56.5 | 15.1 | 1804    | 4 | US-09-548-367D-1    | Sequence 1, Appl1  |
| 32 | 56.5 | 15.1 | 1804    | 4 | US-09-551-853D-1    | Sequence 1, Appl1  |
| 33 | 56.5 | 15.1 | 1862    | 3 | US-08-999-723-1     | Sequence 1, Appl1  |
| 34 | 56.5 | 15.1 | 1862    | 3 | US-09-434-427-1     | Sequence 1, Appl1  |
| 35 | 56.5 | 15.1 | 18596   | 3 | US-09-118-448-11    | Sequence 11, Appl1 |
| 36 | 56.5 | 15.1 | 61663   | 4 | US-09-453-702B-62   | Sequence 62, Appl1 |
| 37 | 56   | 14.9 | 1005    | 4 | US-08-961-527-354   | Sequence 354, App  |
| 38 | 56   | 14.9 | 2022    | 1 | US-08-803-973-6     | Sequence 6, Appl1  |
| 39 | 56   | 14.9 | 2022    | 1 | US-08-803-972-6     | Sequence 6, Appl1  |
| 40 | 56   | 14.9 | 2058    | 1 | US-08-358-117-1     | Sequence 1, Appl1  |
| 41 | 56   | 14.9 | 2058    | 3 | US-08-470-588-1     | Sequence 1, Appl1  |
| 42 | 56   | 14.9 | 2124    | 1 | US-08-803-973-11    | Sequence 11, Appl1 |
| 43 | 56   | 14.9 | 2124    | 1 | US-08-803-972-11    | Sequence 11, Appl1 |
| 44 | 56   | 14.9 | 3089    | 4 | US-09-016-434-1330  | Sequence 1330, Ap  |
| 45 | 56   | 14.9 | 4371    | 1 | US-08-803-973-1     | Sequence 1, Appl1  |

#### ALIGNMENTS

RESULT 1  
US-09-996-243-200  
Sequence 200, Application US/09996243  
Patent No. 6478825  
GENERAL INFORMATION:  
APPLICANT: Aekkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Batton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Rong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996, 243  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16

[illegible]





DB 164 GATCTGGATTGACAACTCTGAGACGCTCTCTGGAGATGTTT-----AAC 208  
QY 23 IleaPlyLeuArgSerAlaPheYsAlaAep---GlupheLeuAsnTrpHisAla--- 40  
DB 209 TTTGACACTTCTGAGAAATTTTAAATCAAGCTGGGTTTATCATCACTGGAGATCCATA 268  
QY 41 -----Leuphe 42  
DB 269 AACAAAGACAGATCCGCCCCAGACCCGAGCCCTCTACTTACGACCGACTCTGG 328  
QY 43 GluSerIleYsArgYsLeuProPheLeuAsnTrpHisAla 56  
DB 329 GAGGATTTCAACAGAACACTCTTCTCAACTGGAAGCA 370  
RESULT 4  
US-09-557-884-1  
Sequence 1, Application US/09557884  
Patent No. 6506581  
GENERAL INFORMATION:  
APPLICANT: Fleischmann et al.  
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/557,884  
FILING DATE: 25-Apr-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476,102  
FILING DATE: JUN-5-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Michelle S. Marks  
REGISTRATION NUMBER: 41,971  
REFERENCE/DOCKET NUMBER: PB186P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8439  
TELEFAX: 301-309-8504  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-557-884-1  
Alignment Scores:  
Pred. No.: 3.09e+04 Length: 1830121  
Score: 67.50 Matches: 13  
Percent Similarity: 66.67% Conservative: 7  
Best Local Similarity: 43.33% Mismatches: 9  
Query Match: 18.00% Indels: 1  
DB: 4 Gaps: 1  
US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-557-884-1 (1-1830121)  
QY 26 LeuArgSerAlaPheYsAlaAepGlupheLeuAsnTrpHisAlaLeuPheGluSerIle 45  
DB 1299803 CTCAAAGTGGCGTAAAGAAACGTTTATGATTGCACTTCATCATATAAAAAATAG 1299862

QY 46 Lys---ArgYsLeuProPheLeuAsnTrp 54  
DB 1299863 AAAGAGAGAAATATAATCCCAATTGG 1299892  
RESULT 5  
US-09-643-990A-1  
Sequence 1, Application US/09643990A  
Patent No. 6528289  
GENERAL INFORMATION:  
APPLICANT: Robert D. Fleischmann  
Mark D. Adams  
Owen White  
Hamilton O. Smith  
J. Craig Venter  
TITLE OF INVENTION: The Haemophilus influenzae Rd Genome, Fragments thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville,  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/643,990A  
FILING DATE: 23-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/487,429  
FILING DATE: 1995-06-07  
APPLICATION NUMBER: 08/426,787  
FILING DATE: 1995-04-21  
ATTORNEY/AGENT INFORMATION:  
NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PB186P1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-610-5790  
TELEFAX: 310-309-8439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-643-990A-1  
Alignment Scores:  
Pred. No.: 3.09e+04 Length: 1830121  
Score: 67.50 Matches: 13  
Percent Similarity: 66.67% Conservative: 7  
Best Local Similarity: 43.33% Mismatches: 9  
Query Match: 18.00% Indels: 1  
DB: 4 Gaps: 1  
US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-643-990A-1 (1-1830121)  
QY 26 LeuArgSerAlaPheYsAlaAepGlupheLeuAsnTrpHisAlaLeuPheGluSerIle 45  
DB 1299803 CTCAAAGTGGCGTAAAGAAACGTTTATGATTGCACTTCATCATATAAAAAATAG 1299862  
QY 46 Lys---ArgYsLeuProPheLeuAsnTrp 54  
DB 1299863 AAAGAGAGAAATATAATCCCAATTGG 1299892



QY 24 AsplysleuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAlaLeu-PheG1 43  
Db 1014 TCACAAAGACGTTATCTATCAACAGTAGACGATGAGTGTCAAGTATGTTGGA 1073  
QY 43 UserlelysaArgLysLeuPro-----PheLeuAsnTrpAspAlaPheProLysLeuLys 61  
Db 1074 AGGTTTCTAAAGAGTTCAGCAACTTAAACCACTGGAAGGTCAACCTCAGGTAA 1133  
QY 61 sGlyLeuArgSerAlaTrpProAspAlaGln 71  
Db 1134 CGCGCAAAAAGCAGCAGCATCCAAATGCTCT 1164  
RESULT 9  
US-09-443-501A-2/c  
Sequence 2, Application US/09443501A  
Patent No. 6303342  
GENERAL INFORMATION:  
APPLICANT: Korean Biosciences, Inc.  
APPLICANT: Julien, Bryan  
APPLICANT: Katz, Leonard  
APPLICANT: Khosla, Chaitan  
APPLICANT: Zierman, Rainer  
TITLE OF INVENTION: Recombinant Methods and Materials for Producing  
FILE REFERENCE: 30062-20031.00  
CURRENT FILING DATE: 1999-11-19  
PRIOR FILING DATE: 1999-04-22  
PRIOR APPLICATION NUMBER: US 60/130,560  
PRIOR FILING DATE: 1999-03-03  
PRIOR APPLICATION NUMBER: US 60/119,386  
PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: US 60/109,401  
PRIOR FILING DATE: 1998-11-20  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 71989  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic construct  
US-09-443-501A-2  
Alignment Scores:  
Pred. No.: 2,04e+03 Length: 71989  
Score: 62.00 Matches: 21  
Percent Similarity: 49.21% Conservative: 10  
Best Local Similarity: 33.33% Mismatches: 22  
Query Match: 16.53% Indels: 10  
Gaps: 5  
US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-443-501A-2 (1-71989)  
QY 12 ArgProGluAlaPheAsnTrpPheLeuAsnIleAspLysLeuArgSerAlaPheLys 31  
Db 64404 CGGCGGAGCGGCTTTCAGCCACATTCCTTCA-----CTATCGCGCTCTTCA 64354  
QY 32 AlaAspGluPheLeu-----AsnTrpHisAlaLeuPheGluSerIleLysArgLys 48  
Db 64353 GGAGATCCCTGTCATCGTTCATGATGACGCTGTG---CAGTGCCTGAGCGCGG 64297  
QY 49 LeuProPheLeuAsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaTrpPro 68  
Db 64296 ACCCGGTAC---TCTTCGCGAGCTTCGCGCGAGGCTGCTCCCTCCGTTCC-----CCC 64246  
QY 69 AspAlaGln 71  
Db 64245 GGGTCCGAG 64237

RESULT 10  
US-08-916-421B-1/c  
Sequence 1, Application US/08916421B  
Patent No. 6503729  
GENERAL INFORMATION:  
APPLICANT: Buit et al.  
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco  
Patent No. 6503729  
FILE REFERENCE: P8275  
CURRENT FILING DATE: 1997-08-22  
PRIOR FILING DATE: 1996-08-22  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 1664976  
TYPE: DNA  
ORGANISM: Methanococcus jannaschii  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (28222)..(28222)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (28257)..(28258)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (84773)..(84773)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (84808)..(84808)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (84812)..(84812)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (98120)..(98120)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (98159)..(98159)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (98239)..(98239)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (98266)..(98266)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (98343)..(98343)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (103598)..(103598)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (148948)..(148948)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (163385)..(163385)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (191989)..(191989)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (231980)..(231980)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (234187)..(234187)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature

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1  OTHER INFORMATION: n equals a, t, c, or g
2  NAME/KEY: misc feature
3  LOCATION: (1310988)..(1310988)
4  OTHER INFORMATION: n equals a, t, c, or g
5  NAME/KEY: misc feature
6  LOCATION: (1313224)..(1313224)
7  OTHER INFORMATION: n equals a, t, c, or g
8  NAME/KEY: misc feature
9  LOCATION: (1349473)..(1349473)
10 OTHER INFORMATION: n equals a, t, c, or g
11 NAME/KEY: misc feature
12 LOCATION: (1349491)..(1349491)
13 OTHER INFORMATION: n equals a, t, c, or g
14 NAME/KEY: misc feature
15 LOCATION: (1470091)..(1470091)
16 OTHER INFORMATION: n equals a, t, c, or g
17 NAME/KEY: misc feature
18 LOCATION: (1569020)..(1569020)
19 OTHER INFORMATION: n equals a, t, c, or g
20 NAME/KEY: misc feature
21 LOCATION: (1602912)..(1602912)
22 OTHER INFORMATION: n equals a, t, c, or g
23 NAME/KEY: misc feature
24 LOCATION: (1603734)..(1603734)
25 OTHER INFORMATION: n equals a, t, c, or g
26 NAME/KEY: misc feature
27 LOCATION: (1637998)..(1637998)
28 OTHER INFORMATION: n equals a, t, c, or g
29 NAME/KEY: misc feature
30 LOCATION: (1664854)..(1664855)
31 OTHER INFORMATION: n equals a, t, c, or g
32 OS-08-916-421B-1

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US-10-059-395-142\_COPY\_29\_99 (1-71) x US-08-916-421B-1 (1-1664976)

QY 8 ASNTYRALASERARGPROGLUALAPHASNTTHRPROPHLEUASNIIEASPLYLEUARG 27

Db 634055 AACTATGCCACAATGATAAGAGATTCTTAAGAGAGATG---ATAAAAAAAGCAGTT 633999

QY 28 SerAlaPheLyAlaAspGluPheLeuAsnTrp---HisAlaLeuPheGluSerIleLys 46

Db 633998 GGAAAAGTAAAAAAGAGATTACGAGAAGTGGTTAACTCTCTGTCGAAAAGGTTAG 633993

4 / ARGVLSLEUPTROFHEUASNTTPASPALAHEPTO 58  
.....

DD 033938 CAAAGACIA--AIAMMMAIIGGGAGCATTCC 033906

US-08-328-962-1/c

Patent No. 5536637

APPLICANT: Jacobs, Kenneth

**TITLE OF INVENTION: AND OTHER SECRETED PROTEINS**

CORRESPONDENCE ADDRESS:

STREET: 87 Cambridgepark Drive

STATE: MA  
COUNTRY: USA

ZIP: 02140  
COMPUTER READABLE FORM

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/328,962  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/045,267  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: McDaniel, Patricia A.  
REGISTRATION NUMBER: 33,194  
REFERENCE/DOCKET NUMBER: GI 5200  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-876-1170  
TELEFAX: 617-876-5851  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1542 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Saccharomyces cerevisiae  
IMMEDIATE SOURCE:  
CLONE: SUC2  
US-08-328-962-1

Alignment Scores:  
Pred. No.: 15.7 Length: 1542  
Score: 60.00 Matches: 17  
Percent Similarity: 57.78% Conservative: 9  
Best Local Similarity: 37.78% Mismatches: 11  
Query Match: 16.00% Indels: 9  
DB: 1 Gaps: 1

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-08-328-962-1 (1-1542)

Qy 19 ProPheLeuAsnIleAspIleuArgSerAlaPheIleuAspGluPheLeuAsnTrp 38  
Db 1025 CCAGATTACATTAATGTTCAATTTGTTGGCTTCAATT-GATCAATTCAGTCTCTGG 967  
Qy 39 HisAlaLeuPheGluSerIleValArgIleu-----Pro 50  
Db 966 ATTACCTGATATTCAGTGTCAAGAAACTTGGCGACCAAGACATGATGATCTCA 907  
Qy 51 PheLeuAsnTrpAsp 55  
Db 906 TGGGTAGTTGGAC 892

RESULT 12  
US-09-328-352-1933  
Sequence 1933, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 1933  
LENGTH: 702  
TYPE: DNA  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-1933

Alignment Scores:  
Pred. No.: 6 Length: 702  
Score: 59.50 Matches: 18

Percent Similarity: 51.72% Conservative: 12  
Best Local Similarity: 31.03% Mismatches: 21  
Query Match: 15.87% Indels: 7  
DB: 4 Gaps: 3

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-328-352-1933 (1-702)

Qy 3 GluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnTrpPheLeuAsn 22  
Db 496 CAGCATGATGATACCTACGACAGT-----GAGAGTTCATACGCGGTCGTAT 549  
Qy 23 -----IleAspIleuArgSerAlaPheIleuAspGluPheLeuAsnTrp 38  
Db 550 GTGATTGCGACGTATGAATTAAGTTCGCGACGTTGTGATGACGATCTTAGAGAAATG 609  
Qy 39 HisAlaLeuPheGluSerIleValArgIleuProPheLeuAsnTrpAspAla 56  
Db 610 CATGACGCTAT--ACCATGGGTGCAAACTTGAATGTTATTTGGGATAGT 660

RESULT 13  
US-09-107-532A-2214  
Sequence 2214, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Arinello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 2214:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2253 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...2253  
SEQUENCE DESCRIPTION: SEQ ID NO: 2214:  
US-09-107-532A-2214

Alignment Scores:  
Pred. No.: 6 Length: 702  
Score: 59.50 Matches: 18

Pred. No.: 32.6 Length: 2253  
Score: 59.50 Matches: 12  
Percent Similarity: 64.29% Conservative: 6  
Best Local Similarity: 42.86% Mismatches: 9  
Query Match: 15.87% Indels: 1  
DB: 4 Gaps: 1

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-107-532A-2214 (1-2253)

QY 38 TTPHIALLeuPheLeuIleuSerIleuValGlyLeuProPheLeuLeuValTTPHIALPhe 57  
DB 1490 TGGATCAGAGTGTACCAATCA--AAAGCGCAGTCCGCGTATGGATGGAGCTTGT 1546

QY 58 ProlLeuLeuGlySer 65  
DB 1547 CTGATGCTGAAAACATACGATCC 1570

RESULT 14  
US-08-311-731A-137/C

Sequence 137, Application US/08311731A  
Patent No. 6583266

GENERAL INFORMATION:

APPLICANT: SMITH, DOUGLAS

APPLICANT: MAO, JEN-I

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR

NUMBER OF SEQUENCES: 411

CORRESPONDENCE ADDRESS:

ADDRESS: WOLF, GREENFIELD & SACKS, P. C.

STREET: 600 ATLANTIC AVENUE

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/311, 731A

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: GATES, EDWARD R.

REGISTRATION NUMBER: 31,616

REFERENCE/DOCKET NUMBER: C0044/7125

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/720-3500

TELEFAX: 617/720-2441

INFORMATION FOR SEQ ID NO: 137:

SEQUENCE CHARACTERISTICS:

LENGTH: 4013 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULAR TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Mycobacterium leprae

US-08-311-731A-137

Alignment Scores:

Pred. No.: 2.55e+03 Length: 40123

Score: 59.00 Matches: 20

Percent Similarity: 47.69% Conservative: 11

Best Local Similarity: 30.77% Mismatches: 26

Query Match: 15.73% Indels: 8

DB: 4 Gaps: 3

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-08-311-731A-137 (1-40123)

QY 11 SerArgProGluAlaPheAsnThrProPheLeuAsnIleAsnIleLeuArgSerAlaPhe 30

DB 19981 AGCAACCTCGACAGCGCGAATCGTCTTCGTGAAGTGAAGACACAGACCTAC 19922

QY 31 LysAlaAspGluPhe-----LeuAsnThrIleAla----LeuPheGluSer 44

DB 19921 GACGGGATCAGATCGCGCGCCATCAAGTTGAGTTGCGCGGATTTGCAACACCG 19862

QY 45 IleValGlyLeuProPheLeuAsnThrAlaPheProLeuLeuGlySer 64

DB 19861 ATCAAGCGC-----GACTTCATGACACCCAGCAATTCCTCAAAATGTTGGGTGACCGA 19808

QY 65 SerAlaThrProAsp 69  
DB 19807 GGCATTTCCATGAC 19793

RESULT 15  
US-08-961-527-197

Sequence 197, Application US/08961527  
Patent No. 6420135

GENERAL INFORMATION:

APPLICANT: Charles Kunach

TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences

NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:

ADDRESS: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,527

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB340P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 197:

SEQUENCE CHARACTERISTICS:

LENGTH: 1062 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-961-527-197

Alignment Scores:

Pred. No.: 18.7 Length: 1062

Score: 58.00 Matches: 18

Percent Similarity: 50.00% Conservative: 16

Best Local Similarity: 26.47% Mismatches: 23

Query Match: 15.47% Indels: 11

DB: 4 Gaps: 2

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-08-961-527-197 (1-1062)

QY 3 GluSerThrIleGluAsnTyrAlaSerArgProGluAla----- 15

DB 355 CAAGCAAGATTCAGAGCTATCTAGACAGACCTGTAGCTGTTTACGATTTGCCAAGGA 414

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QY 16 ---PheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGlu 34
Db 415 ATTTTATCTATTTCTTAGTCGTGAGAACTTGAAAGCTTTTAGAGGACAGATGGC 474
QY 35 PheLeuAsnThrPheAlaLeuPheGluSerIle-LysArgLysLeuProPheLeuAsnTr 54
Db 475 TTGGCTCAGTTTGAGCGCGTGTGCGGTTCAGAGACAGATGCTTACTTGGCA-- 532
QY 54 PAspAlaPheProLysLeuLys 61
Db 533 ----GAGTTTCCTCTATCAGG 550
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Search completed: November 28, 2003, 15:11:03  
Job time : 658 secs



GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: November 28, 2003, 13:33:57 ; Search time 25 Seconds  
(without alignments)  
273.119 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Sequence: 1 EESTIENYASRPEAFNTPF.....LNDAPPKLKGRLSATPDQ 71

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: 1: PIR 76:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                                 |
|------------|-------|-------------|--------|----|---|
| 1          | 74    | 19.7        | 807    | 2  | S29242 sucrose synthase (para-aminobenzoate |
| 2          | 72    | 19.2        | 807    | 2  | G97561 sucrose synthase (para-aminobenzoate |
| 3          | 65.5  | 17.5        | 521    | 2  | S55318 cytochrome P450 1A                   |
| 4          | 65.5  | 17.5        | 521    | 2  | S34184 cytochrome P450 1A                   |
| 5          | 65.5  | 17.5        | 522    | 2  | A28789 cytochrome P450 1A                   |
| 6          | 65.5  | 17.5        | 522    | 2  | S51557 cytochrome P450, 3                   |
| 7          | 65.5  | 17.5        | 2434   | 2  | S44861 DNA topoisomerase                    |
| 8          | 65    | 17.3        | 368    | 2  | A71727 hypothetical prote                   |
| 9          | 65    | 17.3        | 459    | 2  | A75097 hypothetical prote                   |
| 10         | 64.5  | 17.2        | 583    | 2  | S63181 hypothetical prote                   |
| 11         | 64.5  | 17.2        | 583    | 2  | U70395 DNA-binding protei                   |
| 12         | 64.5  | 17.2        | 871    | 2  | B97035 DNA polymerase I,                    |
| 13         | 63.5  | 16.9        | 129    | 2  | A80038 hypothetical prote                   |
| 14         | 63    | 16.8        | 1213   | 2  | T19835 hypothetical prote                   |
| 15         | 62.5  | 16.7        | 522    | 2  | D81900 conserved hypobeth                   |
| 16         | 62.5  | 16.7        | 522    | 2  | A81124 phosphoglycerate m                   |
| 17         | 62    | 16.5        | 253    | 1  | PMRTM hypothetical prote                    |
| 18         | 61.5  | 16.4        | 506    | 2  | T12819 tRNA (guanine-N1-)                   |
| 19         | 61    | 16.3        | 234    | 2  | D81342 hypothetical prote                   |
| 20         | 61    | 16.3        | 254    | 2  | B84071 hypothetical prote                   |
| 21         | 61    | 16.3        | 254    | 2  | D90574 hypothetical prote                   |
| 22         | 61    | 16.3        | 2344   | 2  | T41590 probable sensor-11                   |
| 23         | 60.5  | 16.1        | 276    | 2  | C72298 hypothetical prote                   |
| 24         | 60.5  | 16.1        | 384    | 2  | B43592 outer membrane pro                   |
| 25         | 60.5  | 16.1        | 1232   | 2  | D44413 cobalamin biosynth                   |
| 26         | 60.5  | 16.1        | 4589   | 2  | T41941 dynein beta heavy                    |
| 27         | 60    | 16.0        | 321    | 2  | D64009 hypothetical prote                   |
| 28         | 60    | 16.0        | 321    | 2  | C89823 hypothetical prote                   |
| 29         | 60    | 16.0        | 736    | 2  | S65074 hypothetical prote                   |

|    |      |      |      |   |                           |
|----|------|------|------|---|---------------------------|
| 30 | 60   | 16.0 | 1044 | 2 | T43800 protein kinase hub |
| 31 | 59.5 | 15.9 | 325  | 2 | F71283 outer membrane ant |
| 32 | 59.5 | 15.9 | 481  | 2 | T37505 hypothetical prote |
| 33 | 59   | 15.7 | 161  | 2 | T28413 ORF MS752 tryptop  |
| 34 | 59   | 15.7 | 277  | 2 | A87184 thiosulfate sulfur |
| 35 | 59   | 15.7 | 441  | 2 | D83555 hypothetical prote |
| 36 | 59   | 15.7 | 480  | 2 | T18905 hypothetical prote |
| 37 | 58.5 | 15.6 | 197  | 2 | B84606 probable WRK1-type |
| 38 | 58.5 | 15.6 | 332  | 2 | F82140 C4-dicarboxylate-b |
| 39 | 58   | 15.5 | 128  | 2 | PH0094 Ig heavy chain V r |
| 40 | 58   | 15.5 | 128  | 2 | PH0095 Ig kappa chain V r |
| 41 | 58   | 15.5 | 379  | 2 | T52405 hypothetical prote |
| 42 | 58   | 15.5 | 412  | 2 | A30605 acyl-CoA dehydroge |
| 43 | 58   | 15.5 | 412  | 2 | B30605 acyl-CoA dehydroge |
| 44 | 58   | 15.5 | 529  | 2 | S18453 variant surface gl |
| 45 | 58   | 15.5 | 665  | 1 | H97093 fructose-bisphosph |

## ALIGNMENTS

RESULT 1  
S29242  
sucrose synthase (EC 2.4.1.13) Sal - barley  
N/Alternate names: sucrose-UDP glucosyltransferase; UDPglucose-fructose glucosyltransfer  
C/Species: Hordeum vulgare (barley)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 18-Jun-1999  
C/Accession: S29242; S21494  
R/de la Hoz, P.S.; Vicente-Carabajosa, J.; Mena, M.; Carbonero, P.  
FEBS Lett. 310, 46-50, 1992  
A/Title: Homologous sucrose synthase genes in barley (Hordeum vulgare) are located in ch  
A/Reference number: S29242; WUID:92405741; PMID:1188123  
A/Accession: S29242  
A/Molecule type: mRNA  
A/Residues: 1-807 <HOZ>  
A/Cross-references: EMBL:X65871; NID:G19105; PIDD:CAA46701.1; PID:G19106  
C/Genetic:  
A/Map position: 7H  
C/Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology  
C/Keywords: glycosyltransferase; hexosyltransferase  
F/276-749/Domain: sucrose/sucrose-phosphate synthase homology <SSPs>

Query Match 19.7%; Score 74; DB 2; Length 807;  
Best Local Similarity 27.7%; Pred. No. 1.9;  
Matches 26; Conservative 12; Mismatches 32; Indels 24; Gaps 3;

Qy 2 EESTIENYASR-----EAFNTPPLNIDKLSAFKAUDEFLLNMH---ALFESIKKRLPF 51  
Db 116 KEQLVDEHNSKRKVLDELDPFNASFPBSMSYKGVQFLNRHLSKLFQKESLPL 175

Qy 52 LNM-----DAFPKLGRLSATPDQ 71  
Db 176 LNFLLKHNKYGTTMINDRIQSLRGLQSLARKAE 209

RESULT 2  
G97561  
para-aminobenzoate synthase, component I VC1303 [Imported] - Agrobacterium tumefaciens (C/Species: Agrobacterium tumefaciens  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
C/Accession: G97561  
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Woliam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2322-2328, 2001  
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A/Reference number: A97359; WUID:21608551; PMID:11743194  
A/Accession: G97561  
A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1-390 <KCR>  
A/Cross-references: GB:AE007869; PIDD:AAK87448.1; PID:G15156766; GSPDB:GN00169  
C/Genetic:  
A/Gene: AGR\_C\_3082



QY 7 ENVASRPEAFNTPPLNIDKASAFKADDFLNMHALFESIKRKLPLNMDAPFKLGLRSRA 66  
 C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
 C/Accession: A75097  
 R:anonymous, Genoscope  
 Submitted to the EMBL Data Library, July 1999  
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str  
 A:Reference number: A75001  
 A:Accession: A75097  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-459 <XAM>  
 A:Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50078.1; PID:g545855  
 A:Experimental source: strain Orsay  
 C:Genetics:  
 A:Gene: PAB1598  
 C:Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTH15

Db 157 TPE 159  
 |||  
 |||

RESULT 7  
 S44861  
 DNA topoisomerase II - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 14-Sep-1994 #sequence\_revision 12-May-1995 #text\_change 23-Mar-2001  
 C/Accession: S44861  
 R:Wilson, R.  
 submitted to the EMBL Data Library, December 1992  
 A:Description: Sequence of the C. elegans cosmid R05D3.  
 A:Reference number: S44733  
 A:Accession: S44861  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-2434 <WIL>  
 A:Cross-references: EMBL:L07144; NID:g156412; PID:g156413  
 C:Genetics:  
 A:introns: 32/3; 128/3; 361/3; 506/1; 710/3; 1000/2; 1045/3; 1221/2; 1294/1; 1378/2; 145

Query Match 17.5%; Score 65.5; DB 2; Length 2434;  
 Best Local Similarity 31.6%; Pred. No. 67;  
 Matches 18; Conservative 10; Mismatches 18; Indels 11; Gaps 2;

QY 14 BAFNTPPLNIT---DKLRSAFKADDFLNMHALFESIKRKLPLNMDAPFKLGLRSAT 67  
 C/Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 03-Nov-2000  
 C/Accession: A71727  
 R:Andersson, S.G.E.; Zomrodipour, A.; Andersson, J.O.; Scharitz-Ponten, T.; Alemark, U  
 Nature 396, 133-140, 1998  
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.  
 A:Reference number: A71630; MUID:99039499; PMID:9823893  
 A:Accession: A71727  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-368 <AND>  
 A:Cross-references: GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA14632.1; PID:e134247  
 A:Experimental source: strain Madrid E  
 C:Genetics:  
 A:Gene: RP165  
 C:Superfamily: Rickettsia prowazekii hypothetical protein RP165

Db 206 EVYNAKRNITTTQHQVQINLVLPKINNEKSSSEAVGMFKYLNISGSAVYKAYEYLN 265  
 |||  
 |||

QY 7 ENVASRPEAFNTPPLNIDKASAFKADDFLNMHALFESIKRKLPLNMDAPFKLGLRSAT 37  
 C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
 C/Accession: A75097  
 R:anonymous, Genoscope  
 Submitted to the EMBL Data Library, July 1999  
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str  
 A:Reference number: A75001  
 A:Accession: A75097  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-459 <XAM>  
 A:Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50078.1; PID:g545855  
 A:Experimental source: strain Orsay  
 C:Genetics:  
 A:Gene: PAB1598  
 C:Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTH15

Db 38 WHALFESIKR-----LPLNMD 55  
 |||  
 |||

QY 266 FNKMFEGINNHKLKYFADLQDSAVIPIANWE 296  
 |||  
 |||

RESULT 9  
 A75097  
 hypothetical protein PAB1598 - Pyrococcus abyssi (strain Orsay)

Query Match 17.3%; Score 65; DB 2; Length 368;  
 Best Local Similarity 20.9%; Pred. No. 8.6;  
 Matches 19; Conservative 13; Mismatches 17; Indels 42; Gaps 3;

QY 7 ENVASRPEAFNTPPLNIDKASAFKADDFLNMHALFESIKRKLPLNMDAPFKLGLRSAT 37  
 C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
 C/Accession: A75097  
 R:anonymous, Genoscope  
 Submitted to the EMBL Data Library, July 1999  
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str  
 A:Reference number: A75001  
 A:Accession: A75097  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-459 <XAM>  
 A:Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50078.1; PID:g545855  
 A:Experimental source: strain Orsay  
 C:Genetics:  
 A:Gene: PAB1598  
 C:Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTH15

Db 59 ESETVLEDFSERLAEYFNDFLKNPLR-----NMGAFAYLAGK 98  
 |||  
 |||

QY 1 EBSSTIENYASR-PEAFNTPPLNIDKASAFKADDFLNMHALFESIKR 48  
 C/Date: 27-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 19-Apr-2002  
 C/Accession: S63181; S63189; S67375; S72093  
 R:Diesterhoef, A.; Floeth, M.; Fritz, C.; Heuss-Netzel, D.; Hilbert, H.; Moestl, D.  
 submitted to the Protein Sequence Database, April 1996  
 A:Reference number: S63188  
 A:Accession: S63181  
 A:Molecule type: DNA  
 A:Residues: 1-506 <DUE>  
 A:Cross-references: EMBL:Z71499; NID:g1302242; PID:e239624; PID:g1302243; MTPS:YNL223W  
 A:Experimental source: strain S288C  
 R:Pandolfo, D.; De Antoni, A.; Lanfranchi, G.; Valle, G.  
 submitted to the Protein Sequence Database, April 1996  
 A:Reference number: S63188  
 A:Accession: S63189  
 A:Molecule type: DNA  
 A:Residues: 1-506 <PAN>  
 A:Cross-references: EMBL:Z71499; NID:g1302242; PID:e239624; PID:g1302243; MTPS:YNL223W  
 A:Experimental source: strain S288C  
 R:Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G.  
 submitted to the EMBL Data Library, February 1996  
 A:Description: DNA sequence of cosmid 14-5 from chromosome XIV.  
 A:Reference number: S67355  
 A:Accession: S67375  
 A:Molecule type: DNA  
 A:Residues: 1-506 <PAM>  
 A:Cross-references: EMBL:Z69381; NID:g1183970; PID:e221819; PID:g1183991  
 R:Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G.  
 Yeast 12, 1071-1076, 1996  
 A:Title: The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open reading fra  
 A:Reference number: S72073; MUID:97051596; PMID:8896273  
 A:Accession: S72093  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-506 <PAF>  
 A:Cross-references: EMBL:Z69381; NID:g1183970; PIDN:CAA93375.1; PID:g1183991  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996  
 C:Genetics:  
 A:Gene: SGD:AUT2  
 A:Cross-references: SGD:S0005167  
 A:Map position: 14L  
 A:Note: YNL223W

```

Query Match      17.2%; Score 64.5; DB 2; Length 506;
Best Local Similarity 28.4%; Pred. No. 14;
Matches 19; Conservative 9; Mismatches 16; Indels 23; Gaps 2;

Oy      4 STIENYASPEAENTPF-----LNIDKRSAPKADFLNMHALFESIRK 47
Db      139 STIEDYIANDPCNTDIDGCMGIMRTGSLGALNQLIHLGRDFRVNG-----NESIER 191
Oy      48 KLPFLNW 54
Db      192 ESKFVNW 198

RESULT 11
JT0395
DNA-binding protein homolog - fruit fly (Drosophila melanogaster) transposon jockey
C:Species: Drosophila melanogaster
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Mar-1998
R:Pfimaegi, A.F.; Mizrokh, L.J.; Ilyin, Y.V.
Gene 70, 253-262, 1988
A>Title: The Drosophila mobile element jockey belongs to LINEs and contains coding sequence
A:Reference number: JT0395; MUID:89108005; PMID:2463954
A:Accession: JT0395
A:Molecule type: DNA
A:Residues: 1-583 <PRI>
A:Cross-references: GB:M2874; NID:g157823; PID:g157824
C:Genetics:
A:Gene: FlyBase:jockey
A:Cross-references: FlyBase:FBgn0001283
C:Keywords: DNA binding; zinc finger

Query Match      17.2%; Score 64.5; DB 2; Length 583;
Best Local Similarity 27.0%; Pred. No. 17;
Matches 17; Conservative 10; Mismatches 21; Indels 15; Gaps 3;

Oy      9 YASRPAAENTPFLNIDKRSAPKADFLNMHALFESIRKLPFLNWDAPPKLGRSATP 68
Db      274 YTANPAPFRTAVKELNKLNCQF-----WH---HQLKEKPYR-----VVLKGIHANVP 318
Oy      69 DAQ 71
Db      319 SEQ 321

RESULT 12
E97035
DNA polymerase I, polA [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
R:Noelling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E97035
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-871 <KUR>
A:Cross-references: GB:AE001437; PID:NAK79072.1; PID:g15024015; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1098
C:Superfamily: DNA-directed DNA polymerase I

Query Match      17.2%; Score 64.5; DB 2; Length 871;
Best Local Similarity 28.1%; Pred. No. 27;
Matches 27; Conservative 12; Mismatches 30; Indels 27; Gaps 4;

Oy      3 ESTIENYASRPE-----AFNTPF-LNIDKRSAPKADFLNMHAL-----FESIRKRL 49
Db      226 KENLENTAEBQAVESKCATITNTVPFIEIDIEIRKESDFEGARHLRLRLOPKSIITKTI 285

```

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Oy      50    PELNDA-----FPKLGJRSATPDAQ   71  
           ||| :|| |  
Db      286 PSINVEAKESDPVZEVYNLIDEPFKHELFSAIKDTIE 321
```

RESULT 13

A98038  

hypothetical protein sprl330 [imported] - Streptococcus pneumoniae (strain R6)  
CISpecies: Streptococcus pneumoniae  
CLdate: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #ext\_change 22-Oct-2001  
CAccession: A98038  
R.Hoekstra, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczyk, L.; Burgett, S.; Dehoff, B.S.;  
Y., P.; LeBlanc, D.J.; Lee, I.N.; Leftkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;  
P.; Sun, P.M.; Winler, M.E.  
J.Bacteriol. 183, 5709-5717, 2001  
A.Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.

AltTitle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A.Reference number: A97872; PMID:21429245; FMDI:11544234  
A.Accession: A98038  
A.Molecule type: DNA  
A.Status: preliminary  
A.Residues: 1-129 <Kur>  
A.Cross-references: GB:AEO07317; PIDN:AAL00134.1; PID:g15458975; GSPPDB:GN00174  
C.Genetics:  
A.Gene: sprl330

Query Match            16.9%; Score 63.5; DB 2; Length 129;  
Best Local Similarity     32.7%; Pred.No.3,8;  
Matches       18; Conservative      10; Mismatches    26; Indels     1; Gaps     1;

Oy          7 ENVASRPAPFMTPEFNIDKL-RSFAKDFFLMWHLFSISKRLPLFLNDAPPKL 60  
          :||::|||::|||||:|||||:|::|::|::|::|::|::|::|  
Db          70 KNYSIFEFYMRSFITVDKLVENLGSQAVLDSTHMLMATEKTLPILNMFWQQKL 124  
          ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 14

T19835  

hypothetical protein C38D9.5 - Caenorhabditis elegans  
CISpecies: Caenorhabditis elegans  
CLdate: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #ext\_change 29-Oct-1999  
CAccession: T19835; T27344  
R.Almscough, R.  
submitted to the EMBL Data Library, November 1996  
A.Reference number: Z19184  
A.Accession: T19835  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A.Molecule type: DNA  
A.Residues: 1-1213 <WTL>  
A.Cross-references: EMBL:L281481; PIDN:CAB03951.1; GSPPDB:GN00023; CESP:C38D9.5  
A.Experimental source: clone C3809  
R.Lloyd, C.  
submitted to the EMBL Data Library, March 1997  
A.Reference number: Z20348  
A.Accession: T27344  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A.Molecule type: DNA  
A.Residues: 1-1213 <WT2>  
A.Cross-references: EMBL:L292973; PIDN:CAB07494.1; GSPPDB:GN00023; CESP:C38D9.5  
A.Experimental source: clone Y6G8  
C.Genetic8:  
A.Map position: 5  
A.introns: 32/1, 490/3; 672/1; 770/2; 804/1; 863/1; 967/3; 1000/2; 1072/1

Query Match            16.8%; Score 63; DB 2; Length 1213;  
Best Local Similarity     30.9%; Pred.No.58;  
Matches       21; Conservative       6; Mismatches    13; Indels    28; Gaps     4;

Oy          23 IDKLASAFK-----ADEFLMWHLFSISKRLPLFLNDAPFK-----LKGG 62  
          ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db          465 VQSLSALSAGAAQLTVADT-----IFEVKTKTT--YMWDSTASYNSLSLTGTGLVDALKS 516  
          ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 63 LRSATPDA 70  
 Db 517 LKSNAPDA 524

RESULT 15

D81900  
 hypothetical protein NMA1314 [imported] - Neisseria meningitidis (strain Z2491 serogroup  
 C;Species: Neisseria meningitidis  
 C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
 C;Accession: D81900  
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
 ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
 Nature 404, 502-506, 2000  
 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
 A;Reference number: A81775; MUID:20222556; PMID:10761919  
 A;Accession: D81900  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-522 <PAR>  
 A;Cross-references: GB:AL162755; GB:AL157959; NID:G7379742; PIDN:CAB84566.1; PID:G737999  
 A;Experimental source: serogroup A, strain Z2491  
 C;Genetics:  
 A;Gene: NMA1314  
 C;Superfamily: Haemophilus influenzae hypothetical protein HI1501

Query Match 16.7%; Score 62.5; DB 2; Length 522;  
 Best Local Similarity 29.1%; Pred. No. 25;  
 Matches 23; Conservative 8; Mismatches 23; Indels 25; Gaps 4;

QY 10 ASRPEAFNTPEFLNIDKLSAP---KADEPLNHALPESI-----KKKLPL 52  
 Db 32 AEHPSNFTTP---QKRALPEDASGDIRAQHLELPADIERRDSDIANMGTGRGALLTL 87  
 QY 53 NMDAEPFLKGLRSATPDAQ 71  
 Db 88 NMRVAPP---RNATPEEE 102

Search completed: November 28, 2003, 13:41:04  
 Job time : 31 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:06:01 ; Search time 17 Seconds

(without alignments)  
196,406 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 375  
Sequence: 1 EBBSTIENYASRPBAFNTPF.....LWMDAPPKLKGARSATPAQ 71

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match Length | ID     | Description |
|------------|-------|--------------------|--------|-------------|
| 1          | 74    | 19.7               | 807 1  | SUS1 HORVU  |
| 2          | 68.5  | 18.3               | 413 1  | ACDS_PIG    |
| 3          | 67.5  | 18.0               | 521 1  | CP11_PLAFA  |
| 4          | 65.5  | 17.5               | 521 1  | CP11_PUEPL  |
| 5          | 65.5  | 17.5               | 521 1  | CP11_SEPAU  |
| 6          | 65.5  | 17.5               | 522 1  | CP11_ONCMY  |
| 7          | 65.5  | 17.5               | 1053 1 | TP2M_CABEL  |
| 8          | 65    | 17.3               | 368 1  | Y165_RICPR  |
| 9          | 64.5  | 17.2               | 506 1  | YNM3_YEAST  |
| 10         | 64.5  | 17.2               | 588 1  | GAGD_DROME  |
| 11         | 63.5  | 16.9               | 521 1  | CP11_LIMLI  |
| 12         | 63.5  | 16.9               | 520 1  | CP11_STECH  |
| 13         | 62.5  | 16.7               | 520 1  | CP11_DICLA  |
| 14         | 62    | 16.5               | 252 1  | PMG2_MOUSE  |
| 15         | 62    | 16.5               | 252 1  | PMG2_RAT    |
| 16         | 61    | 16.3               | 234 1  | TRMD_CAMUZ  |
| 17         | 60.5  | 16.1               | 384 1  | TMPE_TREPH  |
| 18         | 60    | 16.0               | 207 1  | Y552_HAEIN  |
| 19         | 60    | 16.0               | 1044 1 | BUB1_SCHPO  |
| 20         | 59.5  | 15.9               | 325 1  | TMPE_TREPA  |
| 21         | 59    | 15.7               | 277 1  | THTR_MYCLE  |
| 22         | 58.5  | 15.6               | 202 1  | WR55_ARATH  |
| 23         | 58.5  | 15.6               | 248 1  | GPMK_METAC  |
| 24         | 58.5  | 15.6               | 380 1  | VINT_BEP21  |
| 25         | 58.5  | 15.6               | 521 1  | CP11_LIZAU  |
| 26         | 58.5  | 15.6               | 521 1  | CP11_LIZSA  |
| 27         | 58    | 15.5               | 273 1  | AROE_BUCAP  |
| 28         | 58    | 15.5               | 412 1  | ACDS_HUMAN  |
| 29         | 58    | 15.5               | 529 1  | VSM6_TREYB  |
| 30         | 58    | 15.5               | 992 1  | VP41_YEAST  |
| 31         | 57.5  | 15.3               | 315 1  | VN35_ROTAL  |
| 32         | 57.5  | 15.3               | 522 1  | CP13_ONCMY  |
| 33         | 57.5  | 15.3               | 669 1  | CYK2_YEAST  |

|    |      |      |        |            |                     |
|----|------|------|--------|------------|---------------------|
| 34 | 57.5 | 15.3 | 1055 1 | UBPP_MOUSE | P57080 mus musculus |
| 35 | 57   | 15.2 | 252 1  | TRT3_COTJA | P06398 coturnix co  |
| 36 | 57   | 15.2 | 262 1  | TRT3_CHICK | P12620 gallus gall  |
| 37 | 57   | 15.2 | 353 1  | YG98_HAEIN | O05083 haemophilus  |
| 38 | 57   | 15.2 | 490 1  | Y035_CLOPE | O06373 clostridium  |
| 39 | 57   | 15.2 | 1709 1 | CHD1_HUMAN | O14646 homo sapien  |
| 40 | 57   | 15.2 | 1711 1 | CHD1_MOUSE | P40201 mus musculus |
| 41 | 57   | 15.2 | 2306 1 | POLG_POL32 | P06209 poliovirus   |
| 42 | 56.5 | 15.1 | 168 1  | DUT_ARCFU  | O29157 archaeoglob  |
| 43 | 56.5 | 15.1 | 460 1  | PGMT_NIEGO | P40390 neisseria g  |
| 44 | 56.5 | 15.1 | 487 1  | MAIO_CLOBU | O59266 clostridium  |
| 45 | 56.5 | 15.1 | 515 1  | CP11_PAGMA | P58181 pagrus major |

## ALIGNMENTS

RESULT 1  
ID SUS1\_HORVU STANDARD; PRT; 807 AA.  
AC P31922;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Sucrose synthase 1 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 1).  
GN SSI.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Abyssinian 2231; TISSUE=Endosperm;  
RX MEDLINE=92405741; PubMed=138123;  
RA Sanchez de la Hoz P., Vicente-Carbalosa J., Mena M., Carbonero P.;  
RT "Homologous sucrose synthase genes in barley (Hordeum vulgare) are  
RT located in chromosomes 7H (syn. 1) and 2H. Evidence for a gene  
RT translocation?";  
RL FEBS Lett. 310:46-50(1992).  
RN [2]  
RP SEQUENCE OF 223-807 FROM N.A.  
RC STRAIN=cv. Pallas;  
RA Brandt J., Thorald-Christensen H., Collinge D.B.;  
RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: SUCROSE-CLEAVING ENZYME THAT PROVIDES UDP-GLUCOSE AND  
CC FRUCTOSE FOR VARIOUS METABOLIC PATHWAYS.  
CC -1- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose  
CC -1- TISSUE-SPECIFICITY: HIGHLY EXPRESSED IN DEVELOPING ENDOSPERM AND  
CC IN ROOTS AND, AT LOWER LEVELS, IN COLEOPTILES AND ALERONE.  
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1. PLANT  
CC SUCROSE SYNTHASE SUBFAMILY.  
CC  
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CC  
CC EMBL; X65871; CAA46701.1; -;  
DR EMBL; X66728; CAA47264.1; -;  
DR PIR; S29242; S29242.  
DR InterPro; IPR001296; Glyco trans 1.  
DR InterPro; IPR000368; Sucrose synth.  
DR Pfam; PF00534; Glycose\_transf\_1;  
DR Pfam; PF00862; Sucrose\_synth; 1.  
KW transferase; Glycosyltransferase; Multigene family.  
FT CONFIDENT 370 370 I -> IL (IN REF. 2).  
FT CONFIDENT 374 374 I -> Y (IN REF. 2).  
FT CONFLICT 392 393 NE -> KO (IN REF. 2).  
SQ SEQUENCE 807 AA; 92211 MW; A863A8C876A060C8 CRC64;



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QY      67 TPD 69
DB      157 TPE 159

RESULT 4
CP11_PLEPL STANDARD; PRT; 521 AA.
ID CP11_PLEPL
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).
GN CYP1A1.
OS Pleuronectes plateasa (Plaice).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Pleuronectidae; Pleuronectes.
OX NCBI_TaxId=8262;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=94251288; PubMed=8193668;
RA Leaver M.J., Pittit L., George S.G.;
RT "Cytochrome P450 1A1 cDNA from plaice (Pleuronectes plateasa) and
RT induction of P450 1A1 mRNA in various tissues by 3-methylcholanthrene
RT and isoflavone."
RL Mol. Biol. Biotechnol. 2:338-345(1993).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- INDUCTION: BY 3-METHYLCOLANTHRENE (3MC) AND ISOCAFAROLE (ISF).
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC
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CC
CC -----
CC DR EMBL; X73631; CAAS2010.1; -.
CC PIR; S34184; S34184.
CC HSSP; P00179; 1DT6.
CC InterPro: IPR001128; Cytochrome_P450.
CC Pfam; PF00067; P450.1.
CC PRINTS; PR00385; P450.
CC PROSITE; PS00086; CYTOCHROME_P450; 1.
CC Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
CC Microsome; Endoplasmic reticulum.
CC FT METAL 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC SEQUENCE 521 AA; 55061 MW; AA7A97CB4578F956 CRC64;
SQ
Query Match 17.5%; Score 65.5; DB 1; Length 521;
Best Local Similarity 30.2%; Pred. No. 4.2;
Matches 19; Conservative 12; Mismatches 23; Indels 9; Gaps 3;
QY 7 ENYASRPEAFTPEFLINDIKRSAPKADFLNWHALFESIKRKLPLINMDAFPLKGLRGA 66
DB 106 DDFAGRPDIYSFRFINAGK-SLAFSTDAQVWRA-----RRKLAYSALRSFSTLBG---T 156
QY 67 TPD 69
DB 157 TPE 159
RESULT 5
CP11_SPAU

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ID CP11_SPAU STANDARD; PRT; 521 AA.
AC 042457; 042458;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).
GN CYP1A1.
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxId=8175;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cousinou M., Lopez-Barea J., Dorado G.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 175-521 FROM N.A.
RC TISSUE=Liver;
RA Tom M.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC
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CC
CC -----
CC DR EMBL; AF011223; AAB64297.1; -.
CC DR EMBL; AF005719; AAB62887.1; -.
CC HSSP; P00179; 1DT6.
CC InterPro: IPR001128; Cytochrome_P450.
CC Pfam; PF00067; P450.1.
CC PRINTS; PR00385; P450.
CC PROSITE; PS00086; CYTOCHROME_P450; 1.
CC Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
CC Microsome; Endoplasmic reticulum.
CC FT METAL 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC FT CONFLICT 175 177 LVK -> GTR (IN REF. 2).
CC FT CONFLICT 209 209 G -> A (IN REF. 2).
CC FT CONFLICT 212 212 Y -> S (IN REF. 2).
CC SEQUENCE 521 AA; 59122 MW; 8FE00D8640B303B CRC64;
SQ
Query Match 17.5%; Score 65.5; DB 1; Length 521;
Best Local Similarity 30.2%; Pred. No. 4.2;
Matches 19; Conservative 13; Mismatches 22; Indels 9; Gaps 3;
QY 7 ENYASRPEAFTPEFLINDIKRSAPKADFLNWHALFESIKRKLPLINMDAFPLKGLRGA 66
DB 106 DDFAGRPDIYSFRFINAGK-SLAFSTDAQVWRA-----RRKLAYSALRSFSTLBG---T 156
QY 67 TPD 69
DB 157 TPE 159
RESULT 6
CP11_ONCMY
ID CP11_ONCMY STANDARD; PRT; 522 AA.
AC 092110; 042195; P10609; P79830;
DT 01-JUL-1989 (Rel. 11, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

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28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1) (CYP1A2).  
 GN CYP1A1.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OK NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=94213487; PubMed=8161204;  
 RA Berntson A.K., Chen T.T.;  
 RT "Two unique CYP1 genes are expressed in response to 3-  
 RT methylcholanthrene treatment in rainbow trout."  
 RL Arch. Biochem. Biophys. 310:187-195(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Bailey G., You L., Harttig U.;  
 RT "Cloning, sequencing and functional expression of two trout CYP1A  
 RT cDNAs in yeast."  
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Bailey G., You L., Harttig U.;  
 RT "Cloning, sequencing and aflatxin B1 metabolism by multiple rainbow  
 RT trout CYP1A cDNAs expressed in yeast."  
 RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89078171; PubMed=3203599;  
 RA Heilmann L.J., Sheen Y.-Y., Bigelow S.W., Nebert D.W.;  
 RT "Trout P4501A1: cDNA and deduced protein sequence, expression in  
 RT liver, and evolutionary significance."  
 RL DNA 7:379-387(1988).  
 CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE  
 CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED  
 CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.  
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
 CC oxidized flavoprotein + H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.  
 CC -1- TISSUE SPECIFICITY: Liver.  
 CC -1- INDUCTION: By 3-methylcholanthrene (3MC).  
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.  
 CC -1- CAUTION: THE SEQUENCE FROM REF 4 WAS A CHIMERA: ITS N-TERMINAL  
 CC PART HAS BEEN SHOWN TO BE DERIVED FROM WHAT IS NOW KNOWN AS THE  
 CC CYP1A3. CYP1A1 HAS ALSO BEEN CALLED CYP1A2.  
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 CC -----  
 DR EMBL: S69278; AAD14036.1; -;  
 DR EMBL: U62797; AAB40627.1; -;  
 DR EMBL: AF015660; AAB69383.1; -;  
 DR EMBL: W21310; AAA49550.1; ALT\_SEQ.  
 DR PIR: A28789; A28789.  
 DR PIR: S51557; S51557.  
 DR HSSP: P00179; 1DT6.  
 DR InterPro: IPR001128; Cytochrome\_P450.  
 DR Pfam: PF00067; P450.1.  
 DR PRINTS: PR00385; P450.  
 DR PROSITE: PS00086; CYTOCHROME\_P450.1.  
 KM Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
 KM Microsome; Endoplasmic reticulum.  
 FT METAL 463 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
 FT CONFLICT 51 51 L -> P (IN REF. 3).  
 FT CONFLICT 97 97 V -> D (IN REF. 3).

FT CONFLICT 124 124 K -> N (IN REF. 3).  
 FT CONFLICT 306 306 Q -> H (IN REF. 3).  
 FT CONFLICT 390 390 T -> I (IN REF. 3).  
 FT CONFLICT 459 459 D -> G (IN REF. 2).  
 FT CONFLICT 470 470 R -> H (IN REF. 3).  
 FT CONFLICT 474 474 Y -> F (IN REF. 1).  
 FT CONFLICT 483 483 R -> K (IN REF. 2).  
 SQ SEQUENCE 522 AA; 59344 MW; 9D063B5891102C89 CRC64;  
 Query Match 17.5%; Score 65.5; DB 1; Length 522;  
 Best Local Similarity 31.7%; Pred. No. 4.2;  
 Matches 20; Conservative 11; Mismatches 23; Indels 9; Gaps 3;  
 QY 7 ENVASPEAPFPTPLNDKLRSAFAKADFLMHALFESIKRKLPLNWDAPFKLGRSA 66  
 DB 106 EDPGRPLVYFKFIN-DKSLATSTDKAGVWRA-----RKLMSALRSATLEG---T 156  
 QY 67 TPD 69  
 DB 157 TPE 159  
 RESULT 7  
 TP2M CAEEL STANDARD; PRT; 1053 AA.  
 AC P34534;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Putative DNA topoisomerase II, mitochondrial precursor (EC 5.99.1.3).  
 GN R05D3.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OK NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
 RA Fulton L., Gardner A., Green P., Hawkes J., Hillier L., Jier M.,  
 RA Johnston L., Jones M., Kersey J., Kirsten J., Lalister N.,  
 RA Latreille P., Lighthouse J., Lloyd C., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showman R.,  
 RA Sims M., Smailson N., Smith A., Smith M., Sonhammer E., Staden R.,  
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
 RA Watson R., Watson A., Weinstock L., Wilkinson-Sprat J.,  
 RA Wohldman P.;  
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RA elegans."  
 RL Nature 368:32-38(1994).  
 RN [2]  
 RP REVISIONS.  
 RA Waterston R.;  
 RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT  
 CC BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II  
 CC MAKES DOUBLE-STRAND BREAKS (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining  
 CC of double-stranded DNA.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.  
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```
CC EMBL: L07144; AAM54162.1; -
DR HSSP: P06786; 18GM
DR WORMBEP; R05D3.1; CB31047.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR001241; DNA_topoisom.
DR InterPro; IPR002205; DNA_topoisom.
DR Pfam; PF00204; DNA_gyraseB.1.
DR Pfam; PF00521; DNA_topoisomIV.1.
DR Pfam; PF02518; HATPase_C.1.
DR PRINTS; PR01158; TOPISMRASEB1.
DR PRINTS; PR00418; TP12FAMILY.
DR ProDom; PD000742; DNA_topoisomIV.1.
DR SMART; SM00433; TOP2C.1.
DR SMART; SM00434; TOP4C.1.
DR PROSITE; PS00117; TOPISOMERASE_II.1.
DR Hypothetical protein; Isomerase; Topoisomerase; DNA-binding;
KW ATP-binding; Mitochondrion; Transil peptide.
FT TRANSIT 1 1053 MITOCHONDRION (POTENTIAL).
FT CHAIN ? 1053 PUTATIVE DNA TOPOISOMERASE II.
FT NP BIND 60 65 ATP (POTENTIAL).
FT ACT_SITE 697 697 DNA CLAVAGE (BY SIMILARITY).
SQ SEQUENCE 1053 AA; 120285 MW; B8167P2E01BFEA45 CRC64;

Query Match 17.5%; Score 65.5; DB 1; Length 1053;
Best Local Similarity 31.6%; Pred. No. 9.1;
Matches 18; Conservative 10; Mismatches 18; Indels 11; Gaps 2;

QY 14 EAFNTPEPLNT---DKRSARFADEFLNWHALFESIKRKLPEFLWDAFPLKIGRSAT 67
Db 474 QSFRTPLKAKKGDVKVASFPSMNEYRKMAVDESGKKIKY-----YKGIQTST 522

RESULT 8
ID Y165_RICPR STANDARD; PRT; 368 AA.
AC 09ZD28;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein RPI65.
GN RPI65.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Madrid E;
RA MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sticheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140(1998).

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CC EMBL: AJ235270; CAA14632.1; -
DR PIR; A71727; A71727.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 368 AA; 41009 MW; 0410168F891F489C CRC64;

Query Match 17.3%; Score 65; DB 1; Length 368;
Best Local Similarity 20.9%; Pred. No. 3.3;
Matches 19; Conservative 13; Mismatches 17; Indels 42; Gaps 3;
```

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QY 7 ENTASRPEAPNT-----PFLNIDKLRSA-----FKADEFLN 37
Db 206 EYVNAKENINTINQHVQINLVLPRINNEKSKSSAVGWFKYLNISSAVYKVAEYLN 265

QY 38 WHALFESIKRK-----LPLNWD 55
Db 266 FNMCFEGINNKLKTRADLQDSAVIPIANWE 296

RESULT 9
ID YNM3_YEAST STANDARD; PRT; 506 AA.
AC P53867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 56.6 kDa protein in UBE2-S5U72 intergenic region.
GN YNL223W OR N1274.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97051596; PubMed=8896273;
RA Pandolfo D., de Antoni A., Lanfranchi G., Valle G.;
RT "The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open
RT reading frames including a novel gene encoding a globin-like
RT domain".
RL Yeast 12:1071-1076(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Duesterhoeft A., Floeth M., Fritze C., Heuss-Netzel D., Hilbert H.,
RA Moestl D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 13-506 FROM N.A.
RA Sun Z., Hampsey M.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.

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CC EMBL: Z69381; CAA3375.1; -
DR EMBL; Z71499; CAA6126.1; -
DR EMBL; U20390; AAA66498.1; -
DR PIR; S63181; S63181.
DR MEROPS; C54.001; -.
DR SCD; S0005167; AUT2.
DR GO; GO:0005875; C:microtubule associated complex; IPI.
DR GO; GO:0008017; F:microtubule binding activity; IPI.
DR GO; GO:0006914; P:autophagy; IMP.
DR GO; GO:0006623; P:protein-vacuolar targeting; IMP.
DR InterPro; IPR005078; Peptidase_C54.
DR Pfam; PF03416; Peptidase_C54; 2.
KM Hypothetical protein.
SQ SEQUENCE 506 AA; 56553 MW; 95EB599DC6DBB6F9 CRC64;

Query Match 17.2%; Score 64.5; DB 1; Length 506;
Best Local Similarity 28.4%; Pred. No. 5.4;
Matches 19; Conservative 9; Mismatches 16; Indels 23; Gaps 2;

QY 4 STTENTASRPEAPNTPF-----LNDIKRSAPKADFLNWHALFESIR 47
Db 139 STIEDIANPDCEFTDIDGWCWIRTGQSILGNALQILHGRDFRVNG-----NESLRR 191
QY 48 KLPLFLNW 54
```

Db 192 ESKFVNW 198

## RESULT 10

GAGJ\_DROME STANDARD; PRT; 568 AA.  
ID GAGJ\_DROME PRT; 568 AA.  
AC P21330;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Nucleic-acid-binding protein (mobile element jockey) (ORF1).  
GN GAG.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_Taxid=7227;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89108009; PubMed=2463954;  
RA Pritamegi A.F., Mizrokh L.J., Ilyin Y.V.;  
RT "Drosophila mobile element jockey is a retroposon and encodes the  
Dok1. Akad. Nauk SSSR 294:1235-1239 (1987)."  
CC CC  
CC -1- FUNCTION: STRONGLY BASIC PROTEIN THAT BINDS DIRECTLY TO  
RETRORVIRAL RNA AND MAY BE INVOLVED IN ITS PACKAGING AND  
IN THE REVERSE TRANSCRIPTION PROCESS.  
CC -1- SIMILARITY: STRONG TO THE EQUIVALENT PROTEIN OF DROSOPHILA  
FUNDBRIS.

CC CC  
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CC CC  
CC EMBL; M22874; AAA28674.1; ALT\_INIT.  
DR EMBL; M38643; AAA28939.1; ALT\_INIT.  
DR Flybase; Fgn0020297; jockey\gag.  
DR InterPro; IPR006579; Pte\_C2HC.  
DR InterPro; IPR001878; Znf\_C2HC.  
DR SMART; SM00596; Pte\_C2HC.1.  
DR SMART; SM00343; Znf\_C2HC.1.  
KW Transposable element; Zinc-finger.  
KW DOMAIN 350 444 THREE ZINC-FINGER-LIKE REGIONS.  
FT ZN\_FING 350 403 POTENTIAL.  
FT ZN\_FING 403 423 POTENTIAL.  
FT ZN\_FING 430 444 POTENTIAL.  
SQ SEQUENCE 568 AA; 62878 MW; DE084834A24C759A CRC64;

Query Match 17.2%; Score 64.5; DB 1; Length 568;  
Best Local Similarity 27.0%; Pred. No. 6.1;  
Matches 17; Conservative 10; Mismatches 21; Indels 15; Gaps 3;

QY 9 YASRPEAFNTPLNTDKLSAFKADEFLMWHALFESIKRKLPLNWDAPPKGLRSATP 68  
DB 259 YRANDAFRTAVKELNKNCQF-----WH---HQLKEKRYR-----VTLKGTHANVP 303  
QY 69 DAQ 71  
DB 304 SSO 306

RESULT 11  
CP11\_LIMLI STANDARD; PRT; 521 AA.  
ID CP11\_LIMLI STANDARD; PRT; 521 AA.  
AC 042430;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).  
GN CYP1A1.  
OS Limanda limanda (Dab).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorphi; Pleuronectiformes;  
OC Pleuronectidae; Pleuronectidae; Limanda.  
OX NCBI\_Taxid=27771;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=21315588; PubMed=11423384;  
RA Craft J.A., Robertson F.E., McPhail M.E., Brown E., Stagg R.M.;  
RT "Measurement of cytochrome P4501A induction in dab (Limanda limanda)  
and other teleosts with species-specific cDNA probes: Isolation and  
characterisation of dab cDNA and its use in expression studies with  
beta-naphthoflavone-treated fish.";  
RL Comp. Biochem. Physiol. 129C:115-127 (2001).  
CC CC  
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF STRUCTURALLY UNRELATED  
MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED  
COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.  
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +  
oxidized flavoprotein + H(2)O.  
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.  
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.

CC CC  
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CC CC  
CC EMBL; AJ001724; CAA04953.1; -.  
DR HSSP; P00179; 1D76.  
DR InterPro; IPR001128; Cytochrome\_P450.  
DR Pfam; PF00067; P450; 1.  
DR PRINTS; PR00385; P450.  
DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;  
KW Microsome; Endoplasmic reticulum.  
KW METAL 463 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
SQ SEQUENCE 521 AA; 59063 MW; 11DE326CA7BDF9 CRC64;

Query Match 16.9%; Score 63.5; DB 1; Length 521;  
Best Local Similarity 30.2%; Pred. No. 7.2;  
Matches 19; Conservative 13; Mismatches 22; Indels 9; Gaps 3;

QY 7 ENYASRPEAFNTPLNTDKLSAFKADEFLMWHALFESIKRKLPLNWDAPPKGLRSATP 66  
DB 106 DDPAGRPLVYFRFINSEK-SLAFSTDKAGIWR-----RKTLVYSLRSATLEG---T 156  
QY 67 TPD 69  
DB 157 TPE 159  
RESULT 12  
CP11\_STECH STANDARD; PRT; 521 AA.  
ID CP11\_STECH STANDARD; PRT; 521 AA.  
AC 092116;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).

```

GN CYP1A1.
OS Stenotomus chrysops (Scup).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Sparidae; Stenotomus.
OX NCBI_TaxID=35579;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95275266; PubMed=7755595;
RA Morrison H.G., Oleksiak M.F., Cornell N.W., Sogin M.L., Stegeman J.J.;
RT "Identification of cytochrome P-450 1A (CYP1A) genes from two teleost
RT fish, coadfish (Opsanus tau) and scup (Stenotomus chrysops), and
RT phylogenetic analysis of CYP1A genes.";
RL Biochem J 308:97-104(1995).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
CC COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
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CC -----
DR EMBL: U14162; AAA74969.1; -.
DR HSSP: P00179; 1DT6.
DR InterPro: IPR001128; Cytochrome_P450.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
DR OXidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT METAL 463 463 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 521 AA; 59019 MW; 8BDC4312074025D4 CRC64;

Query Match 16.7%; Score 63.5; DB 1; Length 521;
Best Local Similarity 30.2%; Pred. No. 7.2;
Matches 19; Conservative 12; Mismatches 23; Indels 9; Gaps 3;

QY 7 ENYASRPAFTPTFLNIDKLSAFKADBEFLNMHALFESIKRKLPELMDAPPKGLKLSA 66
DB 106 DXFAGRPDLYSFRFIN-DGKSLAFSTDAQVWRA-----RKLAYSALRSFATLGG---T 156
QY 67 TPD 69
DB 157 TPE 159

RESULT 13
CP11.DICLA STANDARD; PRT; 520 AA.
ID CP11.DICLA
AC P79716;
DR 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 28-PBB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 1A1 (EC 1.14.14.1) (CYP1A1).
GN CYP1A1.
OS Dicentrarchus labrax (European sea bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Moronidae; Dicentrarchus.
OX NCBI_TaxID=13489;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Liver;
RX MEDLINE=99138413; PubMed=9972466;
RA Stien X., Amichot M., Borge J.B., Lafaurie M.;
RT "Molecular cloning of a CYP1A cDNA from the teleost fish
RT Dicentrarchus labrax.";
RL Comp. Biochem. Physiol. 122C:241-248(1998).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
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CC -----
DR EMBL: U78316; AAB36951.1; -.
DR HSSP: P00179; 1DT6.
DR InterPro: IPR001128; Cytochrome_P450.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
DR OXidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT METAL 464 464 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 520 AA; 58743 MW; 86761584B28E57FB CRC64;

Query Match 16.7%; Score 62.5; DB 1; Length 520;
Best Local Similarity 30.6%; Pred. No. 9.4;
Matches 19; Conservative 9; Mismatches 25; Indels 9; Gaps 3;

QY 7 ENYASRPAFTPTFLNIDKLSAFKADBEFLNMHALFESIKRKLPELMDAPPKGLKLSA 66
DB 106 DXFAGRPDLYSFRFIN-DGKSLAFSTDAQVWRA-----RKLAYSALRSFATLGG---T 156
QY 67 TP 68
DB 157 TP 158

RESULT 14
PMG2_MOUSE STANDARD; PRT; 252 AA.
ID PMG2_MOUSE
AC O70250;
DR 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-SBP-2003 (Rel. 42, Last annotation update)
DE Phosphoglycerate mutase 2 (EC 5.4.2.1) (EC 5.4.2.4) (EC 3.1.3.13)
DE (Phosphoglycerate mutase isozyme M) (PGAM-M) (BPG-dependent PGAM 2)
DE (Muscle-specific phosphoglycerate mutase).
GN PGAM2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu G., Yu L., Tu Q., Jiang Y., Fan Y., Zhao S.;
RT "Cloning and expression analysis of a mouse gene coding
RT phosphoglycerate mutase muscle-specific subunit.".
RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21147938; PubMed=11250083;
RA Zhang J., Yu L., Fu Q., Gao J., Xie Y., Chen J., Zhang P., Liu Q.,

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RA Zhao S.;  
 RT "Mouse phosphoglycerate mutase M and B isozymes: cDNA cloning, enzyme  
 RT activity assay and mapping.";  
 RL Gene 264:273-279(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Meng U., Hsieh F.,  
 RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantini P., Prange C.,  
 RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunatirne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield V.S.N., Krzywinski M.T., Skalska U., Smalins D.E.,  
 RA Schnerich A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Interconversion of 3- and 2-phosphoglycerate with  
 CC 2,3-bisphosphoglycerate as the primer of the reaction. Can also  
 CC catalyze the reaction of EC 5.4.2.4 (synthase) and EC 3.1.3.13  
 CC (phosphatase), but with a reduced activity.  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate + 2,3-diphosphoglycerate  
 CC = 3-phospho-D-glycerate + 2,3-diphosphoglycerate.  
 CC -1- CATALYTIC ACTIVITY: 3-phospho-D-glyceroyl phosphate = 2,3-  
 CC bisphospho-D-glycerate.  
 CC -1- CATALYTIC ACTIVITY: 2,3-diphosphoglycerate + H(2)O = 3-  
 CC phosphoglycerate + phosphate.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- TISSUE SPECIFICITY: In mammalian tissues there are two types of  
 CC phosphoglycerate mutase isozymes: type-M in muscles and type-B in  
 CC other tissues.  
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE MUTASE FAMILY. BPG-  
 CC DEPENDENT PGAM SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; AF029843; AAC13263.1; -;  
 CC EMBL; AF317587; AAK06662.1; -;  
 CC EMBL; BC010750; AAH0750.1; -;  
 CC DR HSSP; P00950; SPGM.  
 CC DR MGD; MGI:1933118; PGAM2.  
 CC DR SWISS-2DPAGE; O70250; MCODE.  
 CC DR InterPro; IPR001345; PG/BPGM mutase.  
 CC DR InterPro; IPR005952; Phosphogly\_mut1.  
 CC DR Pfam; PF00300; PGAM; 1.  
 CC DR TIGRFAMs; TIGR01258; pgm\_1; 1.  
 CC DR PROSITE; PS00175; PG\_MUTASE; 1.  
 CC KW Isomerase; Hydrolase; Glycolysis.  
 CC FT INT MET 0  
 CC FT ACT\_SITE 10 10 BY SIMILARITY.  
 CC FT ACT\_SITE 61 61 PHOSPHOISTIDINE INTERMEDIATE  
 CC FT ACT\_SITE 185 185 (BY SIMILARITY).  
 CC FT ACT\_SITE 252 252 REQUIRED FOR BINDING CARBOXYL GROUP OF  
 CC FT ACT\_SITE 252 252 AA; 28696 MW; 7EB3F9C4B985B6 CRC64;  
 CC SEQUENCE

Query Match 16.5%; Score 62; DB 1; Length 252;  
 Best Local Similarity 30.5%; Pred. No. 4.9;  
 Matches 18; Conservative 11; Mismatches 18; Indels 12; Gaps 2;  
 Qy 15 AFNTP-----FLINDKLR--SAFRDEFLNHALPESIKRLPFLNMAFPPLK 61  
 Db 117 SFDTPPEPMDEKKNYTSISKDRRYAGLKPDELPTCESLMDTTLRALPFWNEETAPK 175  
 RESULT 15  
 PMG2 RAT STANDARD; PRT; 252 AA.  
 ID PMG2 RAT  
 AC P16290;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Phosphoglycerate mutase 2 (EC 5.4.2.1) (EC 5.4.2.4) (EC 3.1.3.13)  
 DE (Phosphoglycerate mutase isozyme M) (PGAM-M) (Bpg-dependent PGAM 2)  
 DE (Muscle-specific phosphoglycerate mutase).  
 GN PGAM2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=90121247; PubMed=2558656;  
 RA Castellana-Escola U., Montoliu L., Pons G., Puigdomenech P.,  
 RA Cohen-Solal M., Carreras J., Rigau J., Climent F.;  
 RT "Sequence of rat skeletal muscle phosphoglycerate mutase cDNA.";  
 RL Biochem. Biophys. Res. Commun. 165:1345-1351(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95011622; PubMed=7925808;  
 RA Ruiz-Lozano P., de Lecea L., Buena C., Perez de la Osa P.,  
 RA Lepege D., Gualberto A., Walsh K., Pons G.;  
 RT "The gene encoding rat phosphoglycerate mutase subunit M: cloning and  
 RT promoter analysis in skeletal muscle cells.";  
 RL Gene 147:243-248(1994).  
 CC -1- FUNCTION: Interconversion of 3- and 2-phosphoglycerate with  
 CC 2,3-bisphosphoglycerate as the primer of the reaction. Can also  
 CC catalyze the reaction of EC 5.4.2.4 (synthase) and EC 3.1.3.13  
 CC (phosphatase), but with a reduced activity.  
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate + 2,3-diphosphoglycerate  
 CC = 3-phospho-D-glycerate + 2,3-diphosphoglycerate.  
 CC -1- CATALYTIC ACTIVITY: 3-phospho-D-glyceroyl phosphate = 2,3-  
 CC bisphospho-D-glycerate.  
 CC -1- CATALYTIC ACTIVITY: 2,3-diphosphoglycerate + H(2)O = 3-  
 CC phosphoglycerate + phosphate.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- TISSUE SPECIFICITY: In mammalian tissues there are two types of  
 CC phosphoglycerate mutase isozymes: type-M in muscles and type-B in  
 CC other tissues.  
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE MUTASE FAMILY. BPG-  
 CC DEPENDENT PGAM SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC the European Bioinformatics Institute. There are no restrictions on its  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M31835; AAA41835.1; -;  
 CC EMBL; Z17319; CAA78967.1; -;  
 CC DR PIR; A33793; PMRTM.  
 CC DR HSSP; P00950; SPGM.  
 CC DR InterPro; IPR001345; PG/BPGM mutase.  
 CC DR InterPro; IPR005952; Phosphogly\_mut1.  
 CC DR Pfam; PF00300; PGAM; 1.  
 CC DR TIGRFAMs; TIGR01258; pgm\_1; 1.

DR PROSITE; PS00175; PG MUTASE; 1.  
 KM Isomerase; Hydrolase; Glycolysis.  
 FT INIT MET 0 0  
 FT ACT\_SITE 10 10 PHOSPHOISTIDINE INTERMEDIATE,  
 FT ACT\_SITE 61 61 REQUIRED FOR BINDING CARBOXYL GROUP OF  
 FT ACT\_SITE 185 185 PHOSPHOGLYCERATES.  
 SQ SEQUENCE 252 AA; 28624 MW; 4A3F118A0E4AD545 CRC64;

Query Match 16.5%; Score 62; DB 1; Length 252;  
 Best Local Similarity 30.5%; Pred. No. 4.9;  
 Matches 18; Conservative 11; Mismatches 18; Indels 12; Gaps 2;

QY 15 AFNTP-----FLINDKLR--SAFKADEFLNWHALFESIKRGLPFLNWDAPPKK 61  
 Db 117 SFDTPPPMDEKNNYASISKORRYAGLKPDELPTCESLKDTIARALPFWNEELAPKIK 175

Search completed: November 28, 2003, 13:39:28  
 Job time : 21 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:11:21 ; Search time 55 Seconds

(without alignments)  
333.122 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 375

Sequence: 1 EESTSTENASRPEANTPF.....LWMDAPFKUKGSRATPDAG 71

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP\_Archaea:\*  
2: SP\_Bacteria:\*  
3: SP\_Fungi:\*  
4: SP\_Human:\*  
5: SP\_Invertebrate:\*  
6: SP\_Mammal:\*  
7: SP\_Mhc:\*  
8: SP\_Organelle:\*  
9: SP\_Phage:\*  
10: SP\_Plant:\*  
11: SP\_Rodent:\*  
12: SP\_Virus:\*  
13: SP\_Vertebrate:\*  
14: SP\_Unclassified:\*  
15: SP\_Yvlnus:\*  
16: SP\_Bacteriaph:\*  
17: SP\_Archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID        | Description        |
|------------|-------|-------------|--------|-----------|--------------------|
| 1          | 72    | 19.2        | 390    | 16 Q8UES9 | Q8UES9 agrobacteri |
| 2          | 70    | 18.7        | 251    | 16 Q935B8 | Q935B8 salmoneila  |
| 3          | 69.5  | 18.5        | 407    | 11 Q8C4L6 | Q8C4L6 mus musculi |
| 4          | 67.5  | 18.0        | 439    | 13 Q98SG4 | Q98SG4 scophthalmu |
| 5          | 67.5  | 18.0        | 439    | 13 Q98SG7 | Q98SG7 platichthys |
| 6          | 67.5  | 18.0        | 521    | 13 Q90MD4 | Q90MD4 lithognathu |
| 7          | 67    | 17.9        | 203    | 4 Q9BSY6  | Q9BSY6 homo sapien |
| 8          | 67    | 17.9        | 912    | 5 Q8T034  | Q8T034 drosophila  |
| 9          | 66.5  | 17.7        | 521    | 13 Q90XPI | Q90XPI salmo salar |
| 10         | 66.5  | 17.7        | 522    | 13 Q8QGP2 | Q8QGP2 salmo salar |
| 11         | 66.5  | 17.7        | 522    | 13 Q9PRH3 | Q9PRH3 oncorhynch  |
| 12         | 66    | 17.6        | 808    | 10 Q83073 | Q83073 triticum ae |
| 13         | 65.5  | 17.5        | 258    | 16 Q8DSX6 | Q8DSX6 streptococc |
| 14         | 65    | 17.3        | 137    | 4 Q96EM8  | Q96EM8 homo sapien |
| 15         | 65    | 17.3        | 459    | 17 Q9UZH9 | Q9UZH9 pyrococcus  |
| 16         | 64.5  | 17.2        | 254    | 5 Q95W96  | Q95W96 heliocidari |

|    |      |      |      |           |                    |
|----|------|------|------|-----------|--------------------|
| 17 | 64.5 | 17.2 | 291  | 2 Q9FT8   | Q9FT8 acidovorax   |
| 18 | 64.5 | 17.2 | 871  | 16 Q9TK2  | Q9TK2 clostridium  |
| 19 | 64   | 17.1 | 519  | 13 Q9TY6  | Q9TY6 anguilla ja  |
| 20 | 64   | 17.1 | 519  | 13 Q9TY7  | Q9TY7 anguilla ja  |
| 21 | 64   | 17.1 | 521  | 13 Q8QG18 | Q8QG18 anguilla an |
| 22 | 64   | 17.1 | 819  | 16 Q8DEP2 | Q8DEP2 vibrio vuln |
| 23 | 63.5 | 16.9 | 129  | 16 Q8CYK6 | Q8CYK6 streptococc |
| 24 | 63   | 16.8 | 304  | 16 Q8XVQ2 | Q8XVQ2 raietonia s |
| 25 | 63   | 16.8 | 521  | 13 Q9Y164 | Q9Y164 fundulus he |
| 26 | 63   | 16.8 | 1213 | 5 Q9XTC7  | Q9XTC7 caenorhabd  |
| 27 | 62.5 | 16.7 | 359  | 16 Q8R863 | Q8R863 thermoaer   |
| 28 | 62.5 | 16.7 | 519  | 13 Q9PT96 | Q9PT96 dicentrarch |
| 29 | 62.5 | 16.7 | 522  | 16 Q9JZE2 | Q9JZE2 neisseria m |
| 30 | 62.5 | 16.7 | 522  | 16 Q9JZE2 | Q9JZE2 neisseria m |
| 31 | 62   | 16.5 | 253  | 5 Q9SW97  | Q9SW97 heliocidari |
| 32 | 61.5 | 16.4 | 506  | 9 Q64068  | Q64068 bacterioph  |
| 33 | 61.5 | 16.4 | 506  | 16 Q31953 | Q31953 bacillus su |
| 34 | 61.5 | 16.4 | 647  | 16 Q8F0E4 | Q8F0E4 leptospira  |
| 35 | 61   | 16.3 | 244  | 16 Q9K7J1 | Q9K7J1 bacillus ha |
| 36 | 61   | 16.3 | 439  | 13 Q98SK5 | Q98SK5 amodryes m  |
| 37 | 61   | 16.3 | 519  | 13 Q9UW07 | Q9UW07 brachydanio |
| 38 | 61   | 16.3 | 519  | 13 Q8QGS5 | Q8QGS5 brachydanio |
| 39 | 61   | 16.3 | 736  | 16 Q98Q68 | Q98Q68 mycoplasma  |
| 40 | 61   | 16.3 | 2344 | 3 Q74539  | Q74539 schizosacch |
| 41 | 60.5 | 16.1 | 276  | 16 Q9X0H7 | Q9X0H7 thermotoga  |
| 42 | 60.5 | 16.1 | 395  | 13 Q98TES | Q98TES oreochromis |
| 43 | 60.5 | 16.1 | 854  | 12 Q995Z2 | Q995Z2 enterovirus |
| 44 | 60.5 | 16.1 | 854  | 12 Q995Z1 | Q995Z1 enterovirus |
| 45 | 60.5 | 16.1 | 1232 | 17 Q58318 | Q58318 methanococc |

#### ALIGNMENTS

RESULT 1  
Q8UES9 PRELIMINARY; PRT; 390 AA.  
ID Q8UES9  
AC Q8UES9  
AD Q8UES9  
DT 01-UTN-2002 (TRENBLrel. 21, Created)  
DT 01-UTN-2002 (TRENBLrel. 21, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Para-aminobenzoate synthase component I.  
GN PAB3 OR ATU1676 OR AGR C 3082.  
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiales; Rhizobium.  
OC NCBI\_TaxID=176299;  
OX [1]  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21608550; PubMed=11743193;  
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
RA Okura V.K., Zhou Y., Chen L., Wood G.B., Almeida N.F., Jr., Woo L.,  
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,  
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palter A.,  
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,  
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung W., Krespan W., Petry M.,  
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
RA Gordon-Fleming F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
RA Nestor E.W.,  
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
C58".  
RL Science 294:2317-2323(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21608551; PubMed=11743194;  
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
RA Gurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,  
RA Houtmel K., Gordon J., Vaudin M., Tatchell O., Bpp A., Liu P.,  
RA Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Marfelz B.,  
RA Flanagan C., Crowell C., Gursen J., Lomo C., Seer C., Strub G.,  
RA Cielo C., Slater S.,  
RT "Genome sequence of the plant pathogen and biotechnology agent

RT Agrobacterium tumefaciens C58."  
 RL Science 294:2323-2328(2001).  
 DR EMBL; AB009124; AAL42676.1; ALT\_INIT.  
 DR EMBL; AB008089; AAK87448.1; -.  
 DR InterPro; IPR005801; Anth\_synth\_chor.  
 DR Pfam; PF00425; chorismate\_bind.1.  
 DR PRINTS; PR00079; ANTSNTASE1.  
 DR ProDom; PD000779; Anth\_synth\_chor.1.  
 KW Complete proteome.  
 SQ SEQUENCE 390 AA; 43232 MW; 65EB9B0D09E7FF16 CRC64;

Query Match 19.2%; Score 72; DB 16; Length 390;  
 Best Local Similarity 35.6%; Pred. No. 2.5;  
 Matches 26; Conservative 11; Mismatches 24; Indels 12; Gaps 4;

Qy 10 ASRPAFTPTPLNIDKLSAFK-ADEFLNMWA--LFE-----SIKRLPLNDAP-- 57  
 Db 34 ADEPAFTTALORMELRACKYLAGTMSYKGLFEPFLAPFAEPNVPPLNFGVSG 93  
 Qy 58 PRLKGLRSATPDA 70  
 Db 94 PQPDGRFARPDA 106

## RESULT 2

Q935B8 PRELIMINARY; PRT; 251 AA.

AC Q935B8;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical protein HCM2.0044c.  
 GN HCM2.0044c.  
 OS Salmonella typhi.  
 OC Plasmid phCM2.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CT18;  
 RX MEDLINE=21534947; PubMed=1677608;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jaseis K.,  
 RA Krogan A., Larsen T.S., Leachner S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrrell B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 RT enterica serovar Typhi CT18."  
 RL Nature 413:848-852(2001).  
 DR EMBL; AL513384; CAD09911.1; -.  
 KW Hypothetical protein; Plasmid; Complete proteome.  
 SQ SEQUENCE 251 AA; 29282 MW; DA64AB1473B4A3 CRC64;

Query Match 18.7%; Score 70; DB 16; Length 251;  
 Best Local Similarity 28.4%; Pred. No. 2.6;  
 Matches 21; Conservative 13; Mismatches 16; Indels 24; Gaps 4;

Qy 3 ESTIEN--VASRPAFTPTP-----LNIDKLSAFKAD-----BELNMHALFE 43  
 Db 19 DAFVNGRTYASRPIDFNDPALKYLIDFADFDVYKXKFFADNDEKTEBEFLAYSSFD 78  
 Qy 44 SIKRLPLNDAP 57  
 Db 79 ERAR-----SWTAY 87

RESULT 3  
 Q9C4L6 PRELIMINARY; PRT; 407 AA.

AC Q9C4L6;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Interfered: RIKEN CDNA 1110014F24.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK081753; BAC38319.1; -.  
 SQ SEQUENCE 407 AA; 42735 MW; 9D243DA7077983F6 CRC64;

Query Match 18.5%; Score 69.5; DB 11; Length 407;  
 Best Local Similarity 31.1%; Pred. No. 5.3;  
 Matches 19; Conservative 5; Mismatches 16; Indels 21; Gaps 3;

Qy 14 EAFVTPPLNIDKLSAFKA-DEFLNMWA-----LFEISIKRLPLN 53  
 Db 265 DASTLTP--NIDNFMENKSKTRPFLNMDAINKGAPSPSTALYFRKLWENFKSTPFN 323  
 Qy 54 W 54  
 Db 324 W 324

## RESULT 4

Q98SG4 PRELIMINARY; PRT; 439 AA.

AC Q98SG4;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Cytochrome P450A (Fragment).  
 GN CYP1A.  
 OS Scophthalmus maximus (turbot).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 CC Acanthomorphi; Acanthopterygii; Percomorpha; Pleuronectiformes;  
 CC Pleuronectoidae; Scophthalmidae; Scophthalmus.  
 OX NCBI\_TaxID=52904;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Craft J.A., Robertson F.E., McPhail M.E., Brown B., Stagg R.M.;  
 RT "Measurement of cytochrome P450A induction in dab (Limanda limanda)  
 RT and other teleosts with species-specific cDNA probes: isolation and  
 RT characterization of dab cDNA and its use in expression studies with b-  
 RT naphthoflavone-treated fish."  
 RL Comp. Biochem. Physiol. 129:115-127(2001).  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR EMBL; AJ310694; CAC34401.1; -.  
 DR HSSP; P00179; 1D76.  
 DR InterPro; IPR001128; Cytochrome\_P450.  
 DR Pfam; PF00067; P450.1.  
 DR PRINTS; PR00385; P450.  
 DR PROSITE; PS00086; CYTOCHROME\_P450; 1.  
 KW Heme; Monooxygenase; Oxidoreductase.  
 FT NON\_TER 1  
 FT NON\_TER 439  
 SQ SEQUENCE 439 AA; 49589 MW; 564ECC5864C696B5 CRC64;

Query Match 18.0%; Score 67.5; DB 13; Length 439;  
 Best Local Similarity 31.7%; Pred. No. 10;  
 Matches 20; Conservative 11; Mismatches 23; Indels 9; Gaps 3;



```

QY 7 ENVASRPEAFNTPFLNIDKLSAFKADDEFILNWHALFESIKRKLPLFNMWDAFPKLKGLRSA 66
  77 EEFAGRPDLYSRFRFLN-DKSLAFSTDAQVWRA-----RRKLAYSALRSFSTLGG--T 127
Db 67 TPD 69
  128 TPE 130

QY 67 TPD 69
  128 TPE 130

RESULT 5
Q98SG7 PRELIMINARY; PRT; 439 AA.
ID 098SG7;
AC 098SG7;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Cytochrome P4501A (Fragment).
GN CYP1A.
OS Platicthys flesus (European flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoides; Pleuronectidae; Platicthys.
OC NCBI_Taxid=8260;
OX [1]
RN SEQUENCE FROM N.A.
RA Crafe J.A., Robertson F.E., McPhail M.E., Brown E., Stagg R.M.;
RT Measurement of cytochrome P4501A induction in dab (Limanda limanda)
RT and other teleosts with species-specific cDNA probes: Isolation and
RT characterization of dab cDNA and its use in expression studies with b-
RT naphthoflavone-treated fish."
RL Comp. Biochem. Physiol. 129:115-127(2001)
CC -1. SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AJ310693; CAC34310.1; -.
DR HSSP; P00179; IDTG.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450.1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
DR Heme; Monooxygenase; Oxidoreductase.
KW Heme; Monooxygenase; Oxidoreductase.
FT NON_TER 1
FT NON_TER 439
SQ SEQUENCE 439 AA; 49571 MW; A8CE6449C8B12CA CRC64;

Query Match 18.0%; Score 67.5; DB 13; Length 439;
Best Local Similarity 30.2%; Pred. No. 10;
Matches 19; Conservative 13; Mismatches 22; Indels 9; Gaps 3;

QY 7 ENVASRPEAFNTPFLNIDKLSAFKADDEFILNWHALFESIKRKLPLFNMWDAFPKLKGLRSA 66
  77 EEFAGRPDLYSRFRFLN-DKSLAFSTDAQVWRA-----RRKLAYSALRSFSTLGG--T 127
Db 67 TPD 69
  128 TPE 130

QY 67 TPD 69
  128 TPE 130

RESULT 6
Q90WD4 PRELIMINARY; PRT; 521 AA.
ID 090WD4;
AC 090WD4;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Cytochrome P4501A.
OS Lithognathus morrulus (Striped seabream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Lithognathus.
OC NCBI_Taxid=50591;
OX [1]
RN SEQUENCE FROM N.A.

```

```

RC TISSUE=Liver;
RA Tom M.;
RT "A cytochrome P450 (CYP1A) cDNA from the liver of the spard fish
RT Lithognathus morrulus."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1. SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AF264037; AAK69390.1; -.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450.1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 521 AA; 59409 MW; 48B25B37DBDD78B6 CRC64;

Query Match 18.0%; Score 67.5; DB 13; Length 521;
Best Local Similarity 31.7%; Pred. No. 12;
Matches 20; Conservative 11; Mismatches 23; Indels 9; Gaps 3;

QY 7 ENVASRPEAFNTPFLNIDKLSAFKADDEFILNWHALFESIKRKLPLFNMWDAFPKLKGLRSA 66
  106 EEFAGRPDLYSRFRFLN-DKSLAFSTDAQVWRA-----RRKLAYSALRSFSTLGG--T 156
Db 67 TPD 69
  157 TPE 159

QY 67 TPD 69
  157 TPE 159

RESULT 7
Q9BSY6 PRELIMINARY; PRT; 203 AA.
ID 09BSY6;
AC 09BSY6;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE Similar to RIKEN CDNA 1110014F24 gene (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_Taxid=9606;
OX [1]
RN SEQUENCE FROM N.A.
RA Straussberg R.;
RC TISSUE=Uterus;
RA Straussberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004493; AAH04493.1; -.
FT NON_TER 1
FT NON_TER 203
SQ SEQUENCE 203 AA; 22128 MW; F59B8BA9B644A6CC CRC64;

Query Match 17.9%; Score 67; DB 4; Length 203;
Best Local Similarity 28.6%; Pred. No. 4.7;
Matches 20; Conservative 6; Mismatches 22; Indels 22; Gaps 3;

QY 7 ENVASRPEAFNTPFLNIDKLSAFKADDEFILNWHALFESIKRKLPLFNMWDAFPKLKGLRSA 66
  56 DNY--RNSRTSPGMNPFDFWKNFYSKGLFTIMWDAINKNQVPPSTRALLYSRLMEDRK 113
Db 47 RKLPLFNMWDA 56
  114 QNTPLFNMWKA 123

QY 47 RKLPLFNMWDA 56
  114 QNTPLFNMWKA 123

RESULT 8
Q8T034 PRELIMINARY; PRT; 912 AA.
ID 08T034;
AC 08T034;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE LD34564p.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

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```

OC Ephydroidea, Drosophilidae, Drosophila.
OX NCB1_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brockstein P., Hong L., Aghayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Fattah D., Frise E., George R.,
RA Gonzalez M., Guatin H., Li P., Lao G., Miranda A., Mungall C.J.,
RA Munoz J., Paclob J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF065955; AAL39740.1;
DR FlyBase; FBgn0034847; CG3502.
DR InterPro; IPR001930; Ala_peptase.
DR InterPro; IPR006025; Zn_MTPeptide.
DR Pfam; PF01433; Peptidase_M1; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 912 AA, 105630 MW, AF07209CD5EBB2A0 CRC64;

Query Match 17.9%; Score 67; DB 5; Length 912;
Best Local Similarity 31.7%; Pred. No. 27;
Matches 20; Conservative 7; Mismatches 18; Indels 18; Gaps 2;

Qy 24 DKLSAFKADFLNMH-----AL-----PESIRKLPFLWMDAPFKLGKLSA 65
Db 636 DLLEYLKEQDFLPQRAIGILNRLGALLNVAENKFKYWKLLLLYNRPFKLSGIRE 695

Qy 66 ATP 68
Db 696 AKP 698

RESULT 9
Q90XPI PRELIMINARY; PRT; 521 AA.
ID Q90XPI;
AC Q90XPI;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Cytochrome P450 1A.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCB1_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RA Arlwe A.;
RT "Molecular cloning, sequence analysis and expression of the cytochrome
RT P4501A gene in Atlantic salmon (Salmo salar).";
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AF364076; AAK52513.2;
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450.1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KM Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 521 AA, 58574 MW, C1859561E453F5CC CRC64;

Query Match 17.7%; Score 66.5; DB 13; Length 521;
Best Local Similarity 31.7%; Pred. No. 16;
Matches 20; Conservative 12; Mismatches 22; Indels 9; Gaps 3;

Qy 7 ENVASRPKAFNTPLNIDKLSAFKADFLNMHAFESIRKLPFLWMDAPFKLGKLSA 66
Db 106 EDFAGRPDIYSFKFIN-DGKSLAFSTDKAGVWRA-----RRKLMSALRSFATLEG--S 156

Qy 67 TPD 69
Db 157 TPE 159
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RESULT 10
Q90GP2 PRELIMINARY; PRT; 522 AA.
ID Q90GP2;
AC Q90GP2;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Cytochrome P450 1A.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCB1_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RA Rees C.B., Li W.;
RT "Cloning and induction of Atlantic salmon CYP1A.";
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AF361643; AAM00254.1;
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450.1.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KM Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 522 AA, 59192 MW, 560C4E10F704A568 CRC64;

Query Match 17.7%; Score 66.5; DB 13; Length 522;
Best Local Similarity 31.7%; Pred. No. 16;
Matches 20; Conservative 12; Mismatches 22; Indels 9; Gaps 3;

Qy 7 ENVASRPKAFNTPLNIDKLSAFKADFLNMHAFESIRKLPFLWMDAPFKLGKLSA 66
Db 106 EDFAGRPDIYSFKFIN-DGKSLAFSTDKAGVWRA-----RRKLMSALRSFATLEG--S 156

Qy 67 TPD 69
Db 157 TPE 159

RESULT 11
Q9PRH3 PRELIMINARY; PRT; 522 AA.
ID Q9PRH3;
AC Q9PRH3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Cytochrome P450 1A3.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCB1_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUS=Liver;
RA Caravan M.J., III, Ponomareva L.V., Solis W.A., Matlib R.S., Puga A.;
RA Nebert D.W.;
RT "Trout CYP1A3 Gene: Recognition of Fish DNA Motifs by Mouse Regulatory
RT Proteins.";
RL Submitted (APR-1998) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AF059711; AAD45967.1;
DR EMBL; AF059710; AAD45966.1;
DR HSSP; P00179; 1DT6.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450.1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KM Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 522 AA, 59086 MW, AF36786EB19D73DA CRC64;
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Query Match 17.7%; Score 66.5; DB 13; Length 522;  
 Best Local Similarity 31.7%; Pred. No. 16;  
 Matches 20; Conservative 12; Mismatches 22; Indels 9; Gaps 3;

QY 7 ENVASRPEAFNPFLINIDKLSAFKADFLNMAHAFESIKRKLPLINDAPFKLGLRSLA 66  
 DB 106 EDFAGRPDLSPKFLIN-DKSLAFSTDKAGVRA-----RRKLMSALRSFATLGG----S 156

QY 67 TPD 69  
 DB 157 TPE 159

RESULT 12  
 082073 PRELIMINARY; PRT; 808 AA.

AC 082073;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)  
 DE Sucrose synthase type 1.  
 GN SSI.  
 OS Triticum aestivum (Wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticaceae; Triticum.  
 OC NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Chinese Spring; TISSUE=developing endosperm;  
 RA Guerin J.R., Acevedo F.M., Carbonero P.;  
 RT "Complete Triticum aestivum sucrose synthase type 1 mRNA."  
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ001117; CAA04543.1; -  
 DR InterPro; IPR001296; Glyco. trans. 1.  
 DR InterPro; IPR000368; Sucrose synth.  
 DR Pfam; PF00534; Glycos. transf. 1.  
 DR Pfam; PF00862; Sucrose synth.; 1.  
 DR SEQUENCE 808 AA; 92521 MW; 4D8D29C94055BEF CRC64;

Query Match 17.6%; Score 66; DB 10; Length 808;  
 Best Local Similarity 26.6%; Pred. No. 30;  
 Matches 25; Conservative 11; Mismatches 34; Indels 24; Gaps 3;

QY 2 BESTTENTASRP-----EAFNPFLINIDKLSAFKADFLNMAH--ALFESIKRKL 51  
 DB 116 KEQVDEHASSKFLVLELDFEPFNASFPSPMSNSIGKRVQFLNRLSSQLFQDKSLVPL 175

QY 52 LNM-----DAFPKLGLRSATPDAG 71  
 DB 176 LNFLLAHYKGTMMLNDRIGSLRGLQSLARKRAE 209

RESULT 13  
 08DSX6 PRELIMINARY; PRT; 258 AA.

AC 08DSX6;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)  
 DE Purative peptidyl-prolyl cis-trans isomerase.  
 GN SMU.1631.  
 OS Streptococcus mutans.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OC NCBI\_TaxID=1309;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UA159 / ATCC 700610 / Serotype C;  
 RX MEDLINE=22295063; PubMed=12397186;  
 RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,  
 RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,  
 Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;

RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental  
 pathogen.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).  
 DR EMBL; AE014994; AAN59271.1; -  
 KW Isomerase; Complete proteome.  
 SQ SEQUENCE 258 AA; 28657 MW; 98785632CFP345E CRC64;

Query Match 17.5%; Score 65.5; DB 16; Length 258;  
 Best Local Similarity 41.0%; Pred. No. 9.4;  
 Matches 16; Conservative 6; Mismatches 14; Indels 3; Gaps 1;

QY 22 NIDKLSAFKADFLNMAHAFESIKRKLPLINDAPFKL 60  
 DB 20 NIDR---AIKGDKYVNHIAKOKANKKQLKQKADFPOL 55

RESULT 14  
 096EW8 PRELIMINARY; PRT; 137 AA.

AC 096EW8;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE Similar to hypothetical gene ZD52F10.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=uterus;  
 RA Strausberg R.;  
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC011886; AAH11886.1; -  
 SQ SEQUENCE 137 AA; 15484 MW; 5830C737DA329566 CRC64;

Query Match 17.3%; Score 65; DB 4; Length 137;  
 Best Local Similarity 30.9%; Pred. No. 5.2;  
 Matches 17; Conservative 4; Mismatches 14; Indels 20; Gaps 2;

QY 22 NIDKLSAFKAD-FLNMAH-----LPEISIKRKLPLINDA 56  
 DB 3 NFDIFWKNFKSKGLFINWDALNKQVPPSTRALLYSRLLWEDKQNTPLNMA 57

RESULT 15  
 09UZH9 PRELIMINARY; PRT; 459 AA.

AC 09UZH9;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)  
 DE Hypothetical protein PAB1598.  
 GN PAB1598.  
 OS Pyrococcus abyssi.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 OC NCBI\_TaxID=29292;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GES / Ozeay;  
 RA Hellig R.;  
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome  
 structure and evolution.";  
 RL Submitted (Jul-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ248286; CAB50078.1; -  
 DR InterPro; IPR004256; DUF234.  
 DR InterPro; IPR004309; DUF238.  
 DR Pfam; PF03008; DUF234; 1.  
 DR Pfam; PF03075; DUF238; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 459 AA; 53935 MW; E0A154DDA218C539 CRC64;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 08:03:47 ; Search time 19 Seconds

(without alignments)  
501.089 Million cell updates/sec

Title: US-10-059-395-142

Sequence: 1 MKIPVLPAAVLLSLVLSA.....LNMDAFPKLGHSATPDAQ 99

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 8     | 8.1         | 150    | 1 NRBO   | pancreatic ribonuc |
| 2          | 8     | 8.1         | 167    | 2 S20066 | pancreatic-type ri |
| 3          | 8     | 8.1         | 184    | 2 AF0298 | probable yfABCD 1  |
| 4          | 8     | 8.1         | 219    | 2 AG0333 | heme exporter prot |
| 5          | 8     | 8.1         | 222    | 2 B82125 | heme exporter prot |
| 6          | 8     | 8.1         | 428    | 2 D97010 | 5-enolpyruvylshik  |
| 7          | 8     | 8.1         | 480    | 2 D81220 | NADH dehydrogenase |
| 8          | 7     | 7.1         | 125    | 2 D72658 | hypothetical prote |
| 9          | 7     | 7.1         | 132    | 2 H75548 | hypothetical prote |
| 10         | 7     | 7.1         | 133    | 2 E71311 | hypothetical prote |
| 11         | 7     | 7.1         | 202    | 2 A83448 | hypothetical prote |
| 12         | 7     | 7.1         | 213    | 2 F95198 | hypothetical prote |
| 13         | 7     | 7.1         | 218    | 1 S21664 | heme export protel |
| 14         | 7     | 7.1         | 221    | 1 F64166 | conserved hypotet  |
| 15         | 7     | 7.1         | 244    | 2 A69502 | cytochrome-c oxida |
| 16         | 7     | 7.1         | 247    | 1 OBHQMS | cytochrome-c oxida |
| 17         | 7     | 7.1         | 247    | 2 S42736 | cytochrome-c oxida |
| 18         | 7     | 7.1         | 247    | 2 S42737 | cytochrome-c oxida |
| 19         | 7     | 7.1         | 247    | 2 S42739 | cytochrome-c oxida |
| 20         | 7     | 7.1         | 247    | 2 AC2659 | conserved hypotet  |
| 21         | 7     | 7.1         | 260    | 2 C97481 | 1828 [imported] -  |
| 22         | 7     | 7.1         | 311    | 1 BYEBT  | sulfate-binding pr |
| 23         | 7     | 7.1         | 339    | 2 AG0942 | periplasmic sulpha |
| 24         | 7     | 7.1         | 350    | 2 S35631 | genome polypeptid  |
| 25         | 7     | 7.1         | 350    | 2 A70473 | flagellar biosynth |
| 26         | 7     | 7.1         | 361    | 2 I50505 | gene wnt6 protein  |
| 27         | 7     | 7.1         | 372    | 1 WMVZCN | major envelope ant |
| 28         | 7     | 7.1         | 372    | 2 C72155 | E13l protein - var |
| 29         | 7     | 7.1         | 372    | 2 H36840 | C17l protein - var |

|    |   |     |     |          |                    |
|----|---|-----|-----|----------|--------------------|
| 30 | 7 | 7.1 | 372 | 2 T28475 | hypothetical prote |
| 31 | 7 | 7.1 | 372 | 2 G90322 | hypothetical prote |
| 32 | 7 | 7.1 | 386 | 1 S41691 | ubiquinol-cytochro |
| 33 | 7 | 7.1 | 410 | 2 S70647 | neuroserpin precur |
| 34 | 7 | 7.1 | 437 | 2 D69519 | tRNA nucleotidyltr |
| 35 | 7 | 7.1 | 447 | 2 B82490 | probable Na+/H+ an |
| 36 | 7 | 7.1 | 451 | 2 A38099 | glycylpeptide N-te |
| 37 | 7 | 7.1 | 457 | 2 I73636 | neuronal olfactome |
| 38 | 7 | 7.1 | 470 | 2 B87506 | hypothetical prote |
| 39 | 7 | 7.1 | 484 | 2 H63298 | hypothetical prote |
| 40 | 7 | 7.1 | 494 | 2 AC0133 | hypothetical prote |
| 41 | 7 | 7.1 | 519 | 2 T45764 | probable permease  |
| 42 | 7 | 7.1 | 542 | 2 D90944 | hypothetical prote |
| 43 | 7 | 7.1 | 542 | 2 H85792 | hypothetical prote |
| 44 | 7 | 7.1 | 542 | 2 G64942 | hypothetical prote |
| 45 | 7 | 7.1 | 546 | 2 AB0088 | probable flagellar |

#### ALIGNMENTS

##### RESULT 1

NRBO  
pancreatic ribonuclease (BC 3.1.27.5) precursor [validated] - bovine

N:Alternate names: ribonuclease 1; ribonuclease A  
C:Species: Bos primigenius taurus (cattle)

C>Date: 24-Apr-1984 #sequence revision 05-Aug-1994 #text change 15-Sep-2000  
A:Accession: S00897; I45998; A32471; A00804; A92018; A61293; S33757; S03528

R:Carana, A.; Contalonne, E.; Palmieri, M.; Libonatti, M.; Furia, A.  
Nucleic Acids Res. 16, 5491-5502, 1988

A:Title: Structure of the bovine pancreatic ribonuclease gene: the unique intervening se  
A:Reference number: S00897; MUID:88262557; PMID:2838818

A:Accession: S00897  
A:Molecule type: DNA

A:Residues: 1-150 <CAR>

A:Cross-references: EMBL:X07283; NID:9671; PIDN:CAA30263.1; PID:9672

R:Vasanthi, N.; Filipula, D.  
Gene 76, 53-60, 1989

A:Title: Expression of bovine pancreatic ribonuclease A coded by a synthetic gene in Bac  
A:Reference number: I45998; MUID:89306659; PMID:2501158

A:Accession: I45998  
A:Molecule type: DNA

A:Status: translated from GB/EMBL/DBJ

A:Residues: 'M', 27-150 <VAS>

A:Cross-references: EMBL:X15802; NID:993; PIDN:CAA33801.1; PID:994

A>Note: recombinant gene expressed in E. coli  
R:Robertson, A.D.; Purisima, E.O.; Eastman, M.A.; Scheraga, H.A.  
Biochemistry 28, 5930-5938, 1989

A:Title: Proton NMR assignments and regular backbone structure of bovine pancreatic ribo  
A:Reference number: A32471; MUID:89375525; PMID:2775743

A:Accession: A32471  
A:Molecule type: protein

A:Residues: 27-150 <ROB>  
R:Smyley, D.G.; Stein, W.H.; Moore, S.

J. Biol. Chem. 238, 227-234, 1963  
A:Title: The sequence of amino acid residues in bovine pancreatic ribonuclease: revisior

A:Reference number: A92016  
A:Accession: A00804

A:Molecule type: protein  
A:Residues: 27-150 <SMY>

A>Note: disulfide bonds were determined  
R:Plummer Jr., T.H.; Hirs, C.H.W.

J. Biol. Chem. 239, 2530-2538, 1964  
A:Title: On the structure of bovine pancreatic ribonuclease B. Isolation of a glycopepti

A:Reference number: A92018  
A:Accession: A92018

A:Molecule type: protein  
A:Residues: 27-150 <PLU>

R:Numagai, H.; Yoshihara, K.; Umemoto, M.; Igarashi, K.; Hirose, S.; Ohgi, K.; Irie, M.  
J. Biochem. 93, 865-874, 1983

A:Title: Studies on salivary gland ribonucleases. III. Purification and properties of th  
A:Reference number: A61293; MUID:83265672; PMID:6874668

A:Accession: A61293

A.Molecule type: protein  
 A.Residues: 27-40, 'XX', '43, 'X', '45-46 <KIM>  
 R.Yang, H.J.; Teou, C.L.  
 Biochem. J. 305, 379-384, 1995  
 A.Title: Inactivation during denaturation of ribonuclease A by guanidinium chloride is a  
 A.Reference number: S53757; PMID:95134214; PMID:7832749  
 A.Accession: S53757  
 A.Molecule type: protein  
 A.Residues: 27-53;60-63;69-73 <YAN>  
 R.Birdsall, D.L.; McPherson, A.  
 submitted to the Brookhaven Protein Data Bank, August 1992  
 A.Reference number: A51385; PDB:1RTB  
 A.Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 27-150  
 R.Birdsall, D.L.; McPherson, A.  
 J. Biol. Chem. 267, 22330-22336, 1992  
 A.Title: Crystal structure disposition of thymidylate acid tetramer in complex with ribon  
 A.Reference number: A44321; PMID:93054504; PMID:1429575  
 A.Contents: annotation; X-ray crystallography, 2.5 angstroms  
 R.Williams, R.L.; Greene, S.M.; McPherson, A.  
 submitted to the Brookhaven Protein Data Bank, September 1987  
 A.Reference number: A50330; PDB:1RBB  
 A.Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 27-150  
 R.Wlodawer, A.  
 submitted to the Brookhaven Protein Data Bank, April 1985  
 A.Reference number: A50927; PDB:5RSA  
 A.Contents: annotation; X-ray and neutron crystallography, 2.0 angstroms, residues 27-15  
 R.Wlodawer, A.; Bott, R.; Sjolvin, L.  
 J. Biol. Chem. 257, 1325-1332, 1982  
 A.Title: The refined crystal structure of ribonuclease A at 2.0 angstrom resolution.  
 A.Reference number: A92350; PMID:82120062; PMID:6278380  
 A.Contents: annotation; X-ray crystallography, 2.0 angstroms  
 R.Howlin, B.; Moss, D.S.; Harris, G.W.; Palmer, R.A.  
 submitted to the Brookhaven Protein Data Bank, October 1991  
 A.Reference number: A50626; PDB:3RNB  
 A.Contents: annotation; X-ray crystallography, 1.45 angstroms, residues 27-150  
 R.Carlsbe, C.H.; Palmer, R.A.; Mazumdar, S.K.; Gorinsky, B.A.; Teatee, D.G.R.  
 J. Mol. Biol. 85, 1-18, 1974  
 A.Title: The structure of ribonuclease at 2.5 angstrom resolution.  
 A.Reference number: A92949; PMID:74253324; PMID:4835726  
 A.Contents: annotation; X-ray crystallography, 2.5 angstroms  
 R.Wyckoff, H.W.; Tsernoglou, D.; Hanson, A.W.; Knox, J.R.; Lee, B.; Richards, F.M.  
 J. Biol. Chem. 245, 305-328, 1970  
 A.Title: The three-dimensional structure of ribonuclease-S. Interpretation of an electro  
 A.Reference number: A92059; PMID:70092235; PMID:5460889  
 A.Contents: annotation; X-ray crystallography, 2.0 angstroms  
 R.Santoro, J.; Gonzalez, C.; Bruix, M.; Neira, J.L.; Nieto, J.L.; Herranz, J.; Rico, M.  
 submitted to the Brookhaven Protein Data Bank, November 1992  
 A.Reference number: A52045; PDB:2AAS  
 A.Contents: annotation; conformation by (1)H-NMR, residues 27-150  
 R.Rico, M.; Bruix, M.; Santoro, J.; Gonzalez, C.; Neira, J.L.; Nieto, J.L.; Herranz, J.  
 Eur. J. Biochem. 183, 623-638, 1989  
 A.Title: Sequential (1)H-NMR assignment and solution structure of bovine pancreatic ribo  
 A.Reference number: S05528; PMID:89377830; PMID:2776756  
 A.Contents: annotation; confirmation by (1)H-NMR  
 R.Shall, S.; Barnard, E.A.  
 J. Mol. Biol. 41, 237-251, 1969  
 A.Title: Heavy atom-labelled derivatives of bovine pancreatic ribonuclease. I. Specific  
 A.Reference number: A92946; PMID:69260123; PMID:5801478  
 A.Contents: annotation; active site  
 R.Henrikson, R.L.; Stein, W.H.; Crestfield, A.M.; Moore, S.  
 J. Biol. Chem. 240, 2921-2934, 1965  
 A.Title: The reactivities of the histidine residues at the active site of ribonuclease  
 A.Reference number: A92020  
 A.Contents: annotation; active site  
 C.Function:  
 A.Description: ribonuclease endonucleolytically hydrolyzes RNA to produce 3'-phosphomono  
 A.Pathway: ribonucleic acid digestion  
 A.Note: this enzyme can also destabilize or unwind the DNA helix by complexing with sing  
 rginate residues of the enzyme and the phosphate groups of the nucleotides  
 C:superfamily: pancreatic ribonuclease  
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
 F:1-26/Domain: signal sequence #status predicted <SIG>  
 F:27-150/Product: pancreatic ribonuclease #status experimental <MAT>

F:38,67,145/Active site: His, Lys, His #status experimental  
 F:52-110,66-121,84-136,91-98/disulfide bonds: #status experimental  
 F:60/Binding site: carbohydrate (Aen) (covalent) (partial) #status experimental  
 Query Match 8.1%; Score 8; DB 1; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 VLLSLVLT 17  
 DB 7 VLLSLVLT 14  
 RESULT 2  
 S20066  
 pancreatic-type ribonuclease (EC 3.1.27.5) BbD precursor, brain - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 22-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 22-Jun-1999  
 C:Accession: S20066; JX0056  
 R.Sasao, M.P.; Carsana, A.; Confalone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmieri  
 Nucleic Acids Res. 19, 6469-6474, 1991  
 A.Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its e  
 A.Reference number: S20066; PMID:92093604; PMID:1754384  
 A.Accession: S20066  
 A.Molecule type: DNA  
 A.Residues: 1-167 <SAS>  
 A.Cross-References: EMBL:X59767; NID:9150; PIDD:CAA42439.1; PIDD:9151  
 U.Watanabe, H.; Kato, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; I  
 U.Biochem. 104, 939-945, 1988  
 A.Title: Primary structure of a ribonuclease from bovine brain.  
 A.Reference number: JX0056; PMID:89214015; PMID:3243767  
 A.Accession: JX0056  
 A.Molecule type: protein  
 A.Residues: 27-154, 'S', '156-166 <MAT>  
 A.Experimental source: brain  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: glycoprotein; hydrolase  
 F:38,67,145/Active site: His, Lys, His #status predicted  
 F:52-110,66-121,84-136,91-98/disulfide bonds: #status predicted  
 F:88/Binding site: carbohydrate (Aen) (covalent) #status experimental  
 F:155/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F:159/Binding site: carbohydrate (Ser) (covalent) #status experimental  
 Query Match 8.1%; Score 8; DB 2; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 VLLSLVLT 17  
 DB 7 VLLSLVLT 14  
 RESULT 3  
 A90298  
 probable yfeABCD locus regulator yfeB (imported) - Yersinia pestis (strain CO92)  
 C:Species: Yersinia pestis  
 C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Nov-2001  
 C:Accession: AF0298  
 R.Parthill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.E  
 demo-Tarrage, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
 Nature 413, 523-527, 2001  
 A.Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A.Reference number: AB0001; PMID:21470413; PMID:11586360  
 A.Accession: AF0298  
 A>Status: preliminary  
 A.Molecule type: DNA  
 A.Residues: 1-184 <KUR>  
 A.Cross-References: GB:AL590842; PIDD:CAQ91250.1; PIDD:G15980439; GSPDB:GN00175  
 C:Genetics:  
 A:Gene: yfeB  
 C:Superfamily: Escherichia coli probable membrane protein b1726

Query Match 8.1%; Score 8; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 FNTPLINI 51  
|||||  
Db 63 FNTPLINI 70

RESULT 4  
AG0333  
heme exporter protein B [imported] - *Yersinia pestis* (strain CO92)  
C/Species: *Yersinia pestis*  
C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Nov-2001  
C/Accession: AG0333  
R/Fairkill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;  
deno-farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
Nature 413, 523-527, 2001  
A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
A/Reference number: AB0001; MUID:21470413; PMID:11586360  
A/Accession: AG0333  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-219 <KUR>  
A/Cross-references: GB:AE00842; PIDN:CA092974.1; PID:G15980713; GSPDB:GN00175  
C/Genetics:  
A/Gene: ccmB  
C/Superfamily: cytochrome c biogenesis protein Cym

Query Match 8.1%; Score 8; DB 2; Length 219;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLLSLVL 17  
|||||  
Db 158 VLLSLVL 165

RESULT 5  
B82125  
heme exporter protein B VC2056 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)  
C/Species: *Vibrio cholerae*  
C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C/Accession: B82125  
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A/Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
A/Reference number: AB2035; MUID:20406833; PMID:10952301  
A/Accession: B82125  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-222 <HEI>  
A/Cross-references: GB:AE004279; GB:AE003852; NID:G96656590; PIDN:AAF95202.1; GSPDB:GN001  
A/Experimental source: serogroup O1, strain N16961; Biotype EI Tor  
C/Genetics:  
A/Gene: VC2056  
A/Map position: 1  
C/Superfamily: cytochrome c biogenesis protein Cym

Query Match 8.1%; Score 8; DB 2; Length 222;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLLSLVL 17  
|||||  
Db 161 VLLSLVL 168

RESULT 6  
D97010

5-enolpyruvylshikimate-3-phosphate synthase [imported] - *Clostridium acetobutylicum*  
C/Species: *Clostridium acetobutylicum*  
C/Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
C/Accession: D97010  
R/Nolling, U.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J. Bacteriol. 183, 4823-4838, 2001  
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *C.*  
A/Reference number: A96900; MUID:21359325; PMID:21359325  
A/Accession: D97010  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-428 <KUR>  
A/Cross-references: GB:AE001437; PIDN:AAK8871.1; PID:G15023793; GSPDB:GN00168  
A/Experimental source: *Clostridium acetobutylicum* ATCC824  
C/Genetics:  
A/Gene: CAC0895  
C/Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carbox

Query Match 8.1%; Score 8; DB 2; Length 428;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EESTTEN 36  
|||||  
Db 35 EESTTEN 42

RESULT 7  
F81220  
NADH dehydrogenase I, N chain NMB0259 [imported] - *Neisseria meningitidis* (strain MC58 s  
C/Species: *Neisseria meningitidis*  
C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C/Accession: F81220  
R/Fetcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A/Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.  
A/Reference number: AB1000; MUID:20175755; PMID:10720307  
A/Accession: F81220  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-480 <TER>  
A/Cross-references: GB:AE002382; GB:AE002098; NID:G7225470; PIDN:AAF40713.1; PID:G722548  
A/Experimental source: serogroup B, strain MC58  
C/Genetics:  
A/Gene: NMB0259  
C/Superfamily: NADH dehydrogenase (ubiquinone) chain 2

Query Match 8.1%; Score 8; DB 2; Length 480;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLLSLVL 17  
|||||  
Db 16 VLLSLVL 23

RESULT 8  
D72658  
hypothetical protein APE0692 - *Aeropyrum pernix* (strain K1)  
C/Species: *Aeropyrum pernix*  
C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jun-2000  
C/Accession: D72658  
R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haitawa, Y.; Jin-no, K.; Takah  
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K  
DNA Res. 6, 83-101, 1999  
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aeropyr*  
A/Reference number: A72450; MUID:99310339; PMID:10382966  
A/Accession: D72658  
A/Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-125 <KAM>  
A:Cross-references: DBJ:AP000060; NID:g5104188; PIDN:BA9668.1; PID:dl043454; PID:g510  
A:Experimental source: strain K1  
C:Gene: APB0692  
C:Superfamily: Aeropyrum pernix hypothetical protein ABE0692

Query Match 7.1%; Score 7; DB 2; Length 125;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PVLPAVV 10  
|||  
Db 70 PVLPAVV 76

RESULT 9  
H75548  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
C:Accession: H75548  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266  
A:Accession: H75548  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-132 <WHI>  
A:Cross-references: GB:AE001882; GB:AE00513; NID:g6457865; PIDN:AAFO9794.1; PID:g645787  
A:Experimental source: strain R1  
C:Gene: DR0206  
A:Map position: 1

Query Match 7.1%; Score 7; DB 2; Length 132;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 VLSLTV 16  
|||  
Db 107 VLSLTV 113

RESULT 10  
E71311  
hypothetical protein TP0536 - syphilis spirochete  
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C>Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 05-Nov-1999  
C:Accession: E71311  
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin  
neon, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; MCD  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A>Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A:Reference number: A71250; MUID:9832770; PMID:965876  
A:Accession: E71311  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-133 <CO>  
A:Cross-references: GB:AE001229; GB:AE00520; NID:g3322827; PIDN:AA65529.1; PID:g332283  
A:Experimental source: strain Nichols  
C:Gene: TP0536

Query Match 7.1%; Score 7; DB 2; Length 133;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LLSLTV 17  
|||  
Db 112 LLSLTV 118

RESULT 11  
A83448  
hypothetical protein PA1579 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: A83448  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: A83448  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-202 <SNO>  
A:Cross-references: GB:AE004586; GB:AE004091; NID:g9947536; PIDN:AA604968.1; GSPDB:GN0  
A:Experimental source: strain PA01  
C:Gene: PA1579

Query Match 7.1%; Score 7; DB 2; Length 202;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 88 LKGRSA 94  
|||  
Db 192 LKGRSA 198

RESULT 12  
F95198  
hypothetical protein SPI705 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001  
C:Accession: F95198  
R:Tellet, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hel  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple,  
neon, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison  
A>Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: F95198  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-213 <KIR>  
A:Cross-references: GB:AE005672; PIDN:AAK75783.1; PID:g14973199; GSPDB:GN00164; TIGR:SP  
A:Experimental source: strain TIGR4  
C:Gene: SPI705

Query Match 7.1%; Score 7; DB 2; Length 213;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 VLSLTV 16  
|||  
Db 193 VLSLTV 199

RESULT 13  
S23664  
hail protein - Rhodobacter capsulatus  
C:Species: Rhodobacter capsulatus  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S23664  
R:Beckman, D.L.; Tirawick, D.R.; Kranz, R.G.



Genes Dev. 6, 268-283, 1992  
A:/Title: Bacterial cytochromes c biogenesis.  
A:/Reference number: S23662; MUID:92146961; PMID:1110666  
A:/Accession: S23664  
A:/Status: preliminary  
A:/Molecule type: DNA  
A:/Residues: 1-218 <BEC>  
A:/Cross-references: EMBL:X63462; NID:G46022; PIDD:CAA45062.1; PID:G46025  
A:/Superfamily: cytochrome c biogenesis protein CycW  
C:/Keywords: transmembrane protein

Query Match 7.1%; Score 7; DB 1; Length 218;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLSLLVL 17  
DB 158 LLSLLVL 164

## RESULT 14

P64166  
Heme export protein B - Haemophilus influenzae (strain Rd KW20)  
C:/Species: Haemophilus influenzae  
C:/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:/Accession: P64166  
R:/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Doolittle, R.F.; Scott, J.; Shirley, B.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; G.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fritchman, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995  
A:/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A./Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:/Reference number: A64000; MUID:95350630; PMID:7542800  
A:/Accession: P64166  
A:/Status: nucleic acid sequence not shown; translation not shown  
A:/Molecule type: DNA  
A:/Residues: 1-221 <TIGR>  
A:/Cross-references: GB:U32789; GB:I42023; NID:G1574642; PIDD:AAC22747.1; PID:G1574645; T  
C:/Superfamily: cytochrome c biogenesis protein CycW  
C:/Keywords: transmembrane protein

Query Match 7.1%; Score 7; DB 1; Length 221;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLSLLV 16  
DB 159 VLSLLV 165

## RESULT 15

A69502  
conserved hypothetical protein AF2018 - Archaeoglobus fulgidus  
C:/Species: Archaeoglobus fulgidus  
C:/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999  
C:/Accession: A69502  
R:/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997  
A:/Authors: Usterback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Moese, C.R.; Venter, J.C.  
A:/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea  
A:/Reference number: A69250; MUID:98049343; PMID:9389475  
A:/Accession: A69502  
A:/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:/Molecule type: DNA  
A:/Residues: 1-244 <KLE>  
A:/Cross-references: GB:AE000963; GB:AE000782; NID:G2689286; PIDD:AAB89232.1; PID:G264851

Query Match 7.1%; Score 7; DB 2; Length 244;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AVVLSL 14  
DB 226 AVVLSL 232

Search completed: November 28, 2003, 08:05:30  
Job time : 24 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 07:57:12 ; Search time 11 Seconds

(without alignments)  
423.240 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 99  
Sequence: 1 MKIPLPAVVLISLVHSA.....LNMDAFKKGRKATPDQAQ 99

Scoring table: OLIGO

Gapop 60.0 , Gapept 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : Swissprot\_41.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID            | Description        |
|------------|-------|-------------|--------|---------------|--------------------|
| 1          | 8     | 8.1         | 150    | 1 RNP_BOVIN   | P00656 bos taurus  |
| 2          | 8     | 8.1         | 167    | 2 RNR_BOVIN   | P39873 bos taurus  |
| 3          | 8     | 8.1         | 184    | 3 YPER_YERPE  | O56956 yersinia pe |
| 4          | 8     | 8.1         | 428    | 4 AROA_CLOAB  | O97km2 clostridium |
| 5          | 7     | 7.1         | 133    | 5 EPP1_HUMAN  | O95825 homo sapien |
| 6          | 7     | 7.1         | 133    | 6 EPP1_MACMU  | O95d11 macaca mula |
| 7          | 7     | 7.1         | 133    | 7 SECG_TREPA  | O83547 treponema p |
| 8          | 7     | 7.1         | 202    | 8 YF79_PSEAE  | O93438 pseudomonas |
| 9          | 7     | 7.1         | 205    | 9 EF1B_YEAST  | P32671 saccharomyc |
| 10         | 7     | 7.1         | 218    | 10 CMB_RHOCA  | P29860 rhodobacter |
| 11         | 7     | 7.1         | 221    | 11 CMB_HAEIN  | P45033 haemophilus |
| 12         | 7     | 7.1         | 239    | 12 GIDB_CLOPE | O8xm32 clostridium |
| 13         | 7     | 7.1         | 247    | 13 COX2_WILMR | P47918 williopsis  |
| 14         | 7     | 7.1         | 247    | 14 COX2_WILSA | P06029 williopsis  |
| 15         | 7     | 7.1         | 283    | 15 ICAL_CERRA | O49342 cercopithec |
| 16         | 7     | 7.1         | 320    | 16 MCA2_HUMAN | O13155 homo sapien |
| 17         | 7     | 7.1         | 325    | 17 CYR2_ORYSA | O9xsa8 oryza sativ |
| 18         | 7     | 7.1         | 329    | 18 SUB1_SALTU | P02906 salmoneilla |
| 19         | 7     | 7.1         | 350    | 19 FLHB_AQUAE | O67813 aquifex aeo |
| 20         | 7     | 7.1         | 359    | 20 MNT8_BRARE | P51028 brachydanio |
| 21         | 7     | 7.1         | 372    | 21 VENV_VACCC | P20638 vaccinia vi |
| 22         | 7     | 7.1         | 372    | 22 VENV_VACCC | P20638 vaccinia vi |
| 23         | 7     | 7.1         | 373    | 23 MGE1_HUMAN | P33815 variola vir |
| 24         | 7     | 7.1         | 410    | 24 NEUS_CHICK | O9ubd1 homo sapien |
| 25         | 7     | 7.1         | 437    | 25 CCA_ARCFU  | O28035 gallus gall |
| 26         | 7     | 7.1         | 451    | 26 NMT_CANAL  | O28126 archaeglob  |
| 27         | 7     | 7.1         | 532    | 27 YOAD_ECOLI | P30418 candida alb |
| 28         | 7     | 7.1         | 554    | 28 PIGS_SCHRO | P76761 escherichia |
| 29         | 7     | 7.1         | 636    | 29 CTR4_HUMAN | O10551 schizosacch |
| 30         | 7     | 7.1         | 708    | 30 ICAL_HUMAN | O43246 homo sapien |
| 31         | 7     | 7.1         | 713    | 31 ICAL_PIG   | P20810 homo sapien |
| 32         | 7     | 7.1         | 814    | 32 AD15_HUMAN | P12675 sus scrofa  |
| 33         | 7     | 7.1         | 1061   | 33 OAR_MYXXA  | O13444 homo sapien |
|            |       |             |        |               | P38370 myxococcus  |

## ALIGNMENTS

| RESULT 1 | ID   | RNP_BOVIN | STANDARD: | PRT: | 150 AA. |
|----------|--|-----------|-----------|------|---------|
| AC       | P00656;  |           |           |      |         |
| DT       | 21-JUL-1986 (Rel. 01, Created)                                       |           |           |      |         |
| DT       | 01-NOV-1988 (Rel. 09, Last sequence update)                          |           |           |      |         |
| DT       | 15-SEP-2003 (Rel. 42, Last annotation update)                        |           |           |      |         |
| DE       | Ribonuclease pancreatic precursor (EC 3.1.27.5) (RNAse 1) (RNAse A). |           |           |      |         |
| GN       | RNASE1 OR RNS1.  |           |           |      |         |
| OS       | Bos taurus (Bovine), and   |           |           |      |         |
| OS       | Bison bison (American bison).  |           |           |      |         |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;    |           |           |      |         |
| OC       | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;    |           |           |      |         |
| OK       | Bovidae; Bovinae; Bos.   |           |           |      |         |
|          | NCBI_TaxID=9913, 9901;   |           |           |      |         |
|          | [1]  |           |           |      |         |
| RP       | SEQUENCE FROM N.A.   |           |           |      |         |
| RC       | SPECIES=Bovine;  |           |           |      |         |
| RX       | MEDLINE=8826257; PubMed=2838818;                                     |           |           |      |         |
| RA       | Carzana A., Confalone E., Palmieri M., Libonati M., Furia A.;        |           |           |      |         |
| RT       | "Structure of the bovine pancreatic ribonuclease gene: the unique    |           |           |      |         |
| RT       | intervening sequence in the 5' untranslated region contains a        |           |           |      |         |
| RL       | promoter-like element."  |           |           |      |         |
|          | Nucleic Acids Res. 16:5491-5502(1988).                               |           |           |      |         |
|          | [2]  |           |           |      |         |
| RP       | SEQUENCE OF 23-150 FROM N.A.   |           |           |      |         |
| RC       | SPECIES=Bovine;  |           |           |      |         |
| RX       | MEDLINE=96093920; PubMed=7479688;                                    |           |           |      |         |
| RA       | Delcarraye S.B., Ribon M., Yokel E.M., Quirk D.J., Rutter W.J.;      |           |           |      |         |
| RT       | Raines R.T.;   |           |           |      |         |
| RT       | "Engineering ribonuclease A: production, purification and            |           |           |      |         |
| RT       | characterization of wild-type enzyme and mutants at Gln11."          |           |           |      |         |
|          | Protein Eng. 8:261-273(1995).  |           |           |      |         |
|          | [3]  |           |           |      |         |
| RP       | SEQUENCE OF 27-150, AND DISULFIDE BONDS.                             |           |           |      |         |
| RC       | SPECIES=Bovine;  |           |           |      |         |
| RA       | Smith D.G., Stein W.H., Moore S.;                                    |           |           |      |         |
| RT       | "The sequence of amino acid residues in bovine pancreatic            |           |           |      |         |
| RT       | ribonuclease: revisions and confirmations."                          |           |           |      |         |
|          | J. Biol. Chem. 238:227-234(1963).                                    |           |           |      |         |
|          | [4]  |           |           |      |         |
| RP       | SEQUENCE OF 27-150.  |           |           |      |         |
| RC       | SPECIES=Bovine;  |           |           |      |         |
| RA       | Plummer T.H. Jr., Hirs C.H.W.;                                       |           |           |      |         |
| RT       | "on the structure of bovine pancreatic ribonuclease B. Isolation of  |           |           |      |         |
| RT       | a glycopeptide."   |           |           |      |         |
|          | J. Biol. Chem. 239:2530-2538(1964).                                  |           |           |      |         |
|          | [5]  |           |           |      |         |
| RP       | ACTIVE SITE.   |           |           |      |         |
| RC       | SPECIES=Bovine;  |           |           |      |         |
| RA       | Helrikson R.L., Stein W.H., Crestfield A.M., Moore S.;               |           |           |      |         |
| RT       | "The reactivities of the histidine residues at the active site of    |           |           |      |         |
| RT       | ribonuclease toward halo acids of different structures."             |           |           |      |         |
|          | J. Biol. Chem. 240:2921-2934(1965).                                  |           |           |      |         |
|          | [6]  |           |           |      |         |
| RP       | ACTIVE SITE.   |           |           |      |         |

RC SPECIES-Bovine; PubMed=5801478;  
 RX MEDLINE=69260123; PubMed=5801478;  
 RT "Heavy atom-labelled derivatives of bovine pancreatic ribonuclease.  
 RT I. Specific reactions of ribonuclease with N-acetylhomocysteine  
 RT thiolactone and silver ion.";  
 RL J. Mol. Biol. 41:237-251(1969).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RC SPECIES-Bovine;  
 RX MEDLINE=70092235; PubMed=5460889;  
 RA Wyckoff H.W., Tsernoglou D., Hanson A.W., Knox J.R., Lee B.,  
 RA Richards F.M.;  
 RT "The three-dimensional structure of ribonuclease-S. Interpretation of  
 RT an electron density map at a nominal resolution of 2 A.";  
 RL J. Biol. Chem. 245:305-328(1970).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RC SPECIES-Bovine;  
 RX MEDLINE=74253324; PubMed=4835726;  
 RA Carlisle C.H., Palmer R.A., Mazumdar S.K., Gorinsky B.A.;  
 RA Yeates D.G.R.;  
 RT "The structure of ribonuclease at 2.5-A resolution.";  
 RL J. Mol. Biol. 85:1-18(1974).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RC SPECIES-Bovine;  
 RX MEDLINE=82120062; PubMed=6276380;  
 RA Wlodawer A., Bott R., Sjoelin L.;  
 RT "The refined crystal structure of ribonuclease A at 2.0-A  
 RT resolution.";  
 RL J. Biol. Chem. 257:1325-1332(1982).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (1.26 ANGSTROMS).  
 RC SPECIES-Bovine;  
 RX MEDLINE=88294009; PubMed=3401445;  
 RA Wlodawer A., Svensson L.A., Sjoelin L., Gilliland G.L.;  
 RT "Structure of phosphate-free ribonuclease A refined at 1.26 A.";  
 RL Biochemistry 27:2705-2717(1988).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).  
 RC SPECIES-Bovine;  
 RX MEDLINE=97299793; PubMed=9154942;  
 RA Leonidas D.D., Shapiro R., Irons L.I., Russo N., Acharya K.R.;  
 RT "Crystal structures of ribonuclease A complexes with 5'-  
 RT 2'-phosphadenosine 3'-phosphate and 5'-diphosphadenosine  
 RT 2'-phosphate at 1.7-A resolution.";  
 RL Biochemistry 36:5578-5588(1997).  
 RN [12]  
 RP STRUCTURE BY NMR.  
 RC SPECIES-Bovine;  
 RX MEDLINE=89375325; PubMed=2775743;  
 RA Robertson A.D., Furisima E.O., Eastman M.A., Scheraga H.A.;  
 RT "Proton NMR assignments and regular backbone structure of bovine  
 RT pancreatic ribonuclease A in aqueous solution.";  
 RL Biochemistry 28:5930-5938(1989).  
 RN [13]  
 RP STRUCTURE BY NMR.  
 RC SPECIES-Bovine;  
 RX MEDLINE=89377830; PubMed=2776756;  
 RA Rico M., Bruix M., Sanctoro J., Gonzalez C., Neira J.L., Nieto J.L.,  
 RA Herranz J.;  
 RT "Sequential 1H-NMR assignment and solution structure of bovine  
 RT pancreatic ribonuclease A.";  
 RL Eur. J. Biochem. 183:623-638(1989).  
 RN [14]  
 RP STRUCTURE BY NMR.  
 RC SPECIES-Bovine;  
 RX MEDLINE=93044359; PubMed=1941699;  
 RA Rico M., Sanctoro J., Gonzalez C., Bruix M., Neira J.L., Nieto J.L.,  
 RA Herranz J.;  
 RT "3D structure of bovine pancreatic ribonuclease A in aqueous  
 RT solution: an approach to tertiary structure determination from a  
 RT small basis of 1H NMR NOE correlations.";

RL J. Biomol. NMR 1:283-298(1991).  
 RN [15]  
 RP DNA-BINDING.  
 RC SPECIES-Bovine;  
 RX MEDLINE=86179900; PubMed=3961503;  
 RA McPherson A., Brayer G., Cascio D., Williams R.;  
 RT "The mechanism of binding of a polynucleotide chain to pancreatic  
 RT ribonuclease.";  
 RL Science 232:765-768(1986).  
 RN [16]  
 RP SEQUENCE OF 27-150.  
 RC SPECIES=B.bison;  
 RX MEDLINE=76259396; PubMed=955781;  
 RA Mueller F.A.J., Welling G.W., Beintema J.J.;  
 RT "Studies on the primary structure of bison pancreatic ribonuclease.";  
 RL Int. J. Pept. Protein Res. 8:345-348(1976).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 CC with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Pancreas.  
 CC -1- MISCELLANEOUS: RIBONUCLEASE CAN DESTABILIZE OR UNWIND THE DNA  
 CC HELIX BY COMPLEXING WITH SINGLE-STRANDED DNA; THIS COMPLEX ARISES  
 CC BY AN EXTENDED MULTISITE CATION-ANION INTERACTION BETWEEN THE  
 CC LYSINE AND ARGININE RESIDUES OF THE ENZYME AND THE PHOSPHATE  
 CC GROUPS OF THE NUCLEOTIDES.  
 CC -1- MISCELLANEOUS: THE BISON SEQUENCE APPEARS TO BE IDENTICAL WITH  
 CC THAT OF BOVINE.  
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
 CC -1- DATABASE: NME=Washington enzyme manual;  
 CC WWW="http://www.worthington-biochem.com/manual/R/RNase.html".  
 CC -----  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 DR EMBL, X07283; CA30263.1; -;  
 DR EMBL, S80747; AAB35594.1; -;  
 DR PIR, S00897; NRBO.  
 DR PDB, 1RBB; 15-JUL-92.  
 DR PDB, 3RN3; 15-OCT-91.  
 DR PDB, 2RN5; 31-JAN-94.  
 DR PDB, 1RSM; 15-OCT-88.  
 DR PDB, 1SRN; 15-JUL-92.  
 DR PDB, 6RSA; 15-APR-93.  
 DR PDB, 6RSA; 15-OCT-89.  
 DR PDB, 6RSA; 15-JAN-93.  
 DR PDB, 6RSA; 15-APR-91.  
 DR PDB, 1RAT; 15-JUL-93.  
 DR PDB, 1RAT; 15-JUL-93.  
 DR PDB, 3RAT; 15-JUL-93.  
 DR PDB, 2RAT; 15-JUL-93.  
 DR PDB, 4RAT; 15-JUL-93.  
 DR PDB, 5RAT; 15-JUL-93.  
 DR PDB, 6RAT; 15-JUL-93.  
 DR PDB, 7RAT; 15-JUL-93.  
 DR PDB, 8RAT; 15-JUL-93.  
 DR PDB, 9RAT; 15-JUL-93.  
 DR PDB, 1RBC; 31-OCT-93.  
 DR PDB, 1RBD; 31-OCT-93.  
 DR PDB, 1RBE; 31-OCT-93.  
 DR PDB, 1RBF; 31-OCT-93.  
 DR PDB, 1RBG; 31-OCT-93.  
 DR PDB, 1RBI; 31-OCT-93.  
 DR PDB, 1RBJ; 07-DEC-95.  
 DR PDB, 1RBN; 20-DEC-94.  
 DR PDB, 1RBW; 15-OCT-95.  
 DR PDB, 1RBX; 15-OCT-95.

Query Match 8.1%; Score 8; DB 1; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 1.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLSLVL 17  
 |||||  
 DB 7 VLSLVL 14

RESULT 2  
 RNR BOVIN STANDARD; PRT; 167 AA.  
 AC P39873;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).  
 GN BRN.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92093604; PubMed=1754384;  
 RA Sasso M.P., Carzana A., Comalome E., Coei C., Sorrentino S.,  
 RA Viola M., Palmieri M., Russo E., Furla A.,  
 RT "Molecular cloning of the gene encoding the bovine brain ribonuclease  
 and its expression in different regions of the brain".  
 RN Nucleic Acids Res. 19:6469-6474(1991).  
 [2]  
 RP SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.  
 RC TISSUE=Brain;  
 RX MEDLINE=89214015; PubMed=3243767;  
 RA Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,  
 RA Ohgi K., Irie M.,  
 RT "Primary structure of a ribonuclease from bovine brain".  
 RN J. Biochem. 104:939-945(1988).  
 [3]  
 RP SEQUENCE OF 27-167 FROM N.A.  
 RX MEDLINE=96139017; PubMed=858129;  
 RA Confalone E., Beliterna J.J., Sasso M.P., Carzana A., Palmieri M.,  
 RA Vento M.T., Furla A.,  
 RT "Molecular evolution of genes encoding ribonucleases in ruminant  
 species".  
 RN J. Mol. Evol. 41:850-858(1995).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 EMBL; X59767; CA442439.1; -  
 DR EMBL; S81744; AAB36138.1; -  
 DR PIR; S20066; S20066.  
 DR HSSP; P00556; 2RNS.  
 DR GlycoSuiteDB; P39873; -  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; RNaseA; 1.  
 DR PRINTS; PR00794; RIBONUCLEASE.  
 DR ProDom; PD000535; RNaseA; 1.  
 DR SMART; SM00092; RNase\_Pc; 1.  
 DR PROSITE; PS00127; RNASE\_PANCREATIC; 1.  
 DR HydroLase; Nuclease; Endonuclease; Glycoprotein; Signal.  
 FT SIGNAL 1 26  
 FT CHAIN 27 167 RIBONUCLEASE, BRAIN.

FT ACT SITE 38 38 BY SIMILARITY.  
 FT ACT SITE 67 67 BY SIMILARITY.  
 FT ACT SITE 145 145 BY SIMILARITY.  
 FT DISULFID 52 110 BY SIMILARITY.  
 FT DISULFID 66 121 BY SIMILARITY.  
 FT DISULFID 84 136 BY SIMILARITY.  
 FT DISULFID 91 98 BY SIMILARITY.  
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 155 155 /FTID=CAR\_000005.  
 FT CARBOHYD 159 159 O-LINKED.  
 FT CONFLICT 155 155 T -> S (IN REF. 2).  
 SQ SEQUENCE 167 AA; 18450 MM; 681CAAC3CC2C0459 CMC64;

QY 10 VLSLVL 17  
 |||||  
 DB 7 VLSLVL 14

Query Match 8.1%; Score 8; DB 1; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3  
 YFEB YFEBP STANDARD; PRT; 164 AA.  
 ID YFEB YFEBP  
 AC Q56856;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Putative YfearBCD regulator yfEB.  
 GN YFEB OR YP02445 OR Y1891.  
 OS Yersinia pestis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Yersinia.  
 OC NCBI\_TaxID=632;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KIM6;  
 RA Bearden S.W.,  
 RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 RN  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CO-92 / Biovar Orientalis;  
 RX MEDLINE=21470413; PubMed=11586360;  
 RA Parthill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,  
 RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,  
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,  
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
 RA Felwell T., Hamlin N., Holtroyd S., Jagsis K., Kariyeh A.V.,  
 RA Leather S., Mule S., Oyston F.C.F., Quail M., Rutherford K.,  
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,  
 RT "Genome sequence of Yersinia pestis, the causative agent of plague".  
 RN Nature 413:523-527(2001).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KIM5 / Biovar Mediaevalis;  
 RX MEDLINE=22137863; PubMed=12142430;  
 RA Deng W., Burland V., Plunkett G. II, Boutin A., Mayhew G.F., Iass P.,  
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,  
 RA Straley S.C., McConough K.A., Nilles M.L., Watson J.S., Blattner F.R.,  
 RA Perry R.D.,  
 RT "Genome sequence of Yersinia pestis KIM".  
 RN J. Bacteriol. 184:4601-4611(2002).  
 CC -1- FUNCTION: PUTATIVE REGULATOR OF YFEB/BCD. AN ABC TRANSPORTER LOCUS  
 INVOLVED IN INORGANIC IRON TRANSPORT.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: STRONG, TO E.COLI YNIB.  
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DR EMBL; U50903; AAC6451.1; -  
 DR EMBL; AJ141452; AAC61250.1; -  
 DR EMBL; AE013792; AAC65458.1; -  
 DR PIR; AF0298; AF0298.  
 KW Transmembrane; Complete proteome.  
 FT TRANSMEM 15 35 POTENTIAL.  
 FT TRANSMEM 84 104 POTENTIAL.  
 FT TRANSMEM 162 182 POTENTIAL.  
 SQ SEQUENCE 184 AA; 20913 MW; 998608ED024E8A51A CRC64;

Query Match 8.1%; Score 8; DB 1; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 44 ENTREPLNT 51  
 DB 63 ENTREPLNT 70

RESULT 4  
 AROA\_CLOAB STANDARD; PRT; 428 AA.  
 ID AROA\_CLOAB  
 AC Q97KM2;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-  
 EN endopyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).  
 GN AROA OR CAC0895.  
 OS Clostridium acetobutylicum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 CC Clostridium.  
 OK NCBI\_TaxID=1488;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
 RX MEDLINE=21359325, PubMed=11466286;  
 RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,  
 RA Gibson R., Lee H.W., Dubois J., Qiu D., Hitti J., Wolf Y.I.,  
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
 RA Bennett G.N., Koonin E.V., Smith D.R.;  
 RT "Genome sequence and comparative analysis of the solvent-producing  
 bacterium Clostridium acetobutylicum";  
 RL J. Bacteriol. 183:4823-4838(2001).  
 CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =  
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.  
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;  
 CC sixth step.  
 CC -1- SUBUNIT: Monomer (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (probable).  
 CC -1- SIMILARITY: Belongs to the EPSP synthase family.  
 CC -----  
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DR EMBL; AE007605; AAK78871.1; -  
 DR PIR; D97010; D97010.  
 DR HAMAP; MF\_00210; 1.  
 DR InterPro; IPR006264; AROA.  
 DR InterPro; IPR001986; EPSP\_synthase.  
 DR Pfam; PF00275; EPSP\_synthase; 1.  
 DR ProDom; PD001867; EPSP\_synthase; 1.  
 DR Trifam; TRIGR01356; aroA; 1.

DR PROSITE; PS00104; EPSP SYNTHASE\_1; FALSE\_NEG.  
 DR PROSITE; PS00885; EPSP SYNTHASE\_2; 1.  
 KW Aromatic amino acid biosynthesis; Transferase; Complete proteome.  
 SQ SEQUENCE 428 AA; 46960 MW; D3A9BF1F46B3C547 CRC64;

Query Match 8.1%; Score 8; DB 1; Length 428;  
 Best Local Similarity 100.0%; Pred. No. 3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 EESTSTEN 36  
 DB 35 EESTSTEN 42

RESULT 5  
 EPTI\_HUMAN STANDARD; PRT; 133 AA.  
 ID EPTI\_HUMAN  
 AC Q95925; Q96SD7; Q9HD30;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Eppin precursor (Epididymal protease inhibitor) (Serine protease  
 DE inhibitor-like with Kunitz and WAP domains 1).  
 GN SPINLM1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OK NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Epididymis, and testis;  
 RX MEDLINE=21297183, PubMed=11404006;  
 RA Richardson R.T., Sivasubraman P., Hall S.H., Hamli K.G., Moore P.A.,  
 RA Ruben S.M., French F.S., O'Rand M.G.;  
 RT "Cloning and sequencing of human Eppin: a novel family of protease  
 RT inhibitors expressed in the epididymis and testis";  
 RL Gene 270:93-102(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Stevardes G.S., Huckle B.J., Deloukas P.;  
 RL Submitted (SFP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stevardes G., Almeida J.P., Babbage A.K., Bagunley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark A.P., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhand P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Levasseilho M.H., Leverhna M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie I.J., McEay K., McWhirray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showstren R., Sims S.,  
 RA Skuse C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Symmore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,  
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:665-871(2001).  
 CC -1- SUBCELLULAR LOCATION: secreted (Potential).  
 CC -1- ALTERNATIVE PRODUCTS:

```

CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O05925-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O05925-2; Sequence=VSP_006755;
CC -1- TISSUE SPECIFICITY: EXPRESSED IN EPIDIDYMIS AND TESTIS.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF286370; AAG00548.1; -
DR EMBL; AF286369; AAG00547.1; -
DR EMBL; AF286368; AAG00546.1; -
DR EMBL; AL118493; CAB56343.1; -
DR EMBL; AL031663; CAB37635.1; -
DR EMBL; AL031663; CAB37635.1; -
DR HSSP; P00974; IBPI.
DR Genew; HGNC:15932; SPINLM1.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00217; WAP; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4.DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR KW Serine protease inhibitor; Signal; Alternative splicing.
FT SIGNAL 1 21
FT CHAIN 1 21
FT DOMAIN 22 133
FT DOMAIN 29 73
FT DOMAIN 77 127
FT DISULFID 33 61
FT DISULFID 33 61
FT DISULFID 40 65
FT DISULFID 48 60
FT DISULFID 54 69
FT DISULFID 77 127
FT DISULFID 86 110
FT DISULFID 102 123
FT VARSPLIC 1 31
SQ SEQUENCE 133 AA; 15284 MW; F7831B203366D9DC CRC64;
Query Match 7.1%; Score 7; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 LLSLVL 17
DB 6 LLSLVL 12

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OC NCBI_Taxid=9544;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Epithelium; and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epithelium and testis."
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN EPIDIDYMIS AND TESTIS.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC -----
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CC -----
DR EMBL; AF346414; AAK31336.1; -
DR HSSP; P00974; IBPI.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00217; WAP; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21
FT CHAIN 1 21
FT DOMAIN 22 133
FT DOMAIN 29 73
FT DOMAIN 77 127
FT DISULFID 33 61
FT DISULFID 33 61
FT DISULFID 40 65
FT DISULFID 48 60
FT DISULFID 54 69
FT DISULFID 77 127
FT DISULFID 86 110
FT DISULFID 102 123
FT VARSPLIC 1 31
SQ SEQUENCE 133 AA; 15279 MW; 433ABE94639A35E9 CRC64;
Query Match 7.1%; Score 7; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 LLSLVL 17
DB 6 LLSLVL 12

```

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RESULT 6
EPII_MACMU
ID EPII_MACMU STANDARD; PRT; 133 AA.
AC Q9BDL1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Eppin precursor (epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN SPINLM1.
OS Macaca mulatta (Rhesus macaque).

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RESULT 7
SECG_TREPA
ID SECG_TREPA STANDARD; PRT; 133 AA.
AC O83547;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable protein-export membrane protein secg.
GN SECG OR TP0535.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_Taxid=160;
RN (1)

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=96333770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson C.M., Gajin M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Soedjaren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khelak H., Richardson D., Howell J.K., Childsbarrow W., Uteback T.,
RA McDonald L., Artlach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete";
RL Science 281:375-386(1998).
CC -1- FUNCTION: INVOLVED IN PROTEIN EXPORT. PARTICIPATES IN AN EARLY
CC EVENT OF PROTEIN TRANSLLOCATION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SECY FAMILY.
-----
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-----
CC EMBL; AE001229; AAC65529.1; -
CC PIR; E71311; E71311.
CC TIGR; TP0536; -
CC InterPro: IPR004692; SecG.
CC Pfam; PF03840; SecG; 1.
CC PRINTS; PRO1651; SECSEXPORT.
CC TIGRFAMs; TIGR00810; secG; 1.
CC Protein transport; Translocation; Transmembrane; Complete proteome.
CC TRANSMEM 3 23 POTENTIAL.
CC FT TRANSMEM 52 72
CC SEQUENCE 133 AA; 14279 MW; 43557545A91D6DAB CRC64;
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Query Match 7.1%; Score 7; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 LLSLVL 17
DB 112 LLSLVL 118
-----
RESULT 8
VF79_PSEAB STANDARD; PRT; 202 AA.
ID VF79_PSEAB
AC Q913D8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein PA1579.
GN PA1579.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Steyer C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Medman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lattig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).

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RN [2]
RP POTENTIAL FUNCTION.
RX MEDLINE=21173595; PubMed=11276083;
RA Iyer L.M., Koonin E.V., Aravind L.;
RT "Adaptations of the helix-grip fold for ligand binding and catalysis
RT in the START domain superfamily.";
RL Proteins 43:134-144(2001).
CC -1- FUNCTION: May play a role in the interaction of the bacterium with
CC animal cells.
CC -1- SIMILARITY: Contains 1 START domain.
-----
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-----
CC EMBL; AE004586; AAG04968.1; -
CC PIR; A83448; A83448.
CC InterPro: IPR002913; START.
CC Pfam; PF01852; START; 1.
CC PROSITE; PS50848; START; 1.
CC Hypothetical protein; Complete proteome.
CC DOMAIN 1 202 START.
CC SEQUENCE 202 AA; 22110 MW; 9F1C9B71F61ED95E CRC64;
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Query Match 7.1%; Score 7; DB 1; Length 202;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 88 LKGLRSA 94
DB 192 LKGLRSA 198
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RESULT 9
EF1B_YEAST STANDARD; PRT; 205 AA.
ID EF1B_YEAST
AC P32471;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Elongation factor 1-beta (EF-1-beta).
GN EF1B OR TEF5 OR YAL003W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93131037; PubMed=8420802;
RA Hitag K., Suzuki K., Tsuchiya E., Miyakawa T.;
RT "Cloning and characterization of the elongation factor EF-1 beta
RT homologue of Saccharomyces cerevisiae. EF-1 beta is essential for
RT growth.";
RL FEBS Lett. 316:165-169(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=95028152; PubMed=7941740;
RA Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,
RA Delaney S., Quillette B.F.F., Barton A.B., Kaback D.B., Bussey H.;
RT "Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
RT the 42 kbp SPO7-CEN1-CDC15 region.";
RL Yeast 10:535-541(1994).
RN [3]
RP SEQUENCE OF 167-177.
RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;

```

RT "Protein identifications for a *Saccharomyces cerevisiae* protein database".

RL Electrophoresis 15:1466-1486(1994).

RM [4]

RP SEQUENCE OF 13-21 AND 50-55.

RC STRAIN=ATCC 38531 / Y41;

RX MEDLINE=97089742; PubMed=8935650;

RA Norbeck J., Blomberg A.;

RT "Protein expression during exponential growth in 0.7 M NaCl medium of *Saccharomyces cerevisiae*".

RL FEMS Microbiol. Lett. 137:1-8(1996).

RM [5]

RP ACETYLATION, AND PHOSPHORYLATION.

RA Gargale J.I., Fletcher B., Kobayashi R., latter G.I., Schender B.,

RL Volpe T., Warner J.R., McLaughlin C.S.;

CC Submitted (SEP-1994) to the SWISS-PROT data bank.

CC -1- FUNCTION: EF-1-BETA AND EF-1-DELTA STIMULATE THE EXCHANGE OF

CC GDP BOUND TO EF-1-ALPHA TO GTP.

CC -1- SUBUNIT: EF-1 IS COMPOSED OF FOUR SUBUNITS: ALPHA, BETA,

CC DELTA, AND GAMMA.

CC -1- PMW: PHOSPHORYLATED.

CC -1- SIMILARITY: BELONGS TO THE EF-1-BETA/EF-1-DELTA FAMILY.

CC -----

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CC -----

DR EMBL: D14080; BAA03165.1; -

DR EMBL: I22015; AAC04954.1; -

DR PIR: S43445; S43445.

DR PDB: 1F60; 22-NOV-00.

DR PDB: 1G7C; 30-MAY-01.

DR PDB: 1JUE; 06-JUN-01.

DR PDB: 1JUF; 06-JUN-01.

DR SWISS-2DPAGE: P32471; YEAST.

DR SGD: S0000003; EFBI.

DR InterPro: IPR001326; EF1-BD.

DR InterPro: IPR004046; GST-Cterm.

DR Pfam: PF00736; EF1BD.1.

DR PROSITE: PS00824; EF1BD.1; 1.

DR PROSITE: PS00825; EF1BD.2; 1.

KM Elongation factor; Protein biosynthesis; Acetylation; Phosphorylation; 3D-structure.

KW INIT MET 0 0

FT MOD RES 1 1 ACETYLATION.

FT CONFLICT 48 48 F -> S (IN REF. 2).

FT CONFLICT 56 56 F -> S (IN REF. 2).

FT CONFLICT 57 57 W -> L (IN REF. 2).

FT CONFLICT 167 167 L -> E (IN REF. 3).

SO SEQUENCE 205 AA; 22689 MW; E47782908998DE6 CRC64;

Query Match 7.1%; Score 7; DB 1; Length 205;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 AFKADEF 63

DB 55 AFKADEF 61

RESULT 10

CCMB\_RHOCA STANDARD; PRT; 218 AA.

AC P29960;

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DR Heme exporter protein B (Cytochrome c-type biogenesis protein h2b).

HELB.

OS Rhodospirillum rubrum (Rhodospirillum rubrum).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;

OC Rhodospirillaceae; Rhodospirillum.

OX NCBI\_TaxID=1061;

RM [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SB1003 / St Louis;

RX MEDLINE=92145961; PubMed=1310666;

RA Beckman D.L., Trawick D.R., Kranz R.G.;

RT "Bacterial cytochromes c biogenesis".

RL Genes Dev. 6:268-283(1992).

CC -1- FUNCTION: REQUIRED FOR THE EXPORT OF HEME TO THE PERIPLASM FOR THE

CC BIOGENESIS OF C-TYPE CYTOCHROMES.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane

CC (Probable).

CC -1- SIMILARITY: BELONGS TO THE CCMB/CYCW/HELB FAMILY.

CC -----

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CC -----

DR EMBL: X63462; CAA45062.1; -

DR PIR: S23664; S23664.

DR InterPro: IPR003544; Cyc\_c-Comp.

DR Pfam: PF03379; CCMB.1.

DR PRINTS: PR01414; CCMBBIOSNIS.

DR TIGRPFMS: TIGR01190; CCMB.1.

KM Cytochrome c-type biogenesis; Transport; Transmembrane;

KM Inner membrane.

FT TRANSMEM 18 38

FT TRANSMEM 43 63 POTENTIAL.

FT TRANSMEM 99 119 POTENTIAL.

FT TRANSMEM 131 151 POTENTIAL.

FT TRANSMEM 155 175 POTENTIAL.

FT TRANSMEM 185 205 POTENTIAL.

SO SEQUENCE 218 AA; 22611 MW; CA2362FBD447F4 CRC64;

Query Match 7.1%; Score 7; DB 1; Length 218;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLSLVLT 17

DB 158 LLSLVLT 164

RESULT 11

CCMB\_HABIN STANDARD; PRT; 221 AA.

AC P45033;

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DR Heme exporter protein B (Cytochrome c-type biogenesis protein ccmb).

GN CCMB OR H11090.

OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC Pasteurellaceae; Haemophilus.

OX NCBI\_TaxID=727;

RM [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Rd / KW20 / ATCC 51907;

RX MEDLINE=95350630; PubMed=7542800;

RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

RA Kienle A.R., Sutton G., Tomb J.-F., Dougherty B.A., Merrick J.M.,

RA McInerney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,

RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,



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RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RL Science 269:496-512(1995).
CC -1- FUNCTION: REQUIRED FOR THE EXPORT OF HEME TO THE PERIPLASM FOR THE
CC BIOGENESIS OF C-TYPE CYTOCHROMES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -1- SIMILARITY: BELONGS TO THE CCMB/CYCW/HEMB FAMILY.
CC -----
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CC -----
CC EMBL, U32789; AAC22747.1; -.
CC PIR, F64166; F64166.
CC TIGR, H11090; -.
CC InterPro, IPR003544; Cyrc_bioG_CcMB.
CC Pfam, PF03379; CcMB, 1.
CC PRINTS, PR01414; CcMBBIOGNIS.
CC TIGRFAMs, TIGR01190; ccmB, 1.
CC Cytochrome c-type biogenesis; Transport; Transmembrane;
CC Inner membrane; Complete proteome.
CC TRANSMEM 21 41 POTENTIAL.
CC TRANSMEM 46 66 POTENTIAL.
CC TRANSMEM 101 121 POTENTIAL.
CC TRANSMEM 126 146 POTENTIAL.
CC TRANSMEM 157 177 POTENTIAL.
CC TRANSMEM 193 213 POTENTIAL.
CC SEQUENCE 221 AA; 23643 MW; 2F8EAPDC5228EF8 CRC64;
SQ
Query Match 7.1%; Score 7; DB 1; Length 221;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLLSLV 16
DB 159 VLLSLV 165

RESULT 12
GIDB_CLOPE STANDARD; PRT; 239 AA.
ID_GIDB_CLOPE
AC Q8XH32;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methyltransferase gldb (EC 2.1.-.-) (Glucose inhibited division
DE protein B).
GN GIDB OR CPE2653.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_Taxid=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RA MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Onshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -1- FUNCTION: Probable S-adenosyl-L-methionine dependent
CC methyltransferase specific for a sterol and/or lipid substrate (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE GIDB FAMILY.

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CC -----
CC EMBL, AP003194; BAB82359.1; -.
CC HANAP, MF_00074; -.
CC InterPro, IPR003682; Gldb.
CC Pfam, PF02527; Gldb, 1.
CC ProDom, PD004441; Gldb, 1.
CC TIGRFAMs, TIGR00138; gldb, 1.
CC Transferase; Methyltransferase; Complete proteome.
CC SEQUENCE 239 AA; 26886 MW; 5F1024A3E3C1C71E CRC64;
SQ
Query Match 7.1%; Score 7; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 AFKADF 63
DB 62 AFKADF 68

RESULT 13
COX2_WILMR STANDARD; PRT; 247 AA.
ID_COX2_WILMR
AC P47918;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide II precursor (EC 1.9.3.1).
GN COX2.
OS Williopsis mrakii (Yeast) (Hansenula mrakii).
OC Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Williopsis.
OX NCBI_Taxid=4963;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 11707;
RA MEDLINE=94287716; PubMed=8017108;
RA Driessl R., Sor P., Fukuhara H.;
RT "Genes of the linear mitochondrial DNA of Williopsis mrakii: coding
RT sequences for a maturase-like protein, a ribosomal protein VARI
RT homologue, cytochrome oxidase subunit 2 and methionyl tRNA."
RL Yeast 10:391-398(1994).
CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-
CC 3 form the functional core of the enzyme complex. Subunit 2
CC transfers the electrons from cytochrome c via its binuclear copper
CC A center to the binuclear center of the catalytic subunit 1.
CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- COFACTOR: Copper A.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- PTM: THE SIGNAL SEQUENCE OF COX2 IS PROCESSED BY IMP1 (BY
CC SIMILARITY).
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC -----
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CC -----
CC EMBL, X66595; CAA47160.1; -.

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DR PIR; S42736; S42736.  
 DR InterPro; IPR001505; Copper Cua.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper Cua; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 DR Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
 KW Electron transport; Respiratory chain; Signal.  
 FT SIGNAL 1 11  
 FT CHAIN 1 11  
 FT DOMAIN 12 247  
 FT TRANSMEM 39 59  
 FT DOMAIN 60 78  
 FT TRANSMEM 79 101  
 FT DOMAIN 102 247  
 FT METAL 182 182  
 FT METAL 217 217  
 FT METAL 221 221  
 FT METAL 225 225  
 SQ SEQUENCE 247 AA; 27941 MW; 98EF8346730B6ECA CRC64;

Query Match 7.1%; Score 7; DB 1; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LPAVVL 12  
 DB 84 LPAVVL 90

RESULT 14  
 COX2\_WILSA STANDARD; PRT; 247 AA.  
 AC P06029;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide II precursor (EC 1.9.3.1).  
 GN COX2 OR OX11.  
 OS Mitochondrion.  
 OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Williopsis.  
 CC NCBI\_TaxID=4906;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8823501; PubMed=2836090;  
 RA Lawson J.E., Deters D.W.;  
 RT "Nucleotide sequence of the mitochondrial cytochrome oxidase subunit  
 II gene in the yeast *Hansenula saturnus*.";  
 RL Curr. Genet. 9:351-360(1985).  
 CC -1- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 3 form the functional core of the enzyme complex. Subunit 2  
 transfers the electrons from cytochrome c via its binuclear copper  
 A center to the binuclear center of the catalytic subunit 1.  
 CC -1- CATALYTIC ACTIVITY: 4 ferriocytochrome c + O(2) = 4 ferriocytochrome  
 c + 2 H(2)O.  
 CC -1- COFACTOR: Copper A.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 inner membrane.  
 CC -1- PTM: THE SIGNAL SEQUENCE OF COX2 IS PROCESSED BY IMP1 (BY  
 SIMILARITY).  
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
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CC EMBL; X02439; CA26284.1; -  
 CC PIR; S07165; OEHQMS.  
 CC InterPro; IPR001505; Copper Cua.  
 CC InterPro; IPR002429; Cyt\_c\_ox\_2.  
 CC Pfam; PF00116; COX2; 1.  
 CC Pfam; PF02790; COX2\_TM; 1.  
 CC PRINTS; PR01166; CYCOXIDASEII.  
 CC ProDom; PD000131; Copper Cua; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 DR Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
 KW Electron transport; Respiratory chain; Signal.  
 FT SIGNAL 1 11  
 FT CHAIN 1 11  
 FT DOMAIN 12 247  
 FT TRANSMEM 39 59  
 FT DOMAIN 60 78  
 FT TRANSMEM 79 101  
 FT DOMAIN 102 247  
 FT METAL 182 182  
 FT METAL 217 217  
 FT METAL 221 221  
 FT METAL 225 225  
 SQ SEQUENCE 247 AA; 27927 MW; 8AFAE9A1EA249CA CRC64;

Query Match 7.1%; Score 7; DB 1; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LPAVVL 12  
 DB 84 LPAVVL 90

RESULT 15  
 ICAL\_CERAE STANDARD; PRT; 263 AA.  
 AC P49342;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Calpain inhibitor (calpastatin) (fragment).  
 GN CAST.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Cercopithecoidea;  
 CC Cercopithecinae; Cercopithecus.  
 CC NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92235069; PubMed=1569094;  
 RA Lee W.J., Ma H., Takano E., Yang H.Q., Hatanaka M., Maki M.;  
 RT "Molecular diversity in amino-terminal domains of human calpastatin  
 by exon skipping.";  
 RL J. Biol. Chem. 267:8437-8442(1992).  
 CC -1- FUNCTION: Specific inhibition of calpain (calcium-dependent  
 cysteine protease). Plays a key role in postmortem tenderization  
 of meat and have been proposed to be involved in muscle protein  
 degradation in living tissue.  
 CC -1- DOMAIN: HAS FOUR INHIBITORY DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE CALPASTATIN FAMILY.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
 CC EMBL; M86248; AA52753.1; -  
 CC InterPro; IPR001259; Calpain\_inhib.

DR Pfam; PF00748; Calpain\_inhib; 2.  
 KM Repeat; Thiol protease inhibitor; Alternative splicing.  
 FT REPEAT 170 222 INHIBITORY DOMAIN 1.  
 FT NON TER 283 283  
 SQ SEQUENCE 283 AA; 30170 MW; 02743390B5D6F0F8 CRC64;

Query Match 7.1%; Score 7; DB 1; Length 283;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TLGGPPE 30  
 Db 163 TLGGPPE 169

Search completed: November 28, 2003, 08:04:04  
 Job time : 15 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 07:57:48 ; Search time 30 Seconds

(without alignment)  
851.574 Million cell updates/sec

Title: US-10-059-395-142

Sequence: 1 MKIPPLPAVVLISLVHSA.....LNMDAPPKXKGRATPPAQ 99

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP\_RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 8     | 8.1         | 219    | 2     | Q9Z650 Pantoea cit |
| 2          | 8     | 8.1         | 219    | 16    | Q8ZD57             |
| 3          | 8     | 8.1         | 222    | 16    | Q9KOE4             |
| 4          | 8     | 8.1         | 228    | 16    | Q8D0V2             |
| 5          | 8     | 8.1         | 372    | 8     | Q8HN36             |
| 6          | 8     | 8.1         | 390    | 16    | Q8ETM3             |
| 7          | 8     | 8.1         | 404    | 12    | Q9ICB8             |
| 8          | 8     | 8.1         | 409    | 12    | Q9ICB6             |
| 9          | 8     | 8.1         | 414    | 12    | Q8JZH6             |
| 10         | 8     | 8.1         | 422    | 12    | Q9ICB7             |
| 11         | 8     | 8.1         | 480    | 16    | Q9KIA8             |
| 12         | 8     | 8.1         | 956    | 10    | Q9VIB3             |
| 13         | 8     | 8.1         | 1197   | 5     | Q9VIB3             |
| 14         | 7     | 7.1         | 48     | 16    | Q9L204             |
| 15         | 7     | 7.1         | 77     | 6     | Q8H244             |
| 16         | 7     | 7.1         | 77     | 8     | Q9TA10             |

|    |   |     |     |    |        |                     |
|----|---|-----|-----|----|--------|---------------------|
| 17 | 7 | 7.1 | 102 | 10 | Q9FIS3 | Q9FIS3 arabidopsis  |
| 18 | 7 | 7.1 | 103 | 2  | P71310 | P71310 escherichia  |
| 19 | 7 | 7.1 | 110 | 8  | Q9T926 | Q9T926 telestes mu  |
| 20 | 7 | 7.1 | 125 | 11 | Q9IXK8 | Q9IXK8 mus musculus |
| 21 | 7 | 7.1 | 125 | 17 | Q9YER7 | Q9YER7 aeropyrum p  |
| 22 | 7 | 7.1 | 132 | 16 | Q9RXV0 | Q9RXV0 deinococcus  |
| 23 | 7 | 7.1 | 133 | 6  | Q8H245 | Q8H245 papio papio  |
| 24 | 7 | 7.1 | 162 | 2  | Q8G122 | Q8G122 pseudomonas  |
| 25 | 7 | 7.1 | 163 | 2  | Q9AQW7 | Q9AQW7 pseudomonas  |
| 26 | 7 | 7.1 | 170 | 2  | Q9AQW6 | Q9AQW6 pseudomonas  |
| 27 | 7 | 7.1 | 170 | 2  | Q8G121 | Q8G121 pseudomonas  |
| 28 | 7 | 7.1 | 173 | 16 | Q8D808 | Q8D808 vibrio vuln  |
| 29 | 7 | 7.1 | 189 | 8  | Q94S57 | Q94S57 arxiozyma t  |
| 30 | 7 | 7.1 | 190 | 8  | Q94NV5 | Q94NV5 arxiozyma t  |
| 31 | 7 | 7.1 | 190 | 10 | Q8GSB4 | Q8GSB4 oryza sativ  |
| 32 | 7 | 7.1 | 192 | 8  | Q94S58 | Q94S58 arxiozyma t  |
| 33 | 7 | 7.1 | 195 | 5  | Q97369 | Q97369 calpodex et  |
| 34 | 7 | 7.1 | 196 | 8  | Q94S60 | Q94S60 arxiozyma t  |
| 35 | 7 | 7.1 | 200 | 8  | Q94S59 | Q94S59 arxiozyma t  |
| 36 | 7 | 7.1 | 213 | 16 | Q97PD3 | Q97PD3 streptococc  |
| 37 | 7 | 7.1 | 218 | 2  | Q33571 | Q33571 rhodobacter  |
| 38 | 7 | 7.1 | 221 | 16 | Q9CPM1 | Q9CPM1 pasteurella  |
| 39 | 7 | 7.1 | 222 | 8  | Q9MG12 | Q9MG12 kongobatha   |
| 40 | 7 | 7.1 | 227 | 8  | Q8LXM4 | Q8LXM4 myadestes g  |
| 41 | 7 | 7.1 | 227 | 8  | Q9G9A0 | Q9G9A0 myadestes g  |
| 42 | 7 | 7.1 | 227 | 8  | Q8LVM2 | Q8LVM2 myadestes g  |
| 43 | 7 | 7.1 | 229 | 8  | Q9B853 | Q9B853 rhagolepis   |
| 44 | 7 | 7.1 | 229 | 8  | Q8HN00 | Q8HN00 monoleia m   |
| 45 | 7 | 7.1 | 233 | 5  | Q8MNB4 | Q8MNB4 dictyostell  |

## ALIGNMENTS

## RESULT 1

Q9Z650 PRELIMINARY; PRT; 219 AA.  
AC Q9Z650; 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE CMDB.  
GN CMDB.  
OS Pantoea citrea.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Pantoea.  
OX NCBI\_TaxID=53336;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1056R;  
RX MEDLINE=20200361; PubMed=10735866;  
RA Fujol C.J., Kado C.I.;  
RT "Genetic and Biochemical characterization of the pathway in Pantoea citrea leading to pink disease of pineapple.";  
RU J. Bacteriol. 182:2230-2237(2000).  
DR EMBL; AF103874; AAD19538.1; .  
DR InterPro; IPR003544; CycC\_bIog\_CMdb.  
DR Pfam; PF03379; CMdb; 1.  
DR PRINTS; PR01414; CMDBIOGNIS.  
DR TIGRFAW; TIGR01190; CMdb; 1.  
SQ SEQUENCE 219 AA; 23088 MW; A7A86D08EA0E028 CRC64;

Query Match 8.1%; Score 8; DB 2; Length 219;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VLTSLVLT 17  
DB 158 VLTSLVLT 165

RESULT 2  
Q8ZD57

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ID Q82D57 PRELIMINARY; PRT; 219 AA.
AC Q82D57;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Heme exporter protein B.
GN CCMB OR YPO2735.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Tiltball R.W., Holden M.T.G.,
RA Prentice M.B., Sebailia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; AJ414153; CAC92974.1; -
DR InterPro; IPR003544; Cytc_blog_CcMB.
DR Pfam; PF03379; CcMB; 1.
DR PRINTS; PRO1414; CCMBBI0GNSIS.
DR TIGRFAMs; TIGR01190; ccmb; 1.
KW Complete proteome.
SQ SEQUENCE 219 AA; 23127 MW; 2BBE6D12D1093A CRC64;

Query Match 8.1%; Score 8; DB 16; Length 219;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 VLSTLVL 17
Db 158 VLSTLVL 165

RESULT 3
Oy Q9KOE4 PRELIMINARY; PRT; 222 AA.
ID Q9KOE4;
AC Q9KOE4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Heme exporter protein B.
GN VC2056.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eissen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unanue B.A.,
RA Gill S.R., Nelson K.B., Read T.D., Tettelin J., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Baes S., Qin H., Dragol I., Sellers P.,
RA McDonald L., Utcchack T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004279; AAF95202.1; -
DR TIGR; VC2056; -
DR InterPro; IPR003544; Cytc_blog_CcMB.
DR Pfam; PF03379; CcMB; 1.
DR PRINTS; PRO1414; CCMBBI0GNSIS.

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DR TIGRFAMs; TIGR01190; ccmb; 1.
KW Complete proteome.
SQ SEQUENCE 222 AA; 23697 MW; 9F6CD1ECA214EC60 CRC64;

Query Match 8.1%; Score 8; DB 16; Length 222;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 VLSTLVL 17
Db 161 VLSTLVL 168

RESULT 4
Oy Q8D0V2 PRELIMINARY; PRT; 228 AA.
ID Q8D0V2;
AC Q8D0V2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Heme exporter protein B.
GN CCMB OR Y1568.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fehershten S.C., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.J., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AE013760; AAM85137.1; -
SQ SEQUENCE 228 AA; 24114 MW; 3E6AFC5025D7AE55 CRC64;

Query Match 8.1%; Score 8; DB 16; Length 228;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 VLSTLVL 17
Db 167 VLSTLVL 174

RESULT 5
Oy Q8HN36 PRELIMINARY; PRT; 372 AA.
ID Q8HN36;
AC Q8HN36;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Cytochrome b.
GN CYTB.
OS Paragonimus westermani.
OC Mitochondrion.
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Euharyota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OX NCBI_TaxID=34504;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=;
RX Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF540958; AAN15171.1; -
DR Mitochondrion.
SQ SEQUENCE 372 AA; 41636 MW; 7B529C6B241B0BFD CRC64;

Query Match 8.1%; Score 8; DB 8; Length 372;

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Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VVLSLVL 17  
DB 223 VVLSLVL 230

## RESULT 6

Q8ETM3 PRELIMINARY; PRT; 390 AA.  
AC Q8ETM3;  
DT 01-MAR-2003 (TRENBLREL. 23, Created)  
DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)  
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)  
DE Hypothetical protein.  
GN OB0237.  
OS Oceanobacillus theyensis.  
OC Bacteria; Firmicutes; Bacillales; Oceanobacillaceae.  
OX NCBI\_TaxID=182710;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;  
RX MEDLINE=2220767; PubMed=12235376;  
RA Takami H., Takaki Y., Uchiyama I.;  
RT "Genome sequence of Oceanobacillus theyensis isolated from the Iheya  
RT Ridge and its unexpected adaptive capabilities to extreme  
RT environments."  
RL Nucleic Acids Res. 30:3927-3935(2002).  
DR EMBL; AF004593; BAC12193.1;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 390 AA; 43262 MW; B2CE189BE0A63D2B CRC64;

Query Match 8.1%; Score 8; DB 16; Length 390;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 PRLNIDKL 54  
DB 200 PRLNIDKL 207

## RESULT 7

Q91CB8 PRELIMINARY; PRT; 404 AA.  
AC Q91CB8;  
DT 01-DEC-2001 (TRENBLREL. 19, Created)  
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)  
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)  
DE Early E3 48K glycoprotein.  
OS Human adenovirus type 8.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=11545;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Blumh J.H., Deryckere F., Windheim M., Adrian T., Burgert H.G.;  
RT "E3-49K: a novel early region 3 protein expressed by adenoviruses of  
RT subgroup D."  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF233391; AL01120.1;  
DR InterPro; IPR003471; Adeno\_E3\_CR1.  
DR InterPro; IPR003470; Adeno\_E3\_CR2.  
DR Pfam; PF02440; Adeno\_E3\_CR1; 3.  
DR Pfam; PF02439; Adeno\_E3\_CR2; 1.  
SQ SEQUENCE 404 AA; 45541 MW; 5B5B62A9A37E99EF CRC64;

Query Match 8.1%; Score 8; DB 12; Length 404;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VVLSLVL 16  
DB 7 VVLSLVL 14

## RESULT 8

Q91CB6 PRELIMINARY; PRT; 409 AA.  
AC Q91CB6;  
DT 01-DEC-2001 (TRENBLREL. 19, Created)  
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)  
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)  
DE Early E3 46K glycoprotein.  
OS Human adenovirus type 9.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=10527;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Blumh J.H., Deryckere F., Windheim M., Adrian T., Burgert H.G.;  
RT "E3-49K: a novel early region 3 protein expressed by adenoviruses of  
RT subgroup D."  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF233394; AL01123.1;  
DR InterPro; IPR003471; Adeno\_E3\_CR1.  
DR InterPro; IPR003470; Adeno\_E3\_CR2.  
DR InterPro; IPR006895; zf-Sec23\_Sec24.  
DR Pfam; PF02440; Adeno\_E3\_CR1; 3.  
DR Pfam; PF02439; Adeno\_E3\_CR2; 1.  
DR Pfam; PF04810; zf-Sec23\_Sec24; 1.  
SQ SEQUENCE 409 AA; 45846 MW; 562F6807B279A95E CRC64;

Query Match 8.1%; Score 8; DB 12; Length 409;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VVLSLVL 16  
DB 7 VVLSLVL 14

## RESULT 9

Q8JZH6 PRELIMINARY; PRT; 414 AA.  
AC Q8JZH6;  
DT 01-OCT-2002 (TRENBLREL. 22, Created)  
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)  
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)  
DE E3/49K.  
OS Human adenovirus type 19p.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=13640;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=587;  
RA Blumh J.H., Deryckere F., Windheim M., Ruzsics Z., Arnberg N.,  
RA Adrian T., Burgert H.G.;  
RT "E3/49K: A Novel Early Region 3 Protein Specifically Expressed By  
RT Adenoviruses of Subgroup D."  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF271153; AAM3819.1;  
DR InterPro; IPR003471; Adeno\_E3\_CR1.  
DR InterPro; IPR003470; Adeno\_E3\_CR2.  
DR Pfam; PF02440; Adeno\_E3\_CR1; 3.  
DR Pfam; PF02439; Adeno\_E3\_CR2; 1.  
SQ SEQUENCE 414 AA; 46289 MW; D5F388514FC95A92 CRC64;

Query Match 8.1%; Score 8; DB 12; Length 414;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VVLSLVL 16  
DB 7 VVLSLVL 14

## RESULT 10

091CB7  
ID 091CB7 PRELIMINARY; PRT; 422 AA.  
AC 091CB7;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DE Early E3 50K glycoprotein.  
OS Human adenovirus type 15.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
NCBI\_TaxID=28276;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Blusch J.H., Deryckere F., Windeheim M., Adrian T., Burgert H.G.;  
RT "E3-49K: a novel early region 3 protein expressed by adenoviruses of subgroup D.";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF233392; AAL01121.1; -  
DR InterPro; IPR003471; Adeno\_E3\_CR1.  
DR InterPro; IPR003470; Adeno\_E3\_CR2.  
DR Pfam; PF02440; Adeno\_E3\_CR1; 3.  
DR Pfam; PF02439; Adeno\_E3\_CR2; 1.  
SQ SEQUENCE 422 AA; 47877 MW; 6551F6FC54BC8399 CRC64;  
Query Match  
Best Local Similarity 100.0%; Score 8; DB 12; Length 422;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 VLLSLTV 16  
DB 7 VLLSLTV 14  
RESULT 11  
09K1A8  
ID 09K1A8 PRELIMINARY; PRT; 480 AA.  
AC 09K1A8;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE NADH dehydrogenase I, N subunit.  
GN NMB0259.  
OS Neisseria meningitidis (serogroup B).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
NCBI\_TaxID=491;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / Serogroup B;  
RX MEDLINE=20175755; PubMed=10710307;  
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,  
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,  
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey B.K.,  
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,  
RA Mason T., Clecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,  
RA Cotton M.D., Utecht V., Masigian V., Knout H., Qin H., Vamathevan J.,  
RA Gill J., Scarlato V., Masigian V., Pizsa M., Grandi G., Sun L.,  
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;  
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";  
RL Science 287:1869-1815(2000).  
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS CHAINS.  
CC -1- SIMILARITY: TO ONE OF THE POLYPEPTIDE CHAINS OF THE NADH-UBIQUINOL OXIDOREDUCTASE OF CHLOROPLASTS OR MITOCHONDRIA.  
DR EMBL; AF002882; AAF40713.1; -  
DR TIGR; NMB0259; -  
DR InterPro; IPR003916; NADHUB\_oxrds.  
DR InterPro; IPR001750; Oxidored\_g1.  
DR Pfam; PF00361; oxidored\_g1; 1.  
DR PRINTS; PR01434; NADHGNAS5.  
KM NAD; Oxidoreductase; Transmembrane; Complete proteome.

SQ SEQUENCE 480 AA; 52125 MW; D05A272BAB24EB15 CRC64;  
Query Match  
Best Local Similarity 100.0%; Score 8; DB 16; Length 480;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 VLLSLTV 17  
DB 16 VLLSLTV 23  
RESULT 12  
09LKT5  
ID 09LKT5 PRELIMINARY; PRT; 956 AA.  
AC 09LKT5;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE 5' repair endonuclease.  
GN UVAH.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.  
NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Landsberg erecta;  
RX MEDLINE=20484028; PubMed=11027708;  
RA Fidanbet A.L., Mitchell D.L., Britt A.B.;  
RT "The Arabidopsis UVAH Gene is a Homolog of the Yeast Repair Endonuclease RAD1.";  
RL Plant Physiol. 124:579-586(2000).  
DR EMBL; AF273377; AAP81910.1; -  
DR InterPro; IPR006166; ERCC4.  
DR Pfam; PF02732; ERCC4; 1.  
KM Endonuclease.  
SQ SEQUENCE 956 AA; 107458 MW; 9B6A14966BAEB145 CRC64;  
Query Match  
Best Local Similarity 100.0%; Score 8; DB 10; Length 956;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 12 LSLVTVS 19  
DB 830 LSLVTVS 837  
RESULT 13  
09VLB3  
ID 09VLB3 PRELIMINARY; PRT; 1197 AA.  
AC 09VLB3;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE CG3811 protein.  
GN CG3811.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkelley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celinker S.B., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,  
RA Suton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Broctier P.,  
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glaeser K.,  
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpas G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Mervulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier B., Spirdling A.C., Stapleton M., Strong R., Sun E.,  
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yen R.F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195 (2000).  
[2]  
RN SEQUENCE FROM N.A.  
RP Celinker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
RA Barton J., An H., Baldwin D., Barton J., Beeson K.Y., Busan D.A.,  
RA Carlson J.W., Center A., Champs M., Davenport L.B., Dietz S.M.,  
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Drenek D., Farfan D.,  
RA Ferreira S., Fries E., Galle R.F., Garg N.S., George R.A.,  
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
RA Ibegwam C., Jalali M., Kruse D., Li P., Matzel B., Moshrefi A.,  
RA McIntosh T.C., Moy M., Murphy B., Murphy L., Nelson K.A., Nuno J.,  
RA Pacleb J., Paragov V., Park S., Patel S., Pfeiffer B.,  
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
RA Stapleton M., Strong R., Svitskas R., Tector C., Tyler D.,  
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,  
RT "Sequencing of *Drosophila melanogaster* genome.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[3]  
RN SEQUENCE FROM N.A.  
RP Mista S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
RA Hradecky P., Huang Y., Kaminker J.S., Prochik S.E., Smith C.D.,  
RA Tupy J.L., Bergman C., Bergman B., Carlson J.W., Celinker S.B.,  
RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
RA Seale S.M.J., Smith B., Shu S., Smurniak F., Whitfield E.,  
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.B.,  
RT "Annotation of *Drosophila melanogaster* genome.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[4]  
RN SEQUENCE FROM N.A.  
RP Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN  
RN SEQUENCE FROM N.A.  
RP Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RA EMBL: AE003625; AAF52781.2;  
DR FLYBase; FBgn0032123; CG3811.  
DR FLYBase; FBgn0032123; CG3811.  
DR InterPro; IPR007114; MFS.  
DR Pfam; PF03132; OAMP\_N; 1.  
DR PROSITE; PS00850; MFS; 1.

SQ SEQUENCE 1197 AA; 130193 MW; 369C217AA54B754C CRC64;  
Query Match 8.1%; Score 8; DB 5; Length 1197;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 VVLSLIV 16  
DB 173 VVLSLIV 180  
RESULT 14  
ID 09L204 PRELIMINARY; PRT; 48 AA.  
AC 09L204;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Hypothetical protein SC02629.  
GN SC02629 OR SC8E4.04.  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycinae; Streptomyces.  
CX NCB1\_TaxID=1902;  
RN  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2) / M145;  
RX MEDLINE=2196410; PubMed=12000953;  
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
RA Thompson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cionin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,  
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.,  
RT "Complete genome sequence of the model actinomycete *Streptomyces*  
RT *coelicolor* A3(2)."  
RL Nature 417:141-147(2002).  
DR EMBL: AL939113; CAB71804.1;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 48 AA; 5012 MW; 4CC4B4DF265858E CRC64;  
Query Match 7.1%; Score 7; DB 16; Length 48;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 VVLSLIV 16  
DB 17 VVLSLIV 23  
RESULT 15  
ID 08H244 PRELIMINARY; PRT; 77 AA.  
AC 08H244;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Epididymal protease inhibitor 2.  
GN BPIIN.  
OS Papio hamadryas (Hamadryas baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
OC Cercopitheinae; Papio.  
CX NCB1\_TaxID=9557;  
RN  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Siyashanmugam P., O'Rand M.G., Richardson R.T.,  
RT "Characterization of Baboon BpPin.";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.



DR EMBL; AY141975; AAN08509.1; -.  
KW Protease.  
SQ SEQUENCE 77 AA; 8787 MW; B86B5868C57CEBD0 CRC64;

Query Match 7.1%; Score 7; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LLSLIVL 17  
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Db 6 LLSLIVL 12

Search completed: November 28, 2003, 08:04:43  
Job time : 37 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 09:26:39 ; Search time 1716 Seconds  
(without alignments)  
1402.181 Million cell updates/sec

Title: US-10-059-395-142  
Perfect score: 99  
Sequence: 1 MKIPVPAVVLISLVLSHA.....LNWAPFKKGRSATPDQAQ 99

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Word size: 1

Total number of hits satisfying chosen parameters: 45562604

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:  
-MODE=frame+pn.model -DEV=x1h  
-Q/cgn2.1/USPTO.spool/US10059395/runat.25112003.140755.7412/app.query.fasta\_1.263  
-DB=EST -OPMT=fastap -SUFFIX=oli.rst -MTMARCH=0.1 -LOOPL=0 -LOOPEXT=0  
-INITs=bits -START=1 -END=1 -MATRIX=oligo -TRANS=humand0.cdi -LIST=45  
-DOCALLIGN=200 -THR\_SCORE=quality -THR\_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc  
-NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10059395.QCGN.1.1.2810 @runat.25112003.140755.7412 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEBUFFER -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :  
EST.\*  
1: em\_esbba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estcp1:\*  
7: em\_estro:\*  
8: em\_hcc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hcc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gse\_hum:\*  
18: em\_gse\_inv:\*  
19: em\_gse\_pln:\*  
20: em\_gse\_vrt:\*  
21: em\_gse\_fun:\*  
22: em\_gse\_mam:\*  
23: em\_gse\_mus:\*  
24: em\_gse\_pro:\*  
25: em\_gse\_rod:\*  
26: em\_gse\_pig:\*  
27: em\_gse\_vrl:\*  
28: gb\_gse1:\*

29: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 99    | 100.0       | 334    | 9     | AA297512    |
| 2          | 99    | 100.0       | 432    | 13    | EX112106    |
| 3          | 98    | 99.0        | 424    | 14    | W69083      |
| 4          | 88    | 88.9        | 394    | 14    | W60320      |
| 5          | 86    | 86.9        | 348    | 9     | AM238758    |
| 6          | 80    | 80.8        | 381    | 14    | W69108      |
| 7          | 78    | 78.8        | 339    | 9     | AA778414    |
| 8          | 76    | 76.8        | 373    | 9     | AA722894    |
| 9          | 72    | 72.7        | 412    | 14    | W60268      |
| 10         | 72    | 72.7        | 432    | 14    | W69233      |
| 11         | 71    | 71.7        | 318    | 9     | AA586846    |
| 12         | 71    | 71.7        | 359    | 10    | BR465728    |
| 13         | 71    | 71.7        | 362    | 9     | AT140605    |
| 14         | 66    | 66.7        | 326    | 9     | AA297513    |
| 15         | 59    | 58.6        | 431    | 14    | W69227      |
| 16         | 58    | 58.6        | 377    | 9     | AA582988    |
| 17         | 58    | 58.6        | 413    | 9     | AA393296    |
| 18         | 57    | 57.6        | 345    | 9     | AT121765    |
| 19         | 56    | 56.6        | 241    | 9     | AA595989    |
| 20         | 53    | 53.5        | 334    | 9     | BG150312    |
| 21         | 51    | 51.5        | 339    | 10    | AT1217587   |
| 22         | 43    | 43.4        | 345    | 9     | AA583942    |
| 23         | 43    | 43.4        | 376    | 14    | W95920      |
| 24         | 39    | 39.4        | 221    | 9     | AA584333    |
| 25         | 37    | 37.4        | 358    | 9     | AM003825    |
| 26         | 35    | 35.4        | 330    | 14    | W95883      |
| 27         | 33    | 33.3        | 218    | 9     | AA398638    |
| 28         | 33    | 33.3        | 239    | 9     | AA595930    |
| 29         | 29    | 29.3        | 249    | 13    | BX476814    |
| 30         | 27    | 27.3        | 339    | 14    | W52030      |
| 31         | 27    | 27.3        | 378    | 9     | AT184682    |
| 32         | 24    | 24.2        | 368    | 9     | AM260965    |
| 33         | 24    | 24.2        | 436    | 9     | AV597545    |
| 34         | 18    | 18.2        | 163    | 9     | AA776980    |
| 35         | 15    | 15.2        | 377    | 9     | AM260982    |
| 36         | 14    | 14.1        | 421    | 9     | AV618771    |
| 37         | 13    | 13.1        | 581    | 9     | AV597546    |
| 38         | 12    | 12.1        | 323    | 10    | BE715771    |
| 39         | 10    | 10.1        | 601    | 10    | BE033529    |
| 40         | 10    | 10.1        | 612    | 28    | AO587040    |
| 41         | 10    | 10.1        | 766    | 13    | BU327477    |
| 42         | 9     | 9.1         | 523    | 9     | AA066639    |
| 43         | 9     | 9.1         | 528    | 13    | BU829711    |
| 44         | 9     | 9.1         | 532    | 28    | BZ169340    |
| 45         | 9     | 9.1         | 538    | 10    | BE879658    |

#### ALIGNMENTS

RESULT 1  
AA297512  
LOCUS AA297512 334 bp mRNA linear EST 18-APR-1997  
DEFINITION EST113061 Fetal skin Homo sapiens cDNA 5' end, mRNA sequence.  
ACCESSION AA297512  
VERSION AA297512.1 GI:1949866  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
1 (bases 1 to 334)  
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulmer,R.A., Bult



|            |  |     |  |     |
|------------|--|-----|--|-----|
| Oy         |  | 1   | MethylisEP-ovallleProAlValValeuleuSerLeuValleuHISerLa          | 20  |
| Dd         |  | 15  | ATGAAGATCCCGGATCTTCTGCCTGGTGAGTCTCTCTCCTGTGGTCACACTGGCC        | 74  |
| Oy         |  | 21  | GInglYalAthrLeuGlYglYPrOgIuNgIuSerThrIleGluaNtYAlaserZg        | 40  |
| Dd         |  | 75  | CAGGAGGCCACCCTGGGTGTCTCGAGGAAAGAACCATTGAGAAATTAGCCGCASCA       | 134 |
| Oy         |  | 41  | ProGlUAlpheAthrPProPhelEuAnsIleApLySleUArgSerAlaPheLYsAla      | 60  |
| Dd         |  | 135 | CCCAGGCGCTTTAACACCCCGTCTCGTAACATCGACAATTCGATTCGCGTTAAAGCT      | 194 |
| Oy         |  | 61  | AAspIuPheLeuAthrPProLYsLeuLYsAgIYleuArgSerAlaIatrrProAspAlaGln | 99  |
| Dd         |  | 195 | GATAGATTCTCGAACTGGCACGCCCTCTTAGCTATACAAAGAACTTCCTTCTC          | 254 |
| Oy         |  | 81  | AsnTrpAspaIapePProLYsLeuLYsAgIYleuArgSerAlaIatrrProAspAlaGln   | 99  |
| Dd         |  | 255 | AACTCGGATGCTTTCCTTAAGCTGAAGAGACTGAGAGCGCAACTCTGATGCCAG         | 311 |
| RESULT 3   |  |     |  |     |
| LOCUS      |  |     |  |     |
| DEFINITION |  |     |  |     |
| ACCESSION  |  |     |  |     |
| VERSION    |  |     |  |     |
| KEYWORDS   |  |     |  |     |
| SOURCE     |  |     |  |     |
| ORGANISM   |  |     |  |     |
| REFERENCE  |  |     |  |     |
| AUTHORS    |  |     |  |     |
| TITLE      |  |     |  |     |
| JOURNAL    |  |     |  |     |
| COMMENT    |  |     |  |     |
| FEATURES   |  |     |  |     |
| source     |  |     |  |     |

| ORIGIN                                    | BASE COUNT   | 98 a   | 100 c | 129 g  | 97 t            |
|---|--|--|-------|--------|-----------------|
| Alignment Scores:                         |  |  |       |        |                 |
| Pred. No.:                                | 1.35e-85   | Length:  |       | 424    |                 |
| Score:                                    | 98.00  | Matches:   |       | 98     |                 |
| Percent Similarity:                       | 100.00%  | Conservative:  |       | 0      |                 |
| Best Local Similarity:                    | 100.00%  | Mismatches:  |       | 0      |                 |
| Query Match:                              | 98.99%   | Indels:  |       | 0      |                 |
| DB:                                       | 14   | Gaps:  |       | 0      |                 |
| US-10-059-395-142 (1-99) x W69083 (1-424) |  |  |       |        |                 |
| Oy  | 2  | Lys11eProValLeuPProAlaValIleuSerIleuValIleuHisSerAlaGln 21         |       |        |                 |
| Db  | 398  | AAGATCCCGGCTCTTCCGCGGTGCTCTCTCCCTCGTGCCTCACTGCGCAG 339             |       |        |                 |
| Oy  | 22   | GlyAlaThrIleuGlyGlyProGluGluGluSerThrIleGluValIleuValSerAlaPro 41  |       |        |                 |
| Db  | 338  | GGAGCCACCCCTGGGTGGCTGAGAGAAAGAACCACTGGAATATGCTCGACACC 279          |       |        |                 |
| Oy  | 42   | GluAlaIleuAsnThrProPheLeuAsnIleAspIleuArgSerAlaPheIleAlaAsp 61     |       |        |                 |
| Db  | 278  | GAGGCTTTAAACACCCCGTTCCTGAACATGACAAATTGGATTTGGGTTAAAGCTGAT 219      |       |        |                 |
| Oy  | 62   | GluPheLeuAsnThrPheAlaLeuPheGluSerIleIleValArgIlePheProPheLeuAsn 81 |       |        |                 |
| Db  | 218  | GAGTTCCTGAACGCGACGCCCTCTTGAGCTCTATCAAAAGAACTTCTTCCTCAAC 159        |       |        |                 |
| Oy  | 82   | TyrAspAlaPheProIleuValIleuValArgSerAlaThrProAspAlaGln 99           |       |        |                 |
| Db  | 158  | TGGATGCTTTTCTTAAGCTGAAGAGACTGAGAGGCGACACTCTGATGCCAG 105            |       |        |                 |
| RESULT 4                                  |  |  |       |        |                 |
| LOCUS                                     | W60320   | 394 bp   | mRNA  | linear | EST 15-OCT-1996 |
| DEFINITION                                | zcd39g01.81 Soares_fetal_heart_NbHh19W Homo sapiens cDNA clone   |  |       |        |                 |
| ACCESSION                                 | W60320   | IMAGE:342096 3, mRNA sequence.                                     |       |        |                 |
| VERSION                                   | W60320.1   | GI:1367079   |       |        |                 |
| KEYWORDS                                  | EST.   |  |       |        |                 |
| SOURCE                                    | Homo sapiens (human)   |  |       |        |                 |
| ORGANISM                                  | Homo sapiens   |  |       |        |                 |
| REFERENCE                                 | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.   |  |       |        |                 |
| AUTHORS                                   | 1 (bases 1 to 394)<br>Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Holman M., Hulman M., Kucaba T., Le M., Lemon G., Merra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Tevaskis E., Watson R., Williams A., Wohlmann P. and Wilson R.                         |  |       |        |                 |
| TITLE                                     | The Wash-Merck EST Project   |  |       |        |                 |
| JOURNAL                                   | Unpublished  |  |       |        |                 |
| COMMENT                                   | Contact: Wilson RK<br>Washington University School of Medicine<br>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108<br>Tel: 314 286 1800<br>Fax: 314 286 1810<br>Email: est@wustl.edu<br>Web: est@wustl.edu  |  |       |        |                 |
| FEATURES                                  | This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.<br>Insert Length: 476 Std Error: 0.00<br>Seq primer: mob.REGA+ET.   |  |       |        |                 |
| source                                    | Location/Qualifiers<br>1..394<br>/organism="Homo sapiens"<br>/mol_type="mRNA"<br>/db_xref="GDB:1267471"<br>/db_xref="taxon:9606"<br>/clone="IMAGE:342096"<br>/sex="unknown"<br>/dev_stage="19 weeks"<br>/lab_host="DH10B (ampicillin resistant)"<br>/clone_id="Soares_fetal_heart_NbHh19W" |  |       |        |                 |

/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTACCACTGAGTGGAGCGGCGCCATCTTTTCTTTTCTTTT 3'). double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung MbHL19M."

BASE COUNT 94 a 88 c 119 g 91 t 2 others  
ORIGIN

Alignment Scores:  
Pred. No.: 7,15e-76 Length: 394  
Score: 88.00 Matches: 88  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 88.89% Indels: 0  
DB: 14 Gaps: 0

US-10-059-395-142 (1-99) x W60320 (1-394)

QY 12 LeuSerLeuValLeuHisSerAlaGlnGlyAlaThrLeuGlyProGluGluGlu 31  
DB 371 CTCCTCCCTCTGCTGCTCCACTGCGGAGGACACCTGGTGGTCTGAGAGAA 312

QY 32 SerThrIleGluAsnThrAlaSerArgProGluAlaPheAsnThrProPheLeuAsnIle 51  
DB 311 ACCACCATTTGAAATTAATGCGTACGACCGGAGGCTTTTAAACCCCGTCTGAAACATC 252

QY 52 AspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPheIleLeuPheGlu 71  
DB 251 GACCAATTCGCAATCGCTTAAGCTGATGAGTCTCGAATCGGACGCCCTCTTTGAG 192

QY 72 SerIleLysArgLysLeuProPheLeuAsnThrAspAlaPheProLysLeuLysGlyLeu 91  
DB 191 TCTATCAAAAGAAACCTTCCTTCTCAACTGGAGTGCCTTCTTAAGCTGAAAGAAAGACTG 132

QY 92 ArgSerAlaThrProAspAlaGln 99  
DB 131 AGGAGCGCACTCTGATGCCAG 108

RESULT 5  
AM238758 348 bp mRNA linear EST 13-DEC-1999  
LOCUS xp03e08.x1 NCI\_CGAP\_HN8 Homo sapiens cDNA clone IMAGE:2739302 3',  
DEFINITION mRNA sequence.  
ACCESSION AM238758  
VERSION AM238758.1 GI:6571147  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 348)  
NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Edward Shillitoe Ph.D., Silvio Gutkind Ph.D.,  
Chidchanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.  
cDNA library Preparation: David B. Kitzman, Ph.D.  
cDNA library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/INL at:  
www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found  
Seq primer: -40UP from Glibco  
High quality sequence stop: 331.  
Location/Qualifiers

FEATURES  
source  
1..348  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2739302"  
/tissue\_type="well-differentiated invasive carcinoma,  
floor of mouth"  
/lab\_host="DH10B"  
/clone\_id="NCI\_CGAP\_HN8"  
/note="Vector: pAMP10; cDNA made by oligo-dT priming.  
Non-directionally cloned into the UDP sites of pAMP10.  
Size-selected on agarose gel, average insert size 500 bp.  
Primary library; non-amplified. cDNA library  
Preparation: David B. Kitzman, Ph.D (NCI). Reference:  
Kitzman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 82 a 104 c 84 g 78 t  
ORIGIN

Alignment Scores:  
Pred. No.: 5.61e-74 Length: 348  
Score: 86.00 Matches: 86  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 86.87% Indels: 0  
DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x AM238758 (1-348)

QY 14 LeuLeuValLeuHisSerAlaGlnGlyAlaThrLeuGlyProGluGluGluSerThr 33  
DB 36 CTCCTGGTGGCTCCACTGCGGAGGAGCCACCTGGGTGCTGAGAGAAAGAACACC 95

QY 34 IleGluAsnThrAlaSerArgProGluAlaPheAsnThrProPheLeuAsnIleAspLys 53  
DB 96 ATTGAGAAATTAATGATACGACCGGAGGCTTTTAAACCCCGTCTGAAACATGACACAA 155

QY 54 LeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPheIleLeuPheGluSerIle 73  
DB 156 TTGGCATTCGCTTTAAGCTGATGAGTCTGAACTGGACGCCCTCTTTGAGTCTATC 215

QY 74 LysArgLysLeuProPheLeuAsnThrAspAlaPheProLysLeuLysGlyLeuArgSer 93  
DB 216 AAAAGAAACCTTCCTTCTCAACTGGAGTGCCTTCTTAAGCTGAAAGAAAGACTGAGAGC 275

QY 94 AlaThrProAspAlaGln 99  
DB 276 GCAACTCCTGATGCCAG 293

RESULT 6  
W69108 381 bp mRNA linear EST 16-OCT-1996  
LOCUS z44c04.61 Soares\_fetal\_heart\_NbHL19W Homo sapiens cDNA clone  
DEFINITION IMAGE:343494 3', mRNA sequence.  
ACCESSION W69108  
VERSION W69108.1 GI:1378389  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 381)  
Hillier, L., Clark, N., Dubuque, T., Ellison, K., Hawkins, M., Holman,  
M., Hultman, M., Kucab, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
Rifkin, B., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston,  
R., Williamson, A., Wohlmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished  
Contact: Wilson RK  
Washington University School of Medicine



|   |  |
|---|--|
| ACCESSION                                   | AA722694   |
| VERSION                                     | AA722694.1   |
| KEYWORDS                                    | GI:2740401   |
| SOURCE                                      | EST.   |
| ORGANISM                                    | Homo sapiens (human)   |
| REFERENCE                                   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  |
| AUTHORS                                     | 1 (bases 1 to 373)   |
| TITLE                                       | Miller L., Allen M., Bowler L., Dubuque T., Geisel G., Joet S., Kizman D., Kucaba T., Lacy M., Le N., Lemon G., Marra M., Martin J., Moore B., Schnellberg K., Stepien M., Tan F., Theisling B., White Y., Wylie T., Waterston R. and Wilson R.  |
| JOURNAL                                     | Unpublished  |
| COMMENT                                     | Washington University School of Medicine<br>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108<br>Tel: 314 286 1800<br>Fax: 314 286 1810<br>Email: east@watson.wustl.edu<br>This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.<br>Seq primer: -40m3 fwd. RT from Amersham.  |
| FEATURES                                    | Location/Qualifiers  |
| SOURCE                                      | 1..373   |
|   | /organism="Homo sapiens"   |
|   | /mol_type="mRNA"   |
|   | /db_xref="GDB:1307650"   |
|   | /db_xref="taxon:9606"  |
|   | /clone="IMAGE:399827"  |
|   | /sex="unknown"   |
|   | /dev_stage="19 weeks"  |
|   | /lab_host="DH10B (ampicillin resistant)"   |
|   | /note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' GTTACCACTGAGATGGAGCGGCACATCTTTTCTTTTCTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Patima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBRH19W." |
| BASE COUNT                                  | 89 a 81 c 113 g 90 t   |
| ORIGIN                                      | NBRH19W."  |
| Alignment Scores:                           |  |
| Pred. NO:                                   | 3,45e-64 Length: 373   |
| Score:                                      | 76.00 Matches: 76  |
| Percent Similarity:                         | 100.00% Conservative: 0  |
| Best Local Similarity:                      | 100.00% Mismatches: 0  |
| Query Match:                                | 76.77% Indels: 0   |
| DB:   | 9 Gaps: 0  |
| US-10-059-395-142 (1-99) x AA722694 (1-373) |  |
| QY  | 24 ThrleuGIyGLyProGluGIuGIuSerThriIleGIuAenTYAlaSerArgProGluAla 43   |
| Db  | 334 ACCCTGGGTGTCCTGAGGAAGAAACACCATTTGAAATTTAGCTCAGACCCGAGGCC 275   |
| QY  | 44 PheAaenThpProPheIuAenIleAaenTyAlaAGSerAlaPheTyAlaAaenGluPhe 63  |
| Db  | 274 TTTAAACACCCCGTTCCTGAACATCGAACAAATGCAATCGGCTTTAAAGCGTGAAGACTTC 215  |
| QY  | 64 LeuAaenThpIshAlaIuAenPheGIuSerIleTyAaGlyAlaenProPheIuAaenTrpASP 83  |
| Db  | 214 CTGAAGCTGACACCCCTCTTGAAGTCTATCAAAAGAAATCTCTTCTCACTGGGAT 155  |
| QY  | 84 AlaPheProTyAlaenTyGlyAlaenAGSerAlaThrProAaenAlaGln 99   |

```

DB          154  GCCTTCTCCTAGCTGAAGAAGCATGAGGAGCCCACTCTGTATGCCAG 107
RESULT 9
LOCUS       W60268                               412 bp    mRNA    linear    EST 15-Oct-1996
DEFINITION  W60268.1 Soares fetal heart NbhH19W Homo sapiens cDNA clone
IMAGE:342096 5', mRNA sequence.
ACCESSION   W60268
VERSION     W60268.1  GI:1367169
KEYWORDS    EST.

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE   1  (bases 1 to 412)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,
            'M., Hultman,M., Kucaba,T., Le,M., Lemmon,G., Marra,M., Parsons,J.,
            Rikhi,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterson
            ,R., Williamson,A., Woldman,P. and Wilson,R.
            The Mash-Merck EST Project
            Unpublished

TITLE       Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel.: 314 286 1800
            Fax: 314 286 1810
            Email: east@watson.wustl.edu
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.lnl.gov) for further information.
            Putative full length read
            Insert Length: 476    Std Error: 0.00
            Seq primer: mob. REGA+ET
            High quality sequence stop: 385.
            Location/Qualifiers
                1..412
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                    /mol_type="mRNA"
                    /db_xref="GDB:1267471"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:342096"
                    /sex="unknown"
                    /dew_stage="19 weeks"
                    /lab_host="DH10B (ampicillin resistant)"
                    /clone_id="Soares_fetal_heart_NbhH19W"
                    /note="Organ: heart; Vector: pT73 (Pharmacia) with a
                    modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
                    strand cDNA was primed with a Not I - oligo(dT) primer [5'
                    TGTTACCAATCTGAAGCGAGCGCGCGACATCTTTTCTTTTCTTTT 3'],
                    TGTTACCAATCTGAAGCGAGCGCGCGACATCTTTTCTTTTCTTTT 3'],
                    double-stranded cDNA was size selected, ligated to Eco RI
                    adapters (Pharmacia), digested with Not I and cloned into
                    the Not I and Eco RI sites of a modified pT73 vector
                    (Pharmacia). Library went through one round of
                    normalization to a Cot = 5. Library constructed by
                    M.Factina Bonaldo. This library was constructed from the
                    same fetus as the fetal lung library, Soares fetal lung
                    NbhH19W."
BASE COUNT  96 a      127 c      88 g      98 t      3 others
ORIGIN
Alignment Scores:
Pred. No.:      3.07e-60      Length:      412
Score:          72.00         Matches:      72
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 72.00%   Mismatches:  0
Query Match:    72.73%       Indels:      0
                        Gaps:      0
US-10-059-395-142 (1-99) x W60268 (1-412)

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Qy 48 PheLeuAsn1LeuAspLysLeuArgSerAlaPheLeuAlaAspGluPheLeuAsnTrpHis 67  
 Db 154 TTCCTGCAATCGACAAATTCGCATCTGGCTTGAAGCTGATGAGTTCCTGAACTGGCAC 213  
 Qy 68 A1ALeuPheGluSer1LeuArgLysLeuProPheLeuAsnTrpAspAlaPheProLys 87  
 Db 214 GCCCTCTTGAAGTCTATCAAAAGAAACCTTCCTCAACTGGATGCTTCTTAAG 273  
 Qy 88 LeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
 Db 274 CTGAAGGAGCTGAGGAGCGCAACTCTGATGCCAG 309

RESULT 10  
 M69233 432 bp mRNA linear EST 16-OCT-1996  
 LOCUS M69233  
 DEFINITION IMAGB:343494 5', mRNA sequence.  
 ACCESSION W69233  
 VERSION W69233.1 GI:1378493  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 432)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawking, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rittin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Woldman, P. and Wilson, R.  
 The WashU-Merck EST Project  
 Unpublished  
 CONTACT: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGB Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 442 Std Error: 0.00  
 Seq primer: mob.REGA+ET  
 High quality sequence stop: 341.  
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 /clone\_lib="Soares fetal heart NBH19W"  
 /note="Organ: heart; Vector: pT773D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCATCTGAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M. Patricia Bonaldo. This library was constructed from the same fetuses as the fetal lung library, Soares fetal lung NBH19W."

BASE COUNT 106 a 127 c 94 g 102 t 3 others  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3,23e-60 Length: 432  
 Score: 72.00 Matches: 98  
 Percent Similarity: 98.99% Conservative: 0  
 Best Local Similarity: 98.99% Mismatches: 1

Query Match: 72.73% Indels: 1  
 DB: 14 Gaps: 0  
 US-10-059-395-142 (1-99) x W69233 (1-432)

Qy 1 MetLys1LeuProValLeuProAlaValLeuLeuSerLeuLeuValLeuHisSerAla 20  
 Db 13 ATGAAGATCCCGATCTCTCTCCGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCC 72  
 Qy 21 GlnGlyAlaThrLeuGlyGlyProGluGluGluSerThrLeuAsnTrpAlaSerArg 40  
 Db 73 CAGGAGGACCACTCGGTGT-CCTGAGGAGAAACACCATTTGAGATATATGCGACGA 131  
 Qy 41 ProGluAlaPheAsnThrProPheLeuLeuLeuAlaAspLysLeuArgSerAlaPheLysAla 60  
 Db 132 CCGGAGGCTTTTAAACACCCCTCTGAAACATGCAATTCGATCGCTTAAAGCT 191  
 Qy 61 AepGluPheLeuAsnTrpHisAlaLeuPheGluSer1LeuArgLysLeuProPheLeu 80  
 Db 192 GATGAGTCTCTGAACTGGACGCGCTCTTTGATCTTATCAAAAGAAACTTCTTCTC 251

Qy 81 AenTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
 Db 252 AACTGGATGCTTCTTAAGCTGAAGGAGCTGAGAGGCAACTCTGATGCCCA 308

RESULT 11  
 AAS66846 318 bp mRNA linear EST 26-SEP-1997  
 LOCUS AAS66846/c  
 DEFINITION nm67ell.s1 NCI\_CGAP\_Lari Homo sapiens cDNA clone IMAGE:1088972 3', mRNA sequence.  
 ACCESSION AAS66846  
 VERSION AAS66846.1 GI:2397660  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 318)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 Unpublished  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cga@bbs-rcmail.nih.gov  
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Stratagene, Inc.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
 www.bio.lnl.gov/bbrp/image/image.html  
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 Seq primer: -40m13 fwd. ET from Amerham.

FEATURES  
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 /lab\_host="SOLR (kanamycin resistant)"  
 /clone\_lib="NCI\_CGAP\_Lari"  
 /note="Organ: larynx; Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Larynx. 5' adaptor sequence: 5' GAATTCGGCGACGAG 3' 3' adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3' Average insert size: 0.9 kb."

BASE COUNT 76 a 67 c 90 g 85 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,21e-59 Length: 318



Score: 71.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 71.72% Indels: 0  
 DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x AA586646 (1-318)

QY 29 GUGUGUGUSeRTThlEGUaSnTYRAlaSeRArgProGUlUAlaPheAnThrProPhe 48  
 DB 316 GAGGAAGAAAGACCAATTAGATATGCGTCACGACCCGAGCCCTTTAAACCCCGTTC 257  
 QY 49 LeuAnIleAaPlySeRSeRAlaPheYsaIaAaPgluPheLeuAnThrIhSaIa 68  
 DB 256 CTGAACATCGCAAAATTCGATCTGCTTTAAAGCTGATGAGTTCTCTGAACCTGCACGCC 197  
 QY 69 LeuPheGUSeRlIeYsaRglYseuProPheLeuAnThrPaAPAlaPheProlyseu 88  
 DB 196 CTCTTGAGTCTATCAAAAGAAACTCTCTTCTCTCACTGGAGATGCCCTTTCTTAAGCTG 137  
 QY 89 LySGlYleuArgSeRAlaThrProAPAlaGln 99  
 DB 136 AAAGACTGAGAGCGCAACTCTGATGCCAG 104

RESULT 12  
 BE466728/c 359 bp mRNA linear EST 27-JUL-2000  
 LOCUS h224906.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:3208954 3'  
 DEFINITION mRNA sequence.

ACCESSION BE466728  
 VERSION BE466728.1 GI:9512503  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 COMMENT Unpublished  
 Tumor Gene Index

JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL, send email to:  
 info@image.llnl.gov  
 Seq primer: -40UP from Gibco.

FEATURES  
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 1..359  
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 /clone="IMAGE:3208954"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_id="NCI CGAP GC6"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
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 as circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clones  
 1257096-1258631, 1469064-1470983, and 1475592-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."  
 77 a 80 c 96 g 106 t

BASE COUNT  
 ORIGIN

# Alignment Scores:

Pred. No.: 2,51e-59 Length: 359  
 Score: 71.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 71.72% Indels: 0  
 DB: 10 Gaps: 0

US-10-059-395-142 (1-99) x BE466728 (1-359)

QY 29 GUGUGUGUSeRTThlEGUaSnTYRAlaSeRArgProGUlUAlaPheAnThrProPhe 48  
 DB 332 GAGGAAGAAAGACCAATTAGATATGCGTCACGACCCGAGCCCTTTAAACCCCGTTC 273  
 QY 49 LeuAnIleAaPlySeRSeRAlaPheYsaIaAaPgluPheLeuAnThrIhSaIa 68  
 DB 272 CTGAACATCGCAAAATTCGATCTGCTTTAAAGCTGATGAGTTCTCTGAACCTGCACGCC 213  
 QY 69 LeuPheGUSeRlIeYsaRglYseuProPheLeuAnThrPaAPAlaPheProlyseu 88  
 DB 212 CTCTTGAGTCTATCAAAAGAAACTCTCTTCTCTCACTGGAGATGCCCTTTCTTAAGCTG 153  
 QY 89 LySGlYleuArgSeRAlaThrProAPAlaGln 99  
 DB 152 AAAGACTGAGAGCGCAACTCTGATGCCAG 120

RESULT 13  
 A1140605/c 362 bp mRNA linear EST 29-OCT-1998  
 LOCUS ge05f03.x1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1738109  
 DEFINITION 3', mRNA sequence.

ACCESSION A1140605  
 VERSION A1140605.1 GI:3648062  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 COMMENT Unpublished  
 Tumor Gene Index

JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
 Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www-bio.llnl.gov/bdpr/image/image.html  
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 /lab\_host="DH10B"  
 /clone\_id="Soares testis NHT"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
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 was prepared from mRNA obtained from Clontech Laboratories  
 'Inc.' and primed with a Not I - oligo(dT) primer 3'f.  
 TGTTCACCAATCTGAGAGCGCGCCCAATTTTCTTTTCTTTT 3'f.  
 Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT73 vector. Library  
 went through one round of normalization to Cots, and was



High quality sequence stop: 410.

## FEATURES

**source**

Location/Qualifiers

1. .431

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/mol_type="mRNA"
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/sex="unknown"

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/note="Organ: heart; Vector: pT7T3D (Pha
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modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

1000

**ORIGIN**

**Alignment Scores:**

|            |          |         |     |
|------------|----------|---------|-----|
| Pred. No.: | 1.56e-47 | Length: | 431 |
|------------|----------|---------|-----|

|                  |         |          |    |
|------------------|---------|----------|----|
| Score:           | 59.00   | Matches: | 59 |
| Percent correct: | 100.00% |          |    |

|                        |         |               |   |
|------------------------|---------|---------------|---|
| Percent Similarity:    | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches:   | 0 |

```

Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 59.60%  Indels: 0

```

|              |        |        |   |
|--------------|--------|--------|---|
| query match: | 59.60% | Index: | 0 |
| DB:          | 14     | Gaps:  | 0 |

|         |    |   |
|---------|----|---|
| 00:     | 14 | 0 |
| Geduld: |    |   |

US-10-059-395-142 (1-99) X W69227 (1-431)

|    |  |     |   |     |
|----|--|-----|---|-----|
| Qy |  | 4.  | ProG1AlalaphesnthrPhropheueAnilIeapylsleuArgSer1aPhylseAla        | 60  |
| Db |  | 134 | CCCGAGGCCCTTTAAcACCCCGTTCGTGAACAATGCACAAATTGGCAGTTCGCCCTTTAAAGGCT | 193 |
| Qy |  | 61  | AspG1UphleuantnrThIsalaleuPhegiuseRlIelysArgVlyLeuProPheIeu       | 80  |
| Db |  | 194 | GATGAGTTCCTGAACtGGAcCGCCCTCTTGAGTCATCAAAAAGGAACCTTCCTTCTCTC       | 253 |
| Qy |  | 81  | AsnTrpAspalalpheProlysleuYsgIyleuArgSer1aThrProaspAlglN           | 99  |
| Db |  | 254 | AACtGGAGATCCCTTTCTTAAGCTGAAGAAGCATGAGAGCGCACTCTGATGSCCGAG         | 310 |

Search completed: November 28, 2003, 10:52:28  
Job time : 1720 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 07:55:01 ! Search time 22 Seconds

(without alignments)  
190.399 Million cell updates/sec

Title: US-10-059-395-142

Sequence: 1 MKRIPVPAVLTSLVTHSA.....LWMDARPKLGRSARPPAQ 99

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: /cgn2\_6/ptodata/2/1aa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCITUS COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID                  | Description        |
|------------|-------|-------------|--------|------------------------|--------------------|
| 1          | 510   | 100.0       | 99     | 4 US-09-996-243-201    | Sequence 201, App  |
| 2          | 66.5  | 13.0        | 692    | 4 US-09-198-452A-966   | Sequence 966, App  |
| 3          | 65.5  | 12.8        | 77     | 4 US-09-107-532A-5662  | Sequence 5662, App |
| 4          | 64.5  | 12.6        | 1350   | 2 US-08-319-866-9      | Sequence 9, App11  |
| 5          | 62    | 12.2        | 311    | 4 US-09-252-991A-18334 | Sequence 18334, A  |
| 6          | 62    | 12.2        | 400    | 4 US-09-150-347-1      | Sequence 1, App11  |
| 7          | 62    | 12.2        | 400    | 4 US-09-665-313-1      | Sequence 1, App11  |
| 8          | 62    | 12.2        | 432    | 4 US-09-403-089A-1     | Sequence 1, App11  |
| 9          | 61.5  | 12.1        | 276    | 4 US-09-328-352-7013   | Sequence 7013, App |
| 10         | 61    | 12.0        | 182    | 4 US-09-134-001C-5386  | Sequence 5386, App |
| 11         | 61    | 12.0        | 256    | 4 US-09-252-991A-29587 | Sequence 29587, A  |
| 12         | 60.5  | 11.9        | 232    | 4 US-09-051-755-10     | Sequence 10, App11 |
| 13         | 60.5  | 11.9        | 934    | 4 US-09-252-991A-19515 | Sequence 19515, A  |
| 14         | 59.5  | 11.7        | 233    | 4 US-09-328-352-6059   | Sequence 6059, App |
| 15         | 59.5  | 11.7        | 15281  | 2 US-08-471-119A-2     | Sequence 2, App11  |
| 16         | 59    | 11.6        | 324    | 4 US-08-311-731A-262   | Sequence 262, App  |
| 17         | 59    | 11.6        | 2509   | 4 US-09-252-991A-16642 | Sequence 16642, A  |
| 18         | 58.5  | 11.5        | 174    | 4 US-09-107-532A-5920  | Sequence 5920, App |
| 19         | 58    | 11.4        | 174    | 4 US-09-252-991A-16812 | Sequence 16812, A  |
| 20         | 58    | 11.4        | 713    | 3 US-08-872-855-5      | Sequence 5, App11  |
| 21         | 57.5  | 11.3        | 93     | 4 US-09-134-001C-3205  | Sequence 3205, App |
| 22         | 57    | 11.2        | 252    | 2 US-07-885-089B-7     | Sequence 7, App11  |
| 23         | 57    | 11.2        | 281    | 4 US-09-107-532A-4985  | Sequence 4985, App |
| 24         | 57    | 11.2        | 505    | 4 US-09-627-216A-12    | Sequence 12, App11 |
| 25         | 57    | 11.2        | 505    | 4 US-09-126-420A-22    | Sequence 22, App11 |
| 26         | 57    | 11.2        | 505    | 4 US-09-765-873A-12    | Sequence 12, App11 |
| 27         | 57    | 11.2        | 1070   | 2 US-08-633-770A-2     | Sequence 2, App11  |

|    |      |      |      |                        |                    |
|----|------|------|------|------------------------|--------------------|
| 28 | 57   | 11.2 | 3724 | 2 US-08-804-227C-10    | Sequence 10, App1  |
| 29 | 57   | 11.2 | 3724 | 2 US-08-804-198-4      | Sequence 4, App11  |
| 30 | 56.5 | 11.1 | 374  | 4 US-09-252-991A-18651 | Sequence 18651, A  |
| 31 | 56.5 | 11.1 | 400  | 4 US-09-150-347-2      | Sequence 2, App11  |
| 32 | 56.5 | 11.1 | 400  | 4 US-09-665-313-2      | Sequence 2, App11  |
| 33 | 56.5 | 11.1 | 429  | 2 US-09-074-512-1      | Sequence 1, App11  |
| 34 | 56.5 | 11.1 | 518  | 3 US-08-999-723-2      | Sequence 2, App11  |
| 35 | 56.5 | 11.1 | 518  | 3 US-09-434-427-2      | Sequence 2, App11  |
| 36 | 56.5 | 11.1 | 518  | 4 US-09-548-372D-2     | Sequence 2, App11  |
| 37 | 56.5 | 11.1 | 518  | 4 US-09-548-367D-2     | Sequence 2, App11  |
| 38 | 56.5 | 11.1 | 518  | 4 US-09-551-853D-2     | Sequence 2, App11  |
| 39 | 56.5 | 11.1 | 543  | 4 US-09-252-991A-30375 | Sequence 30375, A  |
| 40 | 56.5 | 11.1 | 1066 | 2 US-08-633-770A-1     | Sequence 1, App11  |
| 41 | 56   | 11.0 | 135  | 4 US-09-288-143-69     | Sequence 69, App1  |
| 42 | 56   | 11.0 | 373  | 4 US-09-328-352-7009   | Sequence 7009, App |
| 43 | 55.5 | 10.9 | 186  | 1 US-08-117-083-22     | Sequence 22, App1  |
| 44 | 55   | 10.8 | 431  | 4 US-09-134-001C-3051  | Sequence 3051, App |
| 45 | 55   | 10.8 | 513  | 4 US-09-595-857B-30    | Sequence 30, App1  |

#### ALIGNMENTS

RESULT 1  
US-09-996-243-201  
Sequence 201, Application US/09996243

Patent No. 6478825

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferreira, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C13

CURRENT APPLICATION NUMBER: US/09/996,243

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

[illegible]

PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 510; DB 4; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.8e-59;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVPAVVLISLVLSAAGATLGGPEESTIENYASRPEAFNTPFLNIDKLSAFKA 60  
DB 1 MKIPVPAVVLISLVLSAAGATLGGPEESTIENYASRPEAFNTPFLNIDKLSAFKA 60

QY 61 DEFLNWHALFESIKRKLPLNWDAPFKLGLRSATPDAQ 99  
DB 61 DEFLNWHALFESIKRKLPLNWDAPFKLGLRSATPDAQ 99

## RESULT 2

US-09-198-452A-966  
Sequence 966, Application US/09198452A  
Patent No. 6559294

GENERAL INFORMATION:  
APPLICANT: Griffeis, R.  
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
FILE REFERENCE: 9710-003-999  
CURRENT APPLICATION NUMBER: US/09/198,452A  
CURRENT FILING DATE: 1998-11-24  
NUMBER OF SEQ ID NOS: 6849  
SEQ ID NO 966  
LENGTH: 692  
TYPE: PRT  
ORGANISM: Chlamydia pneumoniae

US-09-198-452A-966

Query Match 13.0%; Score 66.5; DB 4; Length 692;  
Best Local Similarity 29.2%; Pred. No. 5.6;  
Matches 19; Conservative 11; Mismatches 28; Indels 7; Gaps 1;

QY 11 LLSLVLSAAGATLGGPEESTIENYASRPEAFNTPFLNIDKLSAFKADFLNWHALF 70  
DB 200 LNNLVVITIDYNNVVDGYNLISVEDTKRFRAYGMEYEID-----GYDFTIHETP 252

QY 71 ESIRK 75  
DB 253 SSIRK 257

## RESULT 3

US-09-107-532A-5662  
Sequence 5662, Application US/09107532A  
Patent No. 6583275

GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESS: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354

COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997

## ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277

## INFORMATION FOR SEQ ID NO: 5662:

SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES

## ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium  
FEATURE:

NAME/KEY: misc feature  
LOCATION: (8) LOCATION 1...77  
SEQUENCE DESCRIPTION: SEQ ID NO: 5662:

US-09-107-532A-5662

Query Match 12.8%; Score 65.5; DB 4; Length 77;  
Best Local Similarity 26.4%; Pred. No. 0.377; 33; Indels 21; Gaps 4;  
Matches 24; Conservative 13; Mismatches 33; Indels 21; Gaps 4;

QY 4 PVLPAVVLISLVLSAAGATLGGPEESTIENYASRPEAFNTPFLNIDKLSAFKAD 61  
DB 6 PILP-----SHGTTLPDPAIQLYEMV---PRVLTPIVGSNTBALSMT 50

QY 62 EFLNWHALFESIKRKLPLNWDAPFKLGLR 92  
DB 51 SFENFREIEFGTKT---NEWSLPKAOQLR 77

## RESULT 4

US-08-319-866-9  
Sequence 9, Application US/08319866  
Patent No. 5929223

GENERAL INFORMATION:  
APPLICANT: Tully, Timothy P.  
APPLICANT: Regulski, Michael  
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES ASSOCIATED WITH LONG-TERM MEMORY  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,866  
FILING DATE: 7-OCT-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

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ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1350 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-319-866-9

Query Match
Best Local Similarity 12.6%; Score 64.5; DB 2; Length 1350;
Pred. No. 26;
Matches 19; Conservative 9; Mismatches 19; Indels 7; Gaps 1;

Qy 8 AVVLSTLVHSAQATLGPEESTIENYASRPAFTPTPLNIDKLSAFKAD 61
Db 543 AVVENNIIVLHSHYGRNV-----TIVDHTHASSFSFMKHPENESKLNCGCAD 589

RESULT 5
US-09-252-991A-18334
Sequence 18334, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18334
LENGTH: 311
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18334

Query Match
Best Local Similarity 12.2%; Score 62; DB 4; Length 311;
Pred. No. 7.2;
Matches 25; Conservative 20; Mismatches 23; Indels 20; Gaps 5;

Qy 18 HSAQATLGPEESTIENYASRPAFTPTPLNIDKLSAFKAD-----FLNWH 68
Db 218 NASVHSAFGGSEHPRDLASR---FS---VNLKLGQAPOHDEIRALRSVAIKWHY 271

Qy 69 LFESEIK---RKLPL-LNWDAPFKLGL 91
Db 272 IEKSLRNYNQNSVPLVKNKADRIDGL 299

RESULT 6
US-09-150-347-1
Sequence 1, Application US/09150347
Patent No. 6372269
GENERAL INFORMATION:
APPLICANT: Rangel-Aldao, Rafael
APPLICANT: Bravo, Adriana
APPLICANT: Sanchez, Beatriz
APPLICANT: Galindo-Castro, Ivan
TITLE OF INVENTION: Malt Beverage Having Stabilized Flavor and Methods of Production
FILE REFERENCE: 1390.0070004
CURRENT APPLICATION NUMBER: US/09/150,347
```

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CURRENT FILING DATE: 1998-09-09
EARLIER APPLICATION NUMBER: 60/058,398
EARLIER FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 400
TYPE: PRT
ORGANISM: Saccharomyces carlsbergensis
US-09-150-347-1

Query Match
Best Local Similarity 12.2%; Score 62; DB 4; Length 400;
Pred. No. 10;
Matches 18; Conservative 10; Mismatches 31; Indels 18; Gaps 3;

Qy 28 PEESTIENYASRPE-----AFNTPL-NIDKLSAFKADFLNWHALFESIKRX 76
Db 49 PNRDVAEYTYQRQRPCTMTITGAFISPGAGYDNPAGVSEQWEMTKIFVIAHEK 108

Qy 77 LPF-----LNWDAPF 86
Db 109 KSFVWQVLWVGWNAFP 125

RESULT 7
US-09-665-313-1
Sequence 1, Application US/09665313
Patent No. 6468567
GENERAL INFORMATION:
APPLICANT: Rangel-Aldao, Rafael
APPLICANT: Bravo, Adriana
APPLICANT: Sanchez, Beatriz
APPLICANT: Galindo-Castro, Ivan
TITLE OF INVENTION: Malt Beverage Having Stabilized Flavor and Methods of Production
FILE REFERENCE: 1390.0070004
CURRENT APPLICATION NUMBER: US/09/665,313
CURRENT FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/150,347
PRIOR FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 400
TYPE: PRT
ORGANISM: Saccharomyces carlsbergensis
US-09-665-313-1

Query Match
Best Local Similarity 12.2%; Score 62; DB 4; Length 400;
Pred. No. 10;
Matches 18; Conservative 10; Mismatches 31; Indels 18; Gaps 3;

Qy 28 PEESTIENYASRPE-----AFNTPL-NIDKLSAFKADFLNWHALFESIKRX 76
Db 49 PNRDVAEYTYQRQRPCTMTITGAFISPGAGYDNPAGVSEQWEMTKIFVIAHEK 108

Qy 77 LPF-----LNWDAPF 86
Db 109 KSFVWQVLWVGWNAFP 125

RESULT 8
US-09-403-089A-1
Sequence 1, Application US/09403089A
Patent No. 6429286
GENERAL INFORMATION:
APPLICANT: Sugimura, Kazuhisa
TITLE OF INVENTION: Immunoregulatory Molecules and Processes for Preparing the Same
FILE REFERENCE: 0020-4637P
CURRENT APPLICATION NUMBER: US/09/403,089A
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/J997/02540
PRIOR FILING DATE: 1997-07-23
```

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; PRIOR APPLICATION NUMBER: JP 9/115303
; PRIOR FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 432
; TYPE: PRT
; ORGANISM: bacteriophage(fd-tet)
US-09-403-089A-1

Query Match
Best Local Similarity 12.2%; Score 62; DB 4; Length 432;
Matches 21; Conservative 14; Mismatches 22; Indels 10; Gaps 3;

QY 5 VLPAVVLSTLVLHSAQAGTTLGGPEESTENTYASRPEAFNTPLNIDKLSAFKRADEFL 64
DB 4 ILFAIPLVVPFYSHSADGAGAGAB---TVESCLAPHTENS-FTNV-----WDDKTL 53
QY 65 NMHALFE 71
DB 54 DRYANFE 60

RESULT 9
US-09-328-352-7013
; Sequence 7013, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7013
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7013

Query Match
Best Local Similarity 12.1%; Score 61.5; DB 4; Length 276;
Matches 18; Conservative 14; Mismatches 29; Indels 5; Gaps 2;

QY 22 GATLGGPEESTENTYASRPEAFNTPLNIDKLS-AFPADEFLNMHALFESIKRKLPL 80
DB 102 GQLSPHSKDTLIKRYAENPDQYDVCTIVGDGHSARAIENAMIAFTALSEQIOGE---- 157
QY 81 NMDAPP 86
DB 158 NMSLAP 163

RESULT 10
US-09-134-001C-5386
; Sequence 5386, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5386
; LENGTH: 192
; TYPE: PRT
```

```

; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5386

Query Match
Best Local Similarity 12.0%; Score 61; DB 4; Length 192;
Matches 31; Conservative 18; Mismatches 37; Indels 38; Gaps 6;

QY 10 VLSTLVLHSAQAGT-----LGGPEESTENTYASRPEAFNTPLNIDKLSAFKRADEFL 47
DB 4 IMKGLITIGSAQVGSHTNALSKYIKGLGDEHVEVIEDLEKPHOLDFACTQAVDEI 63
QY 48 PLNIDKLSAFKRADEFL-----NMHALFESI-KRKLPLNMDAPPKLRK-----GLR 92
DB 64 KNNVSLQSKMEADFLILGTPNTHGSGILKALDHLNMDHF-KMRFVGLICNSGIV 122
QY 93 SATP 96
DB 123 SEEP 126

RESULT 11
US-09-252-991A-29587
; Sequence 29587, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29587
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29587

Query Match
Best Local Similarity 12.0%; Score 61; DB 4; Length 256;
Matches 29; Conservative 15; Mismatches 33; Indels 30; Gaps 5;

QY 1 MKIPVLPAVVLSTLVLHSA---QGATLGG-----PEESTI--ENYASRPEAFNTPF 48
DB 20 MKYPPSSRVVWGILSLSTLANAGITLGGTRVVLQAPAKKALIVRNQASQDV----- 73
QY 49 LNIDKLSAFKRADEFLNMHALFESIKRKLPLNMDAPPKLRKRSAT 95
DB 74 ---MIQSWVEADNGAD-----KREVPFVITPALSRLGNKQOT 108

RESULT 12
US-09-051-755-10
; Sequence 10, Application US/09051755
; Patent No. 6506389
; GENERAL INFORMATION:
; APPLICANT: LEER, Robert J
; APPLICANT: POWELS, Pieter H
; APPLICANT: CONWAY, Patricia L
; TITLE OF INVENTION: NOVEL ADHERENCE FACTORS OF NON PATHOGENIC
; TITLE OF INVENTION: MICROORGANISMS AND APPLICATIONS THEREOF FOR SCREENING
; TITLE OF INVENTION: MICROORGANISMS FOR SPECIFIC PROBIOTIC PROPERTIES; NOVEL
; FILE REFERENCE: LEER et al. 09/051,755
; CURRENT APPLICATION NUMBER: US/09/051,755
; PRIOR FILING DATE: 1998-09-30
; EARLIER APPLICATION NUMBER: PCT/NL95/00367
; EARLIER FILING DATE: 1995-10-20
; EARLIER APPLICATION NUMBER: PCT/NL96/00409
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5835 PFILLALRAAHYRLTGEDATLTGP-----IAN-RNPPELENNIGFVNTQCRIALE 5880

Qy 60 ADE-----FLNMHALFESIKRKLPELWDAFPKJGJLSAT 95  
Db 5889 ENDNFESLVRVRSSTATSAFANQDVPEFESIVSSL-----LPGRDAS 5930  
Search completed: November 28, 2003, 07:57:05  
Job time : 25 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 09:32:09 ; Search time 55 Seconds

(without alignments)  
794,490 Million cell updates/sec

Title: US-10-059-395-142

Sequence: 1 MKIPVLRVAVLSTLVLSA.....LWMDAPFKLGKRSATPDQ 99

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Xgapop 60.0 , Xgapext 60.0  
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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1135290

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO.spool/US1005395/rn1.25112003.140756.7426/app\_query.fasta\_1.263  
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=humand40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=po -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US1005395@cgn2\_1.1.56@rn1.25112003.140756.7426 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA.\*  
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2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/prodata/2/ina/5A\_COMB.seq.\*  
4: /cgn2\_6/prodata/2/ina/5B\_COMB.seq.\*  
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6: /cgn2\_6/prodata/2/ina/5B\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                            |
|------------|-------|-------------|--------|-------|--|
| 1          | 99    | 100.0       | 415    | 4     | US-09-996-243-200 Sequence 200, App    |
| 2          | 9     | 9.1         | 666    | 4     | US-09-252-991A-5754 Sequence 5754, App |
| 3          | 9     | 9.1         | 837    | 4     | US-09-252-991A-5702 Sequence 5702, App |
| 4          | 3     | 9.1         | 1035   | 4     | US-09-252-991A-5715 Sequence 5715, App |
| 5          | 6     | 9.1         | 1245   | 4     | US-09-252-991A-5725 Sequence 5725, App |
| 6          | 9     | 9.1         | 36159  | 4     | US-09-749-588-3 Sequence 3, Appl1      |
| 7          | 8     | 8.1         | 45     | 2     | US-08-860-882A-8 Sequence 8, Appl1     |
| 8          | 8     | 8.1         | 240    | 4     | US-09-107-532A-3419 Sequence 3419, App |
| 9          | 9     | 8.1         | 278    | 4     | US-09-313-294A-1198 Sequence 1198, App |
| 10         | 8     | 8.1         | 330    | 4     | US-09-107-532A-931 Sequence 931, App   |
| 11         | 11    | 8           | 441    | 4     | US-09-107-532A-2246 Sequence 2246, App |
| 12         | 8     | 8.1         | 1002   | 4     | US-09-107-532A-2821 Sequence 2821, App |

|      |   |     |      |   |                     |                    |
|------|---|-----|------|---|---------------------|--------------------|
| C 13 | 8 | 8.1 | 1059 | 4 | US-09-576-160B-8    | Sequence 8, Appl1  |
| 14   | 8 | 8.1 | 5919 | 4 | US-09-221-017B-584  | Sequence 584, App  |
| 15   | 7 | 7.1 | 61   | 1 | US-08-391-339-31    | Sequence 31, Appl1 |
| 16   | 7 | 7.1 | 61   | 1 | US-08-484-274A-31   | Sequence 31, Appl1 |
| 17   | 7 | 7.1 | 243  | 2 | US-08-747-121-6     | Sequence 6, Appl1  |
| 18   | 7 | 7.1 | 283  | 4 | US-09-313-294A-1241 | Sequence 1241, App |
| 19   | 7 | 7.1 | 340  | 4 | US-09-404-879A-203  | Sequence 203, App  |
| 20   | 7 | 7.1 | 340  | 4 | US-09-338-933-203   | Sequence 203, App  |
| 21   | 7 | 7.1 | 340  | 4 | US-09-215-681-203   | Sequence 203, App  |
| 22   | 7 | 7.1 | 341  | 4 | US-09-404-879A-204  | Sequence 204, App  |
| 23   | 7 | 7.1 | 341  | 4 | US-09-338-933-204   | Sequence 204, App  |
| 24   | 7 | 7.1 | 341  | 4 | US-09-215-681-204   | Sequence 204, App  |
| 25   | 7 | 7.1 | 375  | 4 | US-09-107-532A-1682 | Sequence 1682, App |
| 26   | 7 | 7.1 | 400  | 4 | US-09-404-879A-250  | Sequence 250, App  |
| 27   | 7 | 7.1 | 400  | 4 | US-09-338-933-250   | Sequence 250, App  |
| 28   | 7 | 7.1 | 400  | 4 | US-09-215-681-250   | Sequence 250, App  |
| 29   | 7 | 7.1 | 426  | 4 | US-09-205-258-95    | Sequence 95, Appl1 |
| 30   | 7 | 7.1 | 527  | 4 | US-09-404-879A-172  | Sequence 172, App  |
| 31   | 7 | 7.1 | 527  | 4 | US-09-338-933-172   | Sequence 172, App  |
| 32   | 7 | 7.1 | 527  | 4 | US-09-215-681-172   | Sequence 172, App  |
| 33   | 7 | 7.1 | 572  | 4 | US-09-404-879A-174  | Sequence 174, App  |
| 34   | 7 | 7.1 | 572  | 4 | US-09-338-933-174   | Sequence 174, App  |
| 35   | 7 | 7.1 | 572  | 4 | US-09-215-681-174   | Sequence 174, App  |
| 36   | 7 | 7.1 | 653  | 4 | US-09-404-879A-370  | Sequence 370, App  |
| 37   | 7 | 7.1 | 691  | 4 | US-09-338-933-240   | Sequence 240, App  |
| 38   | 7 | 7.1 | 691  | 4 | US-09-215-681-240   | Sequence 240, App  |
| 39   | 7 | 7.1 | 691  | 4 | US-09-215-681-240   | Sequence 240, App  |
| 40   | 7 | 7.1 | 697  | 4 | US-09-404-879A-243  | Sequence 243, App  |
| 41   | 7 | 7.1 | 697  | 4 | US-09-338-933-243   | Sequence 243, App  |
| 42   | 7 | 7.1 | 697  | 4 | US-09-215-681-243   | Sequence 243, App  |
| 43   | 7 | 7.1 | 723  | 4 | US-09-447-356-4     | Sequence 4, Appl1  |
| 44   | 7 | 7.1 | 747  | 4 | US-09-404-879A-209  | Sequence 209, App  |
| 45   | 7 | 7.1 | 747  | 4 | US-09-338-933-209   | Sequence 209, App  |

#### ALIGNMENTS

RESULT 1  
US-09-996-243-200  
; Sequence 200, Application US/09996243  
; Patent No. 6478825  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerder, Hanspeter  
; APPLICANT: Gerlitsen, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C13  
; CURRENT APPLICATION NUMBER: US/09/996,243  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16

[illegible]

PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

|                        |          |               |     |
|------------------------|----------|---------------|-----|
| Pred. No.:             | 2,32e-92 | Length:       | 415 |
| Score:                 | 99.00    | Matches:      | 99  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 4        | Gaps:         | 0   |

US-10-059-395-142 (1-99) x US-09-996-243-200 (1-415)

Qy 1 MetLysIleProValIleuProAlaValIleuSerLeuValIleuHISerAla 20  
Db 13 ATGAAGATCCCGGCTCTTCTGCGGTGCTCTCTCTCTGCTGCTCTGCTGCC 72

Qy 21 GInGIyAlaThrIeuGIyGIyProGIyGIyGluSerThrIleGluSerYAlaSerArg 40  
Db 73 CAGGAGACCCAGCCGTGGGTGCTCTGAGAGAAAGACCATTTGATTTGCGTCA 132

Qy 41 ProGIyAlaPheSerThrProPheLeuAsnIleAspIySLeuArgSerAlaPheIyAla 60  
Db 133 CCGAGGCGCTTTAAACCCCGCTTCGTAACATCAAAATTCGATCTGCTTAAAGCT 192

Qy 61 AspGIyPheLeuSerThrIleAlaLeuPheGluSerIleIySArgIySLeuProPheLeu 80  
Db 193 GATGAGTCTGAACTGGACGCGCTCTTGAAGTCTATCAAAAGAACTTCTTCTC 252

Qy 81 AsnTrpAspAlaPheProIySLeuIyGIyLeuArgSerAlaThrProAspAlaGln 99  
Db 253 AACGGGATCGCTTCTTAAGCTGAAGAGACTGAGAGCGCACTCTGATGCCAG 309

## RESULT 2

US-09-252-991A-5754/c  
Sequence 5754, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 5754  
LENGTH: 666  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5754

Alignment Scores:  
Pred. No.: 1.97  
Score: 9.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 9.09%  
DB: 4  
Length: 666  
Matches: 9  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-10-059-395-142 (1-99) x US-09-252-991A-5754 (1-666)

Qy 90 GlyLeuArgSerAlaThrProAspAla 98  
Db 62 GGGCTCGGAGCGCCAGCGCGAGCT 36

## RESULT 3

US-09-252-991A-5702

Sequence 5702, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 5702  
LENGTH: 837  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5702

Alignment Scores:  
Pred. No.: 2.47  
Score: 9.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 9.09%  
DB: 4  
Length: 837  
Matches: 9  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-10-059-395-142 (1-99) x US-09-252-991A-5702 (1-837)

Qy 90 GlyLeuArgSerAlaThrProAspAla 98  
Db 218 GGGCTCGGAGCGCCAGCGCGAGCT 244

## RESULT 4

US-09-252-991A-5715

Sequence 5715, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 5715  
LENGTH: 1035  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5715

Alignment Scores:

Pred. No.: 3.05 Length: 1035  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.09% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142 (1-99) x US-09-252-991A-5725 (1-1035)

OY 90 GtyleuArySerAlaThProApAla 98  
DB 628 GGGCTGCGAGCGCCAGCCCGGACGCT 654

RESULT 5

US-09-252-991A-5725/c  
Sequence 5725, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 5725

LENGTH: 1245

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-5725

Alignment Scores:

Pred. No.: 3.66 Length: 1245

Score: 9.00 Matches: 9

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 9.09% Indels: 0

DB: 4 Gaps: 0

US-10-059-395-142 (1-99) x US-09-252-991A-5725 (1-1245)

OY 90 GtyleuArySerAlaThProApAla 98

DB 631 GGGCTGCGAGCGCCAGCCCGGACGCT 605

RESULT 6

US-09-749-588-3

Sequence 3, Application US/09749588

Patent No. 6423521

GENERAL INFORMATION:

APPLICANT: CHANDRAMOULISWARAN, Ishwar et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

FILE REFERENCE: CLO01068

CURRENT APPLICATION NUMBER: US/09/749,588

PRIOR FILING DATE: 2000-12-28

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 36159

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)...(36159)

OTHER INFORMATION: n = A,T,C or G

Alignment Scores:  
Pred. No.: 104 Length: 36159  
Score: 9.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 9.09% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142 (1-99) x US-09-749-588-3 (1-36159)

OY 5 ValIeuProAlaValIleuLeuSer 13

DB 9029 GTTTACCCGAGTGTCTCTTACG 9055

RESULT 7

US-08-860-882A-8

Sequence 8, Application US/08860882A

Patent No. 5985281

GENERAL INFORMATION:

APPLICANT: TAYLORSON, CHRISTOPHER JOHN

APPLICANT: EGGLETE, HENDRIKUS JOHANNES

APPLICANT: TARRAGONA-FIOL, ANTONIO

APPLICANT: RABIN, BRIAN ROBERT

APPLICANT: BOYLE, FRANCIS THOMAS

APPLICANT: HENNAM, JOHN FREDERICK

APPLICANT: BLAKELY, DAVID CHARLES

APPLICANT: MARSHAM, PETER ROBERT

APPLICANT: HEATON, DAVID WILLIAM

TITLE OF INVENTION: CHEMICAL COMPOUNDS

NUMBER OF SEQUENCES: 77

CORRESPONDENCE ADDRESS:

ADDRESS: PILLSBURY, MADISON & SUTRO

STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/860,882A

FILING DATE: JUNE 23, 1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: DONALD J. BIRD

REGISTRATION NUMBER: 25,323

REFERENCE/DOCKET NUMBER: 9901/238653

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 861-3027

TELEFAX: (202) 822-0944

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 45 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-860-882A-8

Alignment Scores:  
Pred. No.: 1.41 Length: 45  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 8.08% Indels: 0  
DB: 2 Gaps: 0

US-10-059-395-142 (1-99) x US-08-860-882A-8 (1-45)

```

OY      10 ValleuSerLeuLeuValleu 17
      |||||
Db      21 GTCTGTTGCTGTTGTTGTTCTG 44

RESULT 8
US-09-107-532A-3419/c
; Sequence 3419, Application US/09107532A
; Patent No. 6581275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3419:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...240
SEQUENCE DESCRIPTION: SEQ ID NO: 3419:
US-09-107-532A-3419

Alignment Scores:
Pred. No.: 7.45 Length: 240
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.08% Indels: 0
DB: 4 Gaps: 0

US-10-059-395-142 (1-99) x US-09-107-532A-3419 (1-240)
OY      10 ValleuSerLeuLeuValleu 17
      |||||
Db      229 GTGCTACTTTGCTACTGCTACTC 206

RESULT 9
US-09-313-294A-1198/c

```

```

; Sequence 1198, Application US/09313294A
; Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Laigudi, Raghunath V.
APPLICANT: Ito, Laura Y.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 1198
LENGTH: 278
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. 6476212 700550532H1
NAME/KEY: unsure
LOCATION: 277
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-1198

Alignment Scores:
Pred. No.:      8.62      Length:      278
Score:          8.00      Matches:     8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:      8.08% Indels:             0
DB:               Gaps:                   0

US-10-059-395-142 (1-99) x US-09-313-294A-1198 (1-278)

Cy      11 leuuSeurleuuValleuhis 18
       |||||
Db      126 C|CCTTCCTCCTCGTCTGCAC 103

RESULT 10
US-09-107-532A-931
; Sequence 931, Application US/09107532A
; Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESSES:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneké
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007

```

TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 931:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (B) LOCATION 1...330  
SEQUENCE DESCRIPTION: SEQ ID NO: 931:  
US-09-107-532A-931  
Alignment Scores:  
Pred. No.: 10.2 Length: 330  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 8.08% Indels: 0  
DB: 4 Gaps: 0  
US-10-059-395-142 (1-99) x US-09-107-532A-931 (1-330)  
Cy 10 ValleuSerLeuValleu 17  
Db 33 GTGCTGCTTGGCTGCTGCTT 56  
RESULT 11  
US-09-107-532A-2246  
Sequence 2246, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 2246:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 441 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (B) LOCATION 1...441  
SEQUENCE DESCRIPTION: SEQ ID NO: 2246:  
US-09-107-532A-2246  
Alignment Scores:  
Pred. No.: 13.6 Length: 441  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 8.08% Indels: 0  
DB: 4 Gaps: 0  
US-10-059-395-142 (1-99) x US-09-107-532A-2246 (1-441)  
Cy 10 ValleuSerLeuValleu 17  
Db 124 GTGCTGCTTGGCTGCTGCTT 147  
RESULT 12  
US-09-107-532A-2821/c  
Sequence 2821, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 2821:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1002 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium



FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...1002  
SEQUENCE DESCRIPTION: SEQ ID NO: 2821  
US-09-107-532A-2821

Alignment Scores:  
Pred. No.: 30.8 Length: 1002  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 8.08% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142 (1-99) x US-09-107-532A-2821 (1-1002)

QY 10 ValLeuLeuSerLeuLeuValLeu 17  
DB 722 GTGCTGCTTTCGCTGCTGCTGCTT 699

RESULT 13  
US-09-576-160B-8/C  
Sequence 8, Application US/09576160B  
Patent No. 6469150  
GENERAL INFORMATION:  
APPLICANT: Horlick, Robert  
APPLICANT: Zhao, Jijunhao  
APPLICANT: Swanson, Robert  
APPLICANT: Webb, Maria  
APPLICANT: Strichl, Barbara  
TITLE OF INVENTION: Cloning and Characterization of Genes Encoding  
TITLE OF INVENTION: Bradykinin B1 Receptor Homologues From Five Mammalian  
FILE REFERENCE: 1073.058  
CURRENT APPLICATION NUMBER: US/09/576,160B  
CURRENT FILING DATE: 2000-05-22  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEO ID NO: 8  
LENGTH: 1059  
TYPE: DNA  
ORGANISM: Macaca mulatta  
US-09-576-160B-8

Alignment Scores:  
Pred. No.: 32.6 Length: 1059  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 8.08% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142 (1-99) x US-09-576-160B-8 (1-1059)

QY 8 AlaValValLeuLeuSerLeuLeu 15  
DB 746 GCTGTGCTTTCGCTGCTGCTGCTG 723

RESULT 14  
US-09-221-017B-584  
Sequence 584, Application US/09221017B  
Patent No. 6444799  
GENERAL INFORMATION:  
APPLICANT: Ross, Bruce C.  
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
NUMBER OF SEQUENCES: 1120  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/221,017B  
FILING DATE: 23-DEC-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP1182  
FILING DATE: 31-DEC-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP1546  
FILING DATE: 30-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP2911  
FILING DATE: 09-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/AU98/01023  
FILING DATE: 10-DEC-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Monroy, Gladys H  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 27340-20021.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 584:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5919 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: UNKNOWN  
ORIGINAL SOURCE:  
ORGANISM: PORCYPHYROMONAS GINGIVALIS  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1...5919  
US-09-221-017B-584

Alignment Scores:  
Pred. No.: 180 Length: 5919  
Score: 8.00 Matches: 8  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 8.08% Indels: 0  
DB: 4 Gaps: 0

US-10-059-395-142 (1-99) x US-09-221-017B-584 (1-5919)

QY 6 LeuProAlaValValLeuLeuSer 13  
DB 3611 TTGCCGGCAGTGTCTGTGTGTG 3634

RESULT 15  
US-08-391-339-31  
Sequence 31, Application US/08391339  
Patent No. 5463175  
GENERAL INFORMATION:  
APPLICANT: Kishore, Ganesh M.  
APPLICANT: Barry, Gerard F.  
TITLE OF INVENTION: Glycosylate Tolerant Plants  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Dennis R. Hoerner, Jr.,  
ADDRESS: Monsanto Co. B&F  
STREET: 700 Chesterfield Village Parkway  
CITY: St. Louis

```

STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
APPLICATION NUMBER: US/07/717,370
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-391-339-31

Alignment Scores:
Pred. NO.: 19.9      Length: 61
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US-10-059-395-142 (1-99) x US-08-391-339-31 (1-61)

QY      10 ValLeuLeuSerLeuLeuVal 16
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Db      24 GTACTGTTGAGTTGCTGCTC 44

Search completed: November 28, 2003, 10:53:33
Job time : 61 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 08:04:08 ; Search time 24 Seconds

(without alignments)  
760.825 Million cell updates/sec

Title: US-10-059-395-142

Sequence: 1 MKIVPLPAVVLSTLVLSA.....LWMDAPFKLGKRSATPPAQ 99

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                    | Description       |
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| 2          | 99    | 100.0       | 99     | 9 US-09-989-723-201   | Sequence 201, App |
| 3          | 99    | 100.0       | 99     | 9 US-09-989-727-201   | Sequence 201, App |
| 4          | 99    | 100.0       | 99     | 9 US-09-989-727-201   | Sequence 201, App |
| 5          | 99    | 100.0       | 99     | 10 US-09-989-721-201  | Sequence 201, App |
| 6          | 99    | 100.0       | 99     | 10 US-09-989-721-201  | Sequence 201, App |
| 7          | 99    | 100.0       | 99     | 10 US-09-991-073-201  | Sequence 201, App |
| 8          | 99    | 100.0       | 99     | 10 US-09-990-442-201  | Sequence 201, App |
| 9          | 99    | 100.0       | 99     | 10 US-09-991-163-201  | Sequence 201, App |
| 10         | 99    | 100.0       | 99     | 10 US-09-993-604-201  | Sequence 201, App |
| 11         | 99    | 100.0       | 99     | 10 US-09-990-456-201  | Sequence 201, App |
| 12         | 99    | 100.0       | 99     | 10 US-09-989-721-201  | Sequence 201, App |
| 13         | 99    | 100.0       | 99     | 10 US-09-992-558-201  | Sequence 201, App |
| 14         | 99    | 100.0       | 99     | 10 US-09-984-245-142  | Sequence 142, App |
| 15         | 99    | 100.0       | 99     | 10 US-09-989-293A-201 | Sequence 201, App |

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| 18 | 99 | 100.0 | 99 | 10 US-09-991-181-201  | Sequence 201, App |
| 19 | 99 | 100.0 | 99 | 10 US-09-989-730-201  | Sequence 201, App |
| 20 | 99 | 100.0 | 99 | 10 US-09-990-436-201  | Sequence 201, App |
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| 30 | 99 | 100.0 | 99 | 11 US-09-989-726-201  | Sequence 201, App |
| 31 | 99 | 100.0 | 99 | 11 US-09-998-156-201  | Sequence 201, App |
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| 37 | 99 | 100.0 | 99 | 11 US-09-966-262-142  | Sequence 142, App |
| 38 | 99 | 100.0 | 99 | 11 US-09-990-726-201  | Sequence 201, App |
| 39 | 99 | 100.0 | 99 | 11 US-09-997-559-201  | Sequence 201, App |
| 40 | 99 | 100.0 | 99 | 11 US-09-997-601-201  | Sequence 201, App |
| 41 | 99 | 100.0 | 99 | 11 US-09-990-443-201  | Sequence 201, App |
| 42 | 99 | 100.0 | 99 | 11 US-09-991-854-201  | Sequence 201, App |
| 43 | 99 | 100.0 | 99 | 11 US-09-997-628-201  | Sequence 201, App |
| 44 | 99 | 100.0 | 99 | 11 US-09-997-683-201  | Sequence 201, App |
| 45 | 99 | 100.0 | 99 | 11 US-09-989-729A-201 | Sequence 201, App |

## ALIGNMENTS

RESULT 1  
US-09-989-722-201  
Sequence 201, Application US/09989722  
Patent No. US20020072067A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napiet, Mary A.  
APPLICANT: Par, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zhenli  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P27301C63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/045787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17

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| PRIOR FILING DATE:        | 1998-06-16 |
| PRIOR APPLICATION NUMBER: | 60/089514  |
| PRIOR FILING DATE:        | 1998-06-16 |
| PRIOR APPLICATION NUMBER: | 60/089532  |
| PRIOR FILING DATE:        | 1998-06-17 |
| PRIOR APPLICATION NUMBER: | 60/089538  |
| PRIOR FILING DATE:        | 1998-06-17 |
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| PRIOR FILING DATE:        | 1998-06-17 |
| PRIOR APPLICATION NUMBER: | 60/089599  |
| PRIOR FILING DATE:        | 1998-06-18 |
| PRIOR APPLICATION NUMBER: | 60/089801  |
| PRIOR FILING DATE:        | 1998-06-18 |
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| PRIOR APPLICATION NUMBER: | 60/089952  |
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| PRIOR APPLICATION NUMBER: | 60/090024  |
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| PRIOR APPLICATION NUMBER: | 60/090025  |
| PRIOR FILING DATE:        | 1998-06-22 |
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| PRIOR APPLICATION NUMBER: | 60/090429  |
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| PRIOR APPLICATION NUMBER: | 60/090431  |
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| PRIOR APPLICATION NUMBER: | 60/090535  |
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| PRIOR APPLICATION NUMBER: | 60/090540  |
| PRIOR FILING DATE:        | 1998-06-25 |
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| PRIOR FILING DATE:        | 1998-06-25 |
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| PRIOR APPLICATION NUMBER: | 60/090682  |
| PRIOR FILING DATE:        | 1998-06-26 |
| PRIOR APPLICATION NUMBER: | 60/090863  |
| PRIOR FILING DATE:        | 1998-06-26 |

PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 99; DB 9; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3,2e-88;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 DEFNMWALFESIKRKLPLNMWAPFKLGLRSATPDAQ 99

## RESULT 2

US-09-989-723-201  
Sequence 201, Application US/09989723  
Patent No. US20020072092A1  
GENERAL INFORMATION:  
APPLICANT: Aehkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: F2730P1C62  
CURRENT APPLICATION NUMBER: US/09/989,723  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE: 1997-11-24  
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PRIOR APPLICATION NUMBER: 60/091360  
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PRIOR FILING DATE: 1998-07-02  
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PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 99; DB 9; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3,2e-88;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
US-09-989-279-201  
Sequence 201, Application us//09989279  
Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC56  
CURRENT APPLICATION NUMBER: US/09/989, 279  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
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/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 99; DB 9; Length 99;
Best Local Similarity 100.0%; Pred. No. 3.2e-88;
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/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gottschalk, Mary E.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2730PIC65
/ CURRENT APPLICATION NUMBER: US/09/989,727
/ CURRENT FILING DATE: 2001-11-19
/ PRIOR APPLICATION NUMBER: 60/049787
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/ PRIOR APPLICATION NUMBER: 60/062250
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/ PRIOR APPLICATION NUMBER: 60/065186
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/ PRIOR FILING DATE: 1997-11-24
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/ PRIOR FILING DATE: 1998-02-25
/ PRIOR APPLICATION NUMBER: 60/078910
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/ PRIOR FILING DATE: 1998-06-17
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/ PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
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PRIOR FILING DATE: 1998-07-02  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 99; DB 9; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.2e-88;  
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QY 61 DEFLNWHALFESIKRRLPFLNWDAPFKLKGSLATPDQ 99  
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RESULT 5  
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Sequence 201, Application US/09989731  
Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC70  
CURRENT APPLICATION NUMBER: US/09/989,731  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
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PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
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PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28

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| 43 | PRIOR FILING DATE: 1998-06-25       |
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| 59 | PRIOR FILING DATE: 1998-07-01       |
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| 61 | PRIOR FILING DATE: 1998-07-02       |
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| 63 | PRIOR FILING DATE: 1998-07-01       |
| 64 | PRIOR APPLICATION NUMBER: 60/091519 |
| 65 | PRIOR FILING DATE: 1998-07-02       |
| 66 | PRIOR APPLICATION NUMBER: 60/091626 |
| 67 | PRIOR FILING DATE: 1998-07-02       |
| 68 | PRIOR APPLICATION NUMBER: 60/091633 |
| 69 | PRIOR FILING DATE: 1998-07-02       |

;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 99; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3,2e+88;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKIPVLPAVLLSLVLSAQAGATLGGPEESTLNNYASPPBAFNTPLNIDKLSAFKA 60

QY 61 DEFLNMHALFESTIKRKLPFLNMWDAFPPLKGLRSATPPAQ 99  
DB 61 DEFLNMHALFESTIKRKLPFLNMWDAFPPLKGLRSATPPAQ 99

## RESULT 6

US-09-989-732-201  
Sequence 201, Application US/09989732  
Patent No. US20020123463A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoves, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Garber, Hanspeter

APPLICANT: Gerltsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavien, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tuma, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

FILE REFERENCE: P2730P1C57

CURRENT APPLICATION NUMBER: US/09/989,732

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

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PRIOR FILING DATE: 1997-11-24

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PRIOR APPLICATION NUMBER: 60/078910

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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982

;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09  
  
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Best Local Similarity 100.0%; Score 99; DB 10; Length 99;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 MIPVLPVAVLSTLVHSAQATLGSPPEESTIENVASRPAPFNTPLINDKLSAFKA 60  
  
Qy 61 DEFVWVHALFESIKRKLPLNWDAPFKLKGARSATPDQ 99  
Db 61 DEFVWVHALFESIKRKLPLNWDAPFKLKGARSATPDQ 99  
  
RESULT 7  
US-09-991-073-201  
Sequence 201, Application US/09991073  
Patent No. US20020127576A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC15  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1998-06-02

[illegible]

Query Match 100.0%; Score 99; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3,2e-86;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 DEFNMHALFESIKRKLPELNDAPPKLGLRSATPDQ 99  
Db 61 DEFNMHALFESIKRKLPELNDAPPKLGLRSATPDQ 99

RESULT 8  
US-09-990-442-201  
Sequence 201. Application US/09990442  
Patent No. US20020132252A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kjaer, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC8  
CURRENT APPLICATION NUMBER: US/09/990,442  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 99; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.2e-88;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 61 DEFLNMHALFESIKRKLPTLNWDAPPKLGASATPPDAQ 99

RESULT 9  
US-09-991-163-201  
Sequence 201, Application US/09991163  
Patent No. US20020132253A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, V. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kjaevin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC17  
CURRENT APPLICATION NUMBER: US/09/991,163  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 99; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.2e-88;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPAVVLISLVHSAQATLGGPEEESTIENYASRDEAFVTPPLNIDKLSAFKA 60



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Db 61 DEFLNMHALFESIKRGLPFLNWDAPFKLGLSATDQAQ 99

## RESULT 10

US-09-993-604-201  
Sequence 201, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC25  
CURRENT APPLICATION NUMBER: US/09/993,604  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
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RESULT 11  
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Sequence 201, Application US/09990456  
Patent No. US20020137890A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC22  
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 99; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.2e-88;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCIPLPAVVLISLVLHSAOGATLGGPBEESTIENVASRPAFMTPLINDKLSAFPA 60  
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RESULT 12  
US-09-989-721-201  
Sequence 201, Application US/09989721  
Patent No. US20020142961A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gueney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC55  
CURRENT APPLICATION NUMBER: US/09/989,721  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 99; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.2e-88;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIPVPAVVLSTLVHSAQATLGGPREESTIENYARPEAFNTPFINIDKLSAFYA 60  
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QY 61 DEFNHALFESIKRKLPLINWDAPFKLGLRSATPDQA 99  
DB 61 DEFNHALFESIKRKLPLINWDAPFKLGLRSATPDQA 99

RESULT 13

US-09-992-598-201  
Sequence 201, Application US/09992598  
Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Godowski, Paul J.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC20  
CURRENT APPLICATION NUMBER: US/09/992,598  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 99; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.2e-88;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPAVVLISLVLSAAGATILGPEEESTIENYASREAFNTPLNTDKLSARXA 60  
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QY 61 DEFLNMHALFESIKRKLPEFLNMDAFPRLKJGHSATPDQ 99  
DB 61 DEFLNMHALFESIKRKLPEFLNMDAFPRLKJGHSATPDQ 99

RESULT 14  
US-09-984-245-142  
; Sequence 142, Application US/09984245  
; Patent No. US20020165374A1

GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 87 Human Secreted Proteins  
FILE REFERENCE: P2004P1  
CURRENT APPLICATION NUMBER: US/09/984,245  
CURRENT FILING DATE: 2001-10-29  
PRIOR APPLICATION NUMBER: 09/154,707  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: PCT/US98/05311  
PRIOR FILING DATE: 1998-03-19  
PRIOR APPLICATION NUMBER: US 60/041,277  
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PRIOR FILING DATE: 1997-10-02  
NUMBER OF SEQ ID NOS: 343  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 142  
LENGTH: 99  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-984-245-142

Query Match 100.0%; Score 99; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.2e-88;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 DEFLNMHALFESIKRKLPTLNDAPPKLGKLSATPDQ 99  
DB 61 DEFLNMHALFESIKRKLPTLNDAPPKLGKLSATPDQ 99

RESULT 15  
US-09-989-293A-201  
Sequence 201, Application US/09989293A  
Patent No. US20020177164A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlgen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gueney, Austin L.  
APPLICANT: Kjaavin, Ivar J.  
APPLICANT: Napier, Mary A.  
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APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C65  
CURRENT APPLICATION NUMBER: US/09/989,293A  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR APPLICATION NUMBER: 60/065186  
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Query Match 100.0%; Score 99; DB 10; Length 99;  
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Db 61 DEFINWHALESIXRKLPLINWDAPPLKGLRSATPDAQ 99

Search completed: November 28, 2003, 08:05:58  
Job time : 25 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 08:57:54 / Search time 2857 Seconds

(without alignments)  
1417.589 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 99

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Searched: 2888711 seqs, 20454813386 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5772138

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 2          | 99    | 100.0        | AR252517   | AR252517 Sequence  |
| 3          | 99    | 100.0        | AX077031   | AX077031 Sequence  |
| 4          | 99    | 100.0        | AX358892   | AX358892 Sequence  |
| 5          | 99    | 100.0        | AX362385   | AX362385 Sequence  |
| 6          | 99    | 100.0        | AX403313   | AX403313 Sequence  |
| 7          | 99    | 100.0        | AX454546   | AX454546 Sequence  |
| 8          | 99    | 100.0        | AX491024   | AX491024 Sequence  |
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| 11         | 99    | 100.0        | AX080817   | AX080817 Sequence  |
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| 15         | 72    | 72.7         | AX080818   | AX080818 Sequence  |
| 16         | 56    | 56.6         | AX041085   | AX041085 Sequence  |
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| 18         | 10    | 10.1         | AC113165   | AC113165 Homo sapi |
| 19         | 10    | 10.1         | AC021395   | AC021395 Homo sapi |
| 20         | 10    | 10.1         | AC104119   | AC104119 Homo sapi |
| 21         | 10    | 10.1         | AL353801   | AL353801 Human DNA |
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| 24         | 9     | 9.1          | AR220021   | AR220021 Sequence  |
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| 28         | 9     | 9.1          | AP000558   | AP000558 Homo sapi |
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| 33         | 9     | 9.1          | AC105312   | AC105312 Homo sapi |
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| 35         | 9     | 9.1          | AL451070   | AL451070 Human DNA |
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RESULT 1

## ALIGNMENTS

AX055438  
LOCUS AX055438 414 bp DNA linear PAT 13-JAN-2001  
DEFINITION Sequence 68 from Patent WO073452.  
ACCESSION AX055438  
VERSION AX055438.1 GI:12228711  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L.,  
Tunas, D., Watanabe, C.K. and Wood, W.I.  
TITLE Compositions and methods for the treatment of immune related  
diseases  
JOURNAL Patent: WO 0073452-A 68 07-DEC-2000;  
Genentech, Inc. (US)  
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source Location/Qualifiers  
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Best Local Similarity: 100.00% Mismatches: 0  
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DB 133 CCCGAGCCCTTTAAACACCCCGTCTCGAACATCGAACAAATTGGATCGCTTAAGCT 192  
QY 61 AspGIuPheLeuAsnThrPheIleAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
DB 193 GATGAGTCTCTGAACCTGGACCGCCCTTTGAGCTATCAAAAGAACTCTCTTCCCTC 252  
QY 81 AsnTYrAspAlaPheProLysLeuLysGIyLeuArgSerAlaThrProAspAlaGln 99  
DB 253 AACTGGAGTGCCTTTCTTAAGCTGAAGAGCTGAGAGCGCAACTCTGATGCCAG 309

RESULT 2  
AR252517 415 bp DNA linear PAT 20-DEC-2002  
LOCUS AR252517  
DEFINITION Sequence 200 from patent US 6478825.  
ACCESSION AR252517  
VERSION AR252517.1 GI:27300425  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS Unclassified.  
TITLE 1 (bases 1 to 415)  
Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.  
Implant, method of making same and use of the implant for the  
treatment of bone defects  
Patent: US 6478825-A 200 12-NOV-2002;  
JOURNAL Location/Qualifiers  
1..415  
source

BASE COUNT 99 a 126 c 92 g 98 t  
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AX077031 415 bp DNA linear PAT 22-FEB-2001  
LOCUS AX077031  
DEFINITION Sequence 19 from Patent WO0105972.  
ACCESSION AX077031  
VERSION AX077031.1 GI:13121661  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Ashkenazi, A.J., Baker, K.P., Fong, S., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Hillan, K.J., Mark, M.R., Masters, S.A., Pitti, R.M.,  
Tunas, D., Watanabe, C.K. and Wood, W.I.  
TITLE Compositions and methods for the treatment of immune related  
diseases  
JOURNAL Patent: WO 0105972-A 19 25-JAN-2001;  
Genentech, Inc. (US)  
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BASE COUNT 99 a 126 c 92 g 98 t  
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Best Local Similarity: 100.00% Mismatches: 0  
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DB 73 CAGGAGCCACCCCTGGTGGTCTCTGAGAAAGAACCATTTAGATTATGGCTACCA 132  
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DB 133 CCCGAGCCCTTTAAACACCCCGTCTCGAACATCGAACAAATTGGATCGCTTAAGCT 192  
QY 61 AspGIuPheLeuAsnThrPheIleAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
DB 193 GATGAGTCTCTGAACCTGGACCGCCCTTTGAGCTATCAAAAGAACTCTCTTCCCTC 252  
QY 81 AsnTYrAspAlaPheProLysLeuLysGIyLeuArgSerAlaThrProAspAlaGln 99  
DB 253 AACTGGAGTGCCTTTCTTAAGCTGAAGAGCTGAGAGCGCAACTCTGATGCCAG 309



Grimaldi, C.J., Gurney, A.L., Kijavina, I., Napier, M.A., Pan, J.,  
Pacini, N.F., Roy, M., Stewart, J.A., Tunnas, D., Watanabe, C.K.,  
Williams, P., Wood, W.I. and Zhang, Z.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
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JOURNAL Patent: WO 0073454-A 200 07-DEC-2000;

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source Location/Qualifiers

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ORIGIN

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DEFINITION Sequence 131 from Patent WO0208284.  
ACCESSION AX454546  
VERSION AX454546.1 GI:21713897  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Pacini, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.  
Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis

TITLE  
JOURNAL  
Genentech, Inc. (US)  
Patent: WO 0208284-A 131 31-JAN-2002;  
(US); Gerber, Hanspeter, Paul J. (US); Gerritsen, Mary E. (US); Goddard,  
Andrew (US); Godowski, Paul J. (US); Gurney, Austin L. (US); Hillan,  
Kennech J. (US); Marsters, Scot A. (US); Pan, James (US)  
; Pacini, Nicholas P. (US); Stephan, Jean-Philippe F. (US);  
Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William  
I. (US)

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Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142 (1-99) x AX454546 (1-415)

QY 1 MetLysIlePProValIleuProAlaValIleuLeuSerLeuValIleuHisSerAla 20  
DB 13 ATGAAGATCCCGGCTCTTCCTCCGCTGCTCTCTCCCTCCCTGCTGCTCACTCTGCC 72  
QY 21 GInGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTyrrAlaSerArg 40  
DB 73 CAGGAGGCCACCCCTGGGTGCTCTGAGGAAGAACCATTTGAAATTCGTCACGA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
DB 133 CCCGAGCCTTTAAACCCCGTTCTCTGAACATCGAATTCGATCTGCGTTAAAGCT 192  
QY 61 AspGluPheLeuAsnThrPheAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
DB 193 GATGAGTTCCTGAACCTGACGACCCCTTGTGATCATCAAAAGAAACCTTCCTCTC 252  
QY 81 AsnTPAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
DB 253 AACTGGATGCTTCTTCTTAAGCTGAAGACTGAAGAGCGCACTCGATGCCAG 309

RESULT 8  
LOCUS AX491024 415 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 131 from Patent WO0200690.  
ACCESSION AX491024  
VERSION AX491024.1 GI:22323849  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Pacini, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.  
Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis

TITLE  
JOURNAL  
Genentech, Inc. (US)  
Patent: WO 0200690-A 131 03-JAN-2002;  
(US); Gerber, Hanspeter, Paul J. (US); Gerritsen, Mary E. (US); Goddard,  
Andrew (US); Godowski, Paul J. (US); Gurney, Austin L. (US); Hillan,  
Kennech J. (US); Marsters, Scot A. (US); Pan, James (US)  
; Pacini, Nicholas P. (US); Stephan, Jean-Philippe F. (US);  
Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William  
I. (US)

FEATURES  
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/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

## Alignment Scores:

Pred. No.: 9,62e-96 Length: 415  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142 (1-99) x AX491024 (1-415)

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| QY  | 1  | MetVysIIEProValIleuProAlaValIleuSerLeuLeuValIleuHISerA       | 20     |
| Db  | 13   | ATGAGATCCGGGTCCTTCCTGGGTCCTCTCTCTCTGGTCTCACCCTGGC            | 72     |
| QY  | 21   | GIInGIyAlaThrLeuGlyGIYProGIuGIuGuseThrIIeGIuAnTyAlaSerArg    | 40     |
| Db  | 73   | CAGGAGGACCACTGGGGTGTCTCGAGGAGAAAGCAACATTGAGATTATGGCTACGA     | 132    |
| QY  | 41   | ProGIuAlaPheAenThrProPheLeuAnIIeAplysLeuArgSerAlaPheIysAla   | 60     |
| Db  | 133  | CCCGAGGCGCTTAAACACCCCGTCTGGAACATCGCAATTCGCATTCGCGTTAAGGCT    | 192    |
| QY  | 61   | AspGIuPheLeuAenThrPheAlaLeuPheGuseTIIeIyAsArgIysLeuProPheLeu | 80     |
| Db  | 193  | GATAGATTCCTGAAGTGGACGACCGCTCTTTGAGTGTATCAAGAAAGAACTTCCTTC    | 252    |
| QY  | 81   | AsnTrpAapAlaPheProIysLeuGlyGIYLeuArgSerAlaThrProAspAlaGln    | 99     |
| Db  | 253  | AACGGAGTGCCTTCTTAAGCTGAAAGACGTAGGAGCGGACGCAACTCGATGGCCAG     | 309    |
| RESULT 9                                    |  |  |        |
| LOCUS                                       | AX574494   | 415 bp   | linear |
| DEFINITION                                  | Sequence 21 from Patent WO0224888.   |  |        |
| ACCESSION                                   | AX574494   |  |        |
| VERSION                                     | AX574494.1   | GI:27551800  |        |
| KEYWORDS                                    |  |  |        |
| SOURCE                                      | Homo sapiens (human)   |  |        |
| ORGANISM                                    | Homo sapiens   |  |        |
| REFERENCE                                   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  |  |        |
| AUTHORS                                     | 1 Baker, K.P., Eaton, D.L., Filvaroff, E., Goddard, A., Grimaldi, J.C., Gunney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., Wood, W.T., Zhang, Z. and Fong, S. |  |        |
| TITLE                                       | Secreted and transmembrane polypeptides and nucleic acids encoding the same  |  |        |
| JOURNAL                                     | Patent: WO 0224888-A 21 28-MAR-2002; GENENTECH, INC. (US)  |  |        |
| FEATURES                                    | Location/Qualifiers  |  |        |
| Source                                      | 1..415   |  |        |
| BASE COUNT                                  | 99 a 126 c 92 g 98 t   |  |        |
| ORIGIN                                      |  |  |        |
| Alignment Scores:                           |  |  |        |
| Pred. NO.:                                  | 9.62e-96   | Length: 415  |        |
| Score:                                      | 99.00  | Matches: 99  |        |
| Percent Similarity:                         | 100.00%  | Conservative: 0  |        |
| Best Local Similarity:                      | 100.00%  | Mismatches: 0  |        |
| Query Match:                                | 100.00%  | Indels: 0  |        |
|   | 6  | Gaps: 0  |        |
| US-10-059-395-142 (1-99) x AX574494 (1-415) |  |  |        |
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| Db  | 13   | ATGAGATCCCGGTCCTTCCTGGGTCCTCTCTCTCTGGTCTCACCCTGGC            | 72     |
| QY  | 21   | GIInGIyAlaThrLeuGlyGIYProGIuGIuGuseThrIIeGIuAnTyAlaSerArg    | 40     |
| Db  | 73   | CAGGAGGACCACTGGGGTGTCTCGAGGAGAAAGCAACATTGAGATTATGGCTACGA     | 132    |
| QY  | 41   | ProGIuAlaPheAenThrProPheLeuAnIIeAplysLeuArgSerAlaPheIysAla   | 60     |
| Db  | 133  | CCCGAGGCGCTTAAACACCCCGTCTGGAACATCGCAATTCGCATTCGCGTTAAGGCT    | 192    |
| QY  | 61   | AspGIuPheLeuAenThrPheAlaLeuPheGuseTIIeIyAsArgIysLeuProPheLeu | 80     |
| Db  | 193  | GATAGATTCCTGAAGTGGACGACCGCTCTTTGAGTGTATCAAGAAAGAACTTCCTTC    | 252    |

[illegible]

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Db      81 CAGGAGGACCGCTGGGTGCTCTGAGGAGAAAGACACATTGAGAAATTATGCGCTCAGCA 140
Qy      41 Proglu1a1aPheAantThrProPheleuAni1eAspLyLeuAgsSer1a1aPheLyA1a 60
Db      141 CCGGAGGCGCTTTAAACACCCGCTTCTGACATCAAAATTGCGATCTGCGCTTTAAAGCT 200
Qy      61 AspGluPheLeuAantThrPhe1a1aLeuPheGluSer1e1eLyAgsLyLeuProPheleu 80
Db      201 GATGAGTTCCTGAACCTGACACGCCCTCTTGAAGTCTATCAAAAGAAACTTCTTCCTC 260
Qy      81 AantThrAspAlaPheProLyLeuLyLeuLyLeuLyLeuLyLeuLyLeuLyLeuLyLeu 99
Db      261 AACTGGAGTGCCTTCTCTTAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 317

RESULT 11
LOCUS      AX080817              490 bp      DNA      linear      PAT 27-FEB-2001
DEFINITION Sequence 63 from Patent WO0109327.
ACCESSION  AX080817
VERSION     AX080817.1  GI:13169786
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Kljavin,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Picti,R.M.,
            Matarabze,C.K. and Wood,W.I.
TITLE       Method of preventing the injury or death of retinal cells and
            treating ocular diseases
JOURNAL     Patent: WO 0109327-A 63 08-FEB-2001;
            Genentech, Inc. (US)
FEATURES
            source
            1..490
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            /mol_type="genomic DNA"
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            /note="Virtual DNA fragment used in the isolation of
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ORIGIN
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Pred. No.:      1.12e-95      Length:      490
Score:          99.00      Matches:      99
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
            Gaps:      0
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Qy      1 MetLyS1leProValLeuProAlaValLeuLeuSerLeuLeuValLeuHisSer1a 20
Db      80 ATGAAGATCCCGGCTTCTGCGCGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 139
Qy      21 GlnGlyAlaThrLeuGlyGlyProGluGluGluSerThr11eGluAantThrAlaSerArg 40
Db      140 CAGGAGGACCGCTTGAACCTGACACGCCCTCTTGAAGTCTATCAAAAGAAACTTCTTCCTC 199
Qy      41 ProGlu1a1aPheAantThrProPheleuAni1eAspLyLeuAgsSer1a1aPheLyA1a 60
Db      200 CCGGAGGCGCTTTAAACACCCGCTTCTGACATCAAAATTGCGATCTGCGCTTTAAAGCT 259
Qy      61 AspGluPheLeuAantThrPhe1a1aLeuPheGluSer1e1eLyAgsLyLeuProPheleu 80
Db      260 GATGAGTTCCTGAACCTGACACGCCCTCTTGAAGTCTATCAAAAGAAACTTCTTCCTC 319
Qy      81 AantThrAspAlaPheProLyLeuLyLeuLyLeuLyLeuLyLeuLyLeuLyLeuLyLeu 99
Db      320 AACTGGAGTGCCTTCTCTTAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 376

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RESULT 12
LOCUS      AX080816              435 bp      DNA      linear      PAT 27-FEB-2001
DEFINITION Sequence 62 from Patent WO0109327.
ACCESSION  AX080816
VERSION     AX080816.1  GI:13169785
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Kljavin,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Picti,R.M.,
            Matarabze,C.K. and Wood,W.I.
TITLE       Method of preventing the injury or death of retinal cells and
            treating ocular diseases
JOURNAL     Patent: WO 0109327-A 62 08-FEB-2001;
            Genentech, Inc. (US)
FEATURES
            source
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            /organism="synthetic construct"
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Percent Similarity: 99.00%      Conservative: 0
Best Local Similarity: 99.00%      Mismatches: 0
Query Match:    86.87%      Indels:      1
            Gaps:      0
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Qy      1 MetLyS1leProValLeuProAlaValLeuLeuSerLeuLeuValLeuHisSer1a 20
Db      15 ATGAAGATCCCGGCTTCTGCGCGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 74
Qy      21 GlnGlyAlaThrLeuGlyGlyProGluGluGluSerThr11eGluAantThrAlaSerArg 40
Db      75 CAGGAGGACCGCTTGAACCTGACACGCCCTCTTGAAGTCTATCAAAAGAAACTTCTTCCTC 134
Qy      41 -ProGlu1a1aPheAantThrProPheleuAni1eAspLyLeuAgsSer1a1aPheLyA1a 60
Db      135 CCGGAGGCGCTTTAAACACCCGCTTCTGACATCAAAATTGCGATCTGCGCTTTAAAGC 194
Qy      60 AspGluPheLeuAantThrPhe1a1aLeuPheGluSer1e1eLyAgsLyLeuProPhele 80
Db      195 TGATGAGTTCCTGAACCTGACACGCCCTCTTGAAGTCTATCAAAAGAAACTTCTTCCTC 254
Qy      80 AantThrAspAlaPheProLyLeuLyLeuLyLeuLyLeuLyLeuLyLeuLyLeuLyLeu 99
Db      255 CAACCTGGAGTGCCTTCTCTTAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 312

RESULT 13
LOCUS      HSA293408              529 bp      mRNA      linear      PRI 06-JAN-2003
DEFINITION Homo sapiens mRNA differentially expressed in malignant melanoma,
            clone NN 15.
ACCESSION  AJ293408
VERSION     AJ293408.1  GI:27526545
KEYWORDS   differential expression; malignant; melanoma.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Delchmann,M., Thome,M., Wacker,J. and Naehrer,H.
TITLE       Genes differentially expressed in malignant melanoma

```





Qy 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspIleLeuArgSerAlaPheIysAla 60  
Db 132 CCCGAGGCGCTTTAAACACCCCGTTCCCTGAAACATGCAAAATGCGATCTGCGTTTAAGGCT 191  
Qy 61 AspGluPheLeuAsnThrPheAlaLeuPheGluSerIleIleArgIleLeuProPheLeu 80  
Db 192 GATGAGTTCTCTGACTGCGACGCGCCCTCTTGTAGTCTATCAAAAGGAACTTCTTCTC 251  
Qy 81 AsnTrpAspAlaPheProIysLeuIysGlyLeuArgSerAlaThrProAspAlaGln 99  
Db 252 AACTGGGATGCGCTTCTCTAAGCTGAAGGACTGAGGAGCGCAACTCTGTATGCCCA 308

Search completed: November 28, 2003, 10:23:47  
Job time : 2863 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 08:40:10 ; Search time 231 Seconds

(without alignments)  
1156.902 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 99

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Searched: 2552756 segs, 1349719017 residues

Word size: 1

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

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| 1          | 99    | 100.0       | 414    | 22 AAC91475 | Human PRO826 cDNA.  |
| 2          | 99    | 100.0       | 414    | 24 ABK28600 | Human DN57694-134   |
| 3          | 99    | 100.0       | 415    | 21 AA265018 | Membrane-bound pro  |
| 4          | 99    | 100.0       | 415    | 22 AAF30059 | Human cDNA encoding |
| 5          | 99    | 100.0       | 415    | 22 AAF44164 | Human PRO826 (UNC4  |
| 6          | 99    | 100.0       | 415    | 22 AAC97491 | Human angiogenesis  |
| 7          | 99    | 100.0       | 415    | 24 AB195626 | Human angiogenesis  |
| 8          | 99    | 100.0       | 415    | 24 ABK69971 | cDNA encoding huma  |
| 9          | 99    | 100.0       | 415    | 24 AB188137 | Human PRO826 cDNA   |
| 10         | 99    | 100.0       | 415    | 24 ABK33608 | cDNA encoding huma  |
| 11         | 99    | 100.0       | 415    | 25 ABX80255 | Novel human secret  |
| 12         | 99    | 100.0       | 415    | 25 ABX80759 | Human secreted/cr   |
| 13         | 99    | 100.0       | 415    | 25 ABX81142 | Novel human secret  |
| 14         | 99    | 100.0       | 415    | 25 ABX90232 | Human secreted/cr   |
| 15         | 99    | 100.0       | 415    | 25 ABX79843 | Human PRO polynuci  |
| 16         | 99    | 100.0       | 415    | 25 ABX79439 | Human secreted/cr   |
| 17         | 99    | 100.0       | 415    | 25 ABX64078 | cDNA encoding huma  |
| 18         | 99    | 100.0       | 415    | 25 ABX17042 | Human PRO polynuci  |
| 19         | 99    | 100.0       | 428    | 24 ABZ11803 | Human polynucleoti  |
| 20         | 99    | 100.0       | 456    | 20 AAX00632 | Human secreted pro  |
| 21         | 89    | 89.9        | 518    | 22 ABA09519 | Human secreted pro  |
| 22         | 56    | 56.6        | 305    | 21 AAC68806 | Human head/neck tu  |
| 23         | 56    | 56.6        | 305    | 24 ABZ11886 | Human polynucleoti  |
| 24         | 44    | 44.4        | 386    | 24 ABZ11804 | Human polynucleoti  |
| 25         | 9     | 9.1         | 36159  | 24 ABN85329 | Human kinase gene.  |
| 26         | 9     | 9.1         | 82938  | 24 ABV72623 | Human transporter   |
| 27         | 8     | 8.1         | 45     | 17 AAT42481 | Primer for Chimera  |
| 28         | 8     | 8.1         | 263    | 22 ABA75510 | Human foetal liver  |
| 29         | 8     | 8.1         | 263    | 22 ABA40130 | Probe #18596 for g  |
| 30         | 8     | 8.1         | 263    | 22 AAK24082 | Human brain expres  |
| 31         | 8     | 8.1         | 263    | 22 AAK50145 | Human bone marrow   |
| 32         | 8     | 8.1         | 263    | 22 AAI21228 | Probe #17161 for g  |
| 33         | 8     | 8.1         | 263    | 23 AAI56085 | Probe #24771 used   |
| 34         | 8     | 8.1         | 263    | 23 ABA49777 | Human liver single  |
| 35         | 8     | 8.1         | 263    | 24 ABA23621 | Human genome-deriv  |
| 36         | 8     | 8.1         | 278    | 25 ABX82738 | Corn ear-derived p  |
| 37         | 8     | 8.1         | 307    | 22 ABA47823 | Human breast cell   |
| 38         | 8     | 8.1         | 307    | 22 ABA65710 | Human foetal liver  |
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| 42         | 8     | 8.1         | 307    | 22 AAI20668 | Probe #10601 for g  |
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## ALIGNMENTS

RESULT 1  
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ID AAC91475 standard; cDNA; 414 BP.  
XX AAC91475;  
AC  
XX 21-MAR-2001 (first entry)  
XX  
XX Human PRO826 cDNA.  
DE  
XX Human; PRO; antiinflammatory; dermatological; antiarthritic;  
XX antirheumatic; cardiac; antianemic; immunosuppressive; antithyroid;  
KW antidiabetic; noctropic; neuroprotective; hepatotropic; virucide;  
KW antiallergic; antirheumatic; immune related disorder;  
KW hepatobiliary disease; autoimmune disease; allergy; se.  
OS Homo sapiens.

XX WO200073452-A2.  
 XX  
 XX 07-DEC-2000.  
 XX  
 XX 02-JUN-2000; 2000WO-US15264.  
 XX  
 XX 02-JUN-1999; 99WO-US12252.  
 XX 20-JUL-1999; 99US-0144732.  
 XX 20-JUL-1999; 99US-0144758.  
 XX 28-JUL-1999; 99US-0146222.  
 XX 01-SEP-1999; 99WO-US20111.  
 XX 13-SEP-1999; 99WO-US21090.  
 XX 15-SEP-1999; 99WO-US21547.  
 XX 29-OCT-1999; 99US-0162506.  
 XX 30-NOV-1999; 99WO-US28313.  
 XX 01-DEC-1999; 99WO-US28634.  
 XX 09-DEC-1999; 99US-0170262.  
 XX 20-DEC-1999; 99WO-US30911.  
 XX 05-JAN-2000; 2000WO-US00219.  
 XX 06-JAN-2000; 2000WO-US00376.  
 XX 11-FEB-2000; 2000WO-US03565.  
 XX 18-FEB-2000; 2000WO-US04341.  
 XX 18-FEB-2000; 2000WO-US04342.  
 XX 22-FEB-2000; 2000WO-US04414.  
 XX 24-FEB-2000; 2000WO-US04914.  
 XX 15-MAR-2000; 2000WO-US06884.  
 XX 20-MAR-2000; 2000WO-US07377.  
 XX 21-MAR-2000; 2000WO-US07532.  
 XX 30-MAR-2000; 2000WO-US08439.  
 XX 17-MAY-2000; 2000WO-US13705.  
 XX 22-MAY-2000; 2000WO-US14042.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL,  
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK,  
 PI Wood WI;  
 XX  
 DR WPI; 2001-025253/03.  
 DR P-PEDB; AAB50916.  
 XX  
 PT Thirty three nucleic acids encoding PRO polypeptides which are useful  
 PT in the diagnosis and treatment of immune related disorders, e.g.  
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 PT thyroiditis and diabetes mellitus -  
 XX  
 PS Claim 48; Fig 29; 218bp; English.  
 XX  
 CC The present sequence is one of thirty three nucleic acids encoding PRO  
 CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and  
 CC antagonists are useful for treating and diagnosing immune related  
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
 CC (such as infectious, autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
 CC food hypersensitivity and urticaria), immunological diseases of the  
 CC lung (such as eosinophilic pneumonia), idiopathic pulmonary fibrosis  
 CC and hypersensitivity pneumonitis), transplantation associated diseases  
 CC including graft rejection and graft-versus-host diseases.  
 XX  
 SO Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:  
 Pred. No.: 7,24e-88 Length: 414  
 Score: 99.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0  
 US-10-059-395-142 (1-99) x AAC91475 (1-414)  
 QY 1 MetLysIleProValIleuProAlaValIleuLeuSerIleuValIleuHisSerAla 20  
 DB 13 ATGAAGATCCCGGCTCTCTCCGCGGTGCTCTCTCCCTCGTGCCTTCACTCGCC 72  
 QY 21 GlnIlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAenThrAlaSerArg 40  
 DB 73 CAGGAGCCACCTGGGTGGTCTTGAAGAGAAAGACCATTTGAAATTATGCGTCACGA 132  
 QY 41 ProGluAlaPheAenThrProPheLeuAenIleAspLysIleuArgSerAlaPheLysAla 60  
 DB 133 CCCGAGGCTTTATCACCCGCTTCTGAACATGCAAAATTGCGATCTGCTTTAAAGCT 192  
 QY 61 AspGluPheLeuAenThrPheAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
 DB 193 GATGAGTTCCTGAACCTGACGCGCCCTTGTGAGCTATCAAAAGAAACTTCTTCCTC 252  
 QY 81 AsnThrAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
 DB 253 AACTGGATGCTTTTCTTAAGCTAAAGAGCTGAGAGCGCACTGCTGATGCCCG 309  
 RESULT 2  
 ID ABR28600 standard; cDNA; 414 BP.  
 XX ABR28600;  
 AC  
 XX 09-APR-2002 (first entry)  
 DT  
 XX  
 DE Human DMS57694-1341 encoding PRO826.  
 XX  
 KW Human; sex: male; PRO; antiinflammatory; ophthalmological; vasotropic;  
 KW retinal cell injury; ocular disease; retinitis pigmentosa;  
 KW macular degeneration; retinal detachment; retinal tear; retinopathy;  
 KW retinal degenerative disease; macular hole; degenerative myopia;  
 KW acute retinal necrosis syndrome; traumatic chorioretinopathy;  
 KW Purtscher's retinopathy; oedema; ischaemic condition;  
 KW retinal vision occlusion; collagen vascular disease;  
 KW thrombocytopenic purpura; uveitis; retinal vasculitis; Pales disease;  
 KW systemic lupus erythematosus; environmental trauma.  
 XX  
 OS Homo sapiens.  
 XX  
 MO200109327-A2.  
 XX  
 PD 08-FEB-2001.  
 PF  
 XX 28-JUL-2000; 2000WO-US20710.  
 XX  
 XX 28-JUL-1999; 99US-146222P.  
 XX 13-SEP-1999; 99WO-US20944.  
 XX 15-SEP-1999; 99WO-US21090.  
 XX 29-NOV-1999; 99WO-US28214.  
 XX 30-NOV-1999; 99WO-US28313.  
 XX 01-DEC-1999; 99WO-US28301.  
 XX 05-JAN-2000; 2000WO-US00219.  
 XX 06-JAN-2000; 2000WO-US00376.  
 XX 11-FEB-2000; 2000WO-US03565.  
 XX 18-FEB-2000; 2000WO-US04341.  
 XX 22-FEB-2000; 2000WO-US04414.  
 XX 24-FEB-2000; 2000WO-US05004.  
 XX 02-MAR-2000; 2000WO-US05841.  
 XX 15-MAR-2000; 2000WO-US06884.

PR 30-MAR-2000; 2000MOW-US08439.  
PR 17-MAY-2000; 2000MOW-US13705.

(GETH ) GENENTECH INC.

XX Abkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;  
PI Kijaviri IU, Tafleuer M, Mark MR, Marsters SA, Pictt RM;  
PI Watanabe CK, Wood WI;  
DR WPI; 2002-130120/17.  
DR P-PDB; AAU81964.

XX Promoting survival of retinal cells, or delaying or preventing retinal  
PT cell injury or death, by contacting retinal cells with PRO175, 220,  
PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132  
PT polypeptide -  
XX  
XX Claim 33; Fig 24; 152pp; English.

The invention relates to promoting the survival of retinal cells, or  
delaying or preventing retinal cell injury or death, by contacting the  
retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO828, PRO826,  
PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
encoding the PRO proteins, a vector comprising the nucleic acid, a host  
cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
useful for promoting survival of retinal cells (retinal neurons such as  
retinal ganglion cells, displaced retinal ganglion cells, amacrine  
cells, displaced amacrine cells, horizontal neurons or bipolar neurons,  
rod photoreceptors, or supportive cells such as Muller cells or pigment  
epithelial cells), or delaying or preventing retinal cell injury or  
death caused by ocular disease (which is or is associated with  
retinitis pigmentosa, macular degenerative disease, retinal detachment, retinal  
tear, retinopathy, retinal degenerative disease, macular hole,  
degenerative myopia, acute retinal necrosis syndrome, traumatic  
choriorretinopathy or contusion, Purtscher's retinopathy, oedema, an  
ischemic condition, central or branch retinal vision occlusion,  
collagen vascular disease, thrombocytopenic purpura, uveitis, retinal  
vasculitis, occlusion associated with Bales disease or systemic lupus  
erythematosus), retinal injury or environmental trauma. The retinal  
cell injury or death is delayed or prevented by substantially not  
causing angiogenesis or mitogenesis. The present sequence is a cDNA  
encoding a PRO protein.

Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:  
Pred. No.: 7, 24e-88 Length: 414  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservativity: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0

US-10-059-395-142 (1-99) \* ABK28600 (1-414)

QY 1 MetIysIIeProValIeuProAlaValIeuLeuSerLeuValIeuHisSerAla 20  
Db 13 ATAAAGATCCCGGTCTTCTTCGCGGGTGCTCCTCCTCCGCTGCCTCATCTGCC 72  
QY 21 GIINGLYALATHrIeuGLyGIyPProGUguIuSertHrIIegIUAsnTYrAlaSerArg 40  
Db 73 CAAGGAGCAACCCCTGGTGCTGCTGAAGAAGAACCAACATTGAAGATTATGCGTCACGA 122  
QY 41 ProGUAlAIPheAsnHrPrPhHeuAnIIeApLyISLauAgSerAlaphylArAla 60  
Db 133 CCCGAGGCTTTAAACCCCCGTTCTTGAACATCGACAATTGCGATTCGCTTTAAAGCT 122  
QY 61 AspGIuPheLSuAsnTrpHisAlaIeuPheGuIsErIIeLYASrGLySLeUProPheLU 80  
Db 193 GATGAGTTCCTGAACAGGAGCACCGCTTTGAGCTTAACAAGAAAATTCTTCTTC 252  
QY 81 AsnTrpAspAlaPheProLySLeULySGILyLeuAgSerAlaThrProAspAlaGln 99

| Db       | 253  | AACTGGAATGCTTCTCTAAGCTGAAGAGGAGCAACTCTGATGCCAG | 308 |
|----------|--|--|-----|
| RESULT 3 |  |  |     |
| AA265018 |  |  |     |
| ID       | AA265018   | standard; cDNA; 415 BP.                        |     |
| XX       | AA265018;  |  |     |
| AC       |  |  |     |
| XX       |  |  |     |
| DT       | 05-APR-2000 (first entry)  |  |     |
| XX       |  |  |     |
| DE       | Membrane-bound protein PRO826 encoding cDNA.                           |  |     |
| XX       |  |  |     |
| KW       | Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; |  |     |
| KM       | pharmacological; receptor immunoadhesin; gene mapping; ss.             |  |     |
| XX       |  |  |     |
| OS       | Homo sapiens.  |  |     |
| XX       |  |  |     |
| PN       | W09963088-A2.  |  |     |
| XX       |  |  |     |
| PD       | 09-DEC-1999.   |  |     |
| XX       |  |  |     |
| PF       | 02-JUN-1999;   | 99WO-US12252.                                  |     |
| XX       |  |  |     |
| PR       | 02-JUN-1998;   | 98US-0087607.                                  |     |
| PR       | 02-JUN-1998;   | 98US-0087609.                                  |     |
| PR       | 02-JUN-1998;   | 98US-0087759.                                  |     |
| PR       | 03-JUN-1998;   | 98US-0087827.                                  |     |
| PR       | 04-JUN-1998;   | 98US-0088021.                                  |     |
| PR       | 04-JUN-1998;   | 98US-0088025.                                  |     |
| PR       | 04-JUN-1998;   | 98US-0088028.                                  |     |
| PR       | 04-JUN-1998;   | 98US-0088029.                                  |     |
| PR       | 04-JUN-1998;   | 98US-0088030.                                  |     |
| PR       | 04-JUN-1998;   | 98US-0088033.                                  |     |
| PR       | 04-JUN-1998;   | 98US-0088326.                                  |     |
| PR       | 05-JUN-1998;   | 98US-0088167.                                  |     |
| PR       | 05-JUN-1998;   | 98US-0088202.                                  |     |
| PR       | 05-JUN-1998;   | 98US-0088212.                                  |     |
| PR       | 05-JUN-1998;   | 98US-0088217.                                  |     |
| PR       | 09-JUN-1998;   | 98US-0088655.                                  |     |
| PR       | 10-JUN-1998;   | 98US-0088722.                                  |     |
| PR       | 10-JUN-1998;   | 98US-0088730.                                  |     |
| PR       | 10-JUN-1998;   | 98US-0088734.                                  |     |
| PR       | 10-JUN-1998;   | 98US-0088738.                                  |     |
| PR       | 10-JUN-1998;   | 98US-0088740.                                  |     |
| PR       | 10-JUN-1998;   | 98US-0088741.                                  |     |
| PR       | 10-JUN-1998;   | 98US-0088742.                                  |     |
| PR       | 10-JUN-1998;   | 98US-0088810.                                  |     |
| PR       | 10-JUN-1998;   | 98US-0088811.                                  |     |
| PR       | 10-JUN-1998;   | 98US-0088824.                                  |     |
| PR       | 10-JUN-1998;   | 98US-0088825.                                  |     |
| PR       | 10-JUN-1998;   | 98US-0088826.                                  |     |
| PR       | 11-JUN-1998;   | 98US-0088858.                                  |     |
| PR       | 11-JUN-1998;   | 98US-0088861.                                  |     |
| PR       | 11-JUN-1998;   | 98US-0088863.                                  |     |
| PR       | 11-JUN-1998;   | 98US-0088876.                                  |     |
| PR       | 12-JUN-1998;   | 98US-0089090.                                  |     |
| PR       | 12-JUN-1998;   | 98US-0089105.                                  |     |
| PR       | 16-JUN-1998;   | 98US-0089340.                                  |     |
| PR       | 16-JUN-1998;   | 98US-0089512.                                  |     |
| PR       | 16-JUN-1998;   | 98US-0089514.                                  |     |
| PR       | 17-JUN-1998;   | 98US-0089532.                                  |     |
| PR       | 17-JUN-1998;   | 98US-0089538.                                  |     |
| PR       | 17-JUN-1998;   | 98US-0089598.                                  |     |
| PR       | 17-JUN-1998;   | 98US-0089599.                                  |     |
| PR       | 17-JUN-1998;   | 98US-0089600.                                  |     |
| PR       | 17-JUN-1998;   | 98US-0089653.                                  |     |
| PR       | 18-JUN-1998;   | 98US-0089601.                                  |     |
| PR       | 18-JUN-1998;   | 98US-0089907.                                  |     |
| PR       | 18-JUN-1998;   | 98US-0089908.                                  |     |
| PR       | 19-JUN-1998;   | 98US-0089947.                                  |     |
| PR       | 19-JUN-1998;   | 98US-0089948.                                  |     |
| PR       | 19-JUN-1998;   | 98US-0089952.                                  |     |

PR 22-JUN-1998; 98US-0090246.  
 PR 22-JUN-1998; 98US-0090252.  
 PR 22-JUN-1998; 98US-0090254.  
 PR 23-JUN-1998; 98US-0090349.  
 PR 23-JUN-1998; 98US-0090355.  
 PR 24-JUN-1998; 98US-0090429.  
 PR 24-JUN-1998; 98US-0090431.  
 PR 24-JUN-1998; 98US-0090435.  
 PR 24-JUN-1998; 98US-0090444.  
 PR 24-JUN-1998; 98US-0090445.  
 PR 24-JUN-1998; 98US-0090461.  
 PR 24-JUN-1998; 98US-0090472.  
 PR 24-JUN-1998; 98US-0090535.  
 PR 24-JUN-1998; 98US-0090538.  
 PR 24-JUN-1998; 98US-0090540.  
 PR 24-JUN-1998; 98US-0090557.  
 PR 25-JUN-1998; 98US-0090676.  
 PR 25-JUN-1998; 98US-0090678.  
 PR 25-JUN-1998; 98US-0090688.  
 PR 25-JUN-1998; 98US-0090690.  
 PR 25-JUN-1998; 98US-0090691.  
 PR 25-JUN-1998; 98US-0090694.  
 PR 25-JUN-1998; 98US-0090695.  
 PR 26-JUN-1998; 98US-0090696.  
 PR 26-JUN-1998; 98US-0090862.  
 PR 26-JUN-1998; 98US-0090863.  
 PR 01-JUL-1998; 98US-0091358.  
 PR 01-JUL-1998; 98US-0091360.  
 PR 02-JUL-1998; 98US-0091478.  
 PR 02-JUL-1998; 98US-0091486.  
 PR 02-JUL-1998; 98US-0091519.  
 PR 02-JUL-1998; 98US-0091626.  
 PR 02-JUL-1998; 98US-0091628.  
 PR 02-JUL-1998; 98US-0091633.  
 PR 02-JUL-1998; 98US-0091646.  
 PR 02-JUL-1998; 98US-0091673.  
 PR 07-JUL-1998; 98US-0091978.  
 PR 09-JUL-1998; 98US-0091982.  
 PR 10-JUL-1998; 98US-0092182.  
 PR 20-JUL-1998; 98US-0092472.  
 PR 30-JUL-1998; 98US-0093339.  
 PR 04-AUG-1998; 98US-0094651.  
 PR 04-AUG-1998; 98US-0095282.  
 PR 04-AUG-1998; 98US-0095285.  
 PR 04-AUG-1998; 98US-0095301.  
 PR 04-AUG-1998; 98US-0095302.  
 PR 04-AUG-1998; 98US-0095318.  
 PR 04-AUG-1998; 98US-0095321.  
 PR 04-AUG-1998; 98US-0095325.  
 PR 10-AUG-1998; 98US-0095916.  
 PR 10-AUG-1998; 98US-0095929.  
 PR 10-AUG-1998; 98US-0096012.  
 PR 11-AUG-1998; 98US-0096143.  
 PR 11-AUG-1998; 98US-0096146.  
 PR 12-AUG-1998; 98US-0096329.  
 PR 17-AUG-1998; 98US-0096757.  
 PR 17-AUG-1998; 98US-0096766.  
 PR 17-AUG-1998; 98US-0096768.  
 PR 17-AUG-1998; 98US-0096773.  
 PR 17-AUG-1998; 98US-0096791.  
 PR 17-AUG-1998; 98US-0096867.  
 PR 17-AUG-1998; 98US-0096891.  
 PR 17-AUG-1998; 98US-0096894.  
 PR 17-AUG-1998; 98US-0096895.  
 PR 17-AUG-1998; 98US-0096897.  
 PR 18-AUG-1998; 98US-0096949.  
 PR 18-AUG-1998; 98US-0096950.  
 PR 18-AUG-1998; 98US-0096959.  
 PR 18-AUG-1998; 98US-0096960.  
 PR 18-AUG-1998; 98US-0097102.  
 PR 19-AUG-1998; 98US-0097141.  
 PR 20-AUG-1998; 98US-0097218.

PR 24-AUG-1998; 98US-0097661.  
 PR 26-AUG-1998; 98US-0097951.  
 PR 26-AUG-1998; 98US-0097952.  
 PR 26-AUG-1998; 98US-0097954.  
 PR 26-AUG-1998; 98US-0097955.  
 PR 26-AUG-1998; 98US-0097971.  
 PR 26-AUG-1998; 98US-0097974.  
 PR 26-AUG-1998; 98US-0097978.  
 PR 26-AUG-1998; 98US-0097979.  
 PR 26-AUG-1998; 98US-0097986.  
 PR 26-AUG-1998; 98US-0098014.  
 PR 31-AUG-1998; 98US-0098525.  
 PR 16-SEP-1998; 98US-0100634.  
 PR 12-JAN-1999; 99US-0115565.

(GENTECH ) GENENTECH INC.

XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 PI Wood WI, Yuan J;  
 XX

DR MPI; 2000-072883/06.  
 P-PSDB; AAY66681.

XX Membrane-bound proteins and related nucleotide sequences  
 XX Claim 2; Fig 12a; 822pp; English.

CC The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, TIR  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
 CC will also be useful for the preparation of PRO polypeptides, especially  
 CC by recombinant techniques.

XX SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:

|                        |          |               |     |
|------------------------|----------|---------------|-----|
| Pred. No.:             | 7,266-88 | Length:       | 415 |
| Score:                 | 99.00    | Matches:      | 99  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 21       | Gaps:         | 0   |

US-10-059-395-142 (1-99) x AAZ65018 (1-415)

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | MettysilleProValleuProAlaValleuLeuSerleuValleuHisSerAla      | 20  |
| DB | 13  | ATGAAGATCCCGCTCTCCGCGTGTCTCTCCCTCCGCGTCTCACTGCGC             | 72  |
| QY | 21  | GlnGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAlaSerArg       | 40  |
| DB | 73  | CAGGAGCCACCTGGTGGTGGTCTGAGAGAAAGACCATTTGAATTATTCGTCACGA      | 132 |
| QY | 41  | ProGluAlaPheAsnThrProPheLeuAsnIleAspIysLeuArgSerAlaPheIysAla | 60  |
| DB | 133 | CCCGAGGCTTTAACCACCCGCTCTCAATGACAAATTCGATTCGCTTAAGGCT         | 192 |
| QY | 61  | AspGluPheLeuAsnThrPheAlaLeuPheGluSerIleIysAspGlyLeuProPheLeu | 80  |
| DB | 193 | GATGAGTCTCGAATGACGACGCTCTTGAAGTCTCAAAAGAAACCTTCCTTCCTC       | 252 |
| QY | 81  | AsnTrpAspAlaPheProIysLeuIysGlyLeuArgSerAlaThrProAspAlaGln    | 99  |
| DB | 253 | AACGTGGATGCTTCTTCAAGCTGAAGACTGAGAGCCCACTCTGATGCCAG           | 309 |

RESULT 4  
AAAF30059  
ID AAAF30059 standard; cDNA; 415 BP.  
XX  
AC AAAF30059;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Human cDNA encoding PRO826.  
XX  
XX PRO826; UNQ467; human; immune disease; autoimmune disease;  
KM antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
KM immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
KM hepatotropic; virucide; dermatological; antipsoriatic;  
KM antiaesthetic; antiallergic; immunostimulant; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 13..312  
FT /tag= a  
FT sig\_peptide 13..78  
FT /tag= b  
FT mat\_peptide 79..309  
FT /tag= c  
XX  
XX WO200105972-A1.  
XX  
XX 25-JAN-2001.  
XX  
XX 15-MAR-2000; 2000MO-US06884.  
XX  
XX 20-JUL-1999; 99US-0144758.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL,  
PI Hillan KJ, Mark MR, Marsters SA, Pizzi RM, Tumas D, Watanabe CK,  
PI Wood WI;  
XX  
XX WPI; 2001-103149/11.  
XX P-PSDB; AAB20117.  
XX  
XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
PT diagnosing and treating immune-related disorders, such as multiple  
PT sclerosis, rheumatoid arthritis and diabetes -  
XX  
XX Claim 21; Fig 19; 127pp; English.  
XX  
XX The present sequence is that of cDNA clone DN57694-1341 (ATCC 203017)  
CC encoding novel human immunomodulator protein PRO826 (UNQ467) (see  
CC AAB20117). The clone was isolated following a database search by  
CC applying a signal sequence algorithm. The predicted protein has a  
CC mol.wt. of 11 kDa and a pI of 7.47. The invention provides  
CC polynucleotides (see AAF30050-62) encoding novel human PRO proteins  
CC (see AAB20108-20) including PRO826. Claimed compositions  
CC comprising these proteins or their agonists are useful for increasing  
CC infiltration of inflammatory cells into a tissue of a mammal,  
CC stimulating or enhancing an immune response in a mammal, or  
CC increasing the proliferation of T-lymphocytes in a mammal in response  
CC to an antigen. Claimed compositions comprising the PRO polypeptide  
CC or its antagonist have the opposite effect. A claimed method for  
CC treating an immune related disorder, such as a T cell disorder,  
CC involves administering the PRO polypeptide, an agonist antibody or  
CC an antagonist antibody. The disorder is selected from systemic  
CC lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, spondyloarthropathy, systemic  
CC sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome,  
CC systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia,  
CC autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,  
CC immune-mediated renal disease, demyelinated diseases (such as  
CC multiple sclerosis), autoimmune chronic active hepatitis, primary

CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
CC inflammatory bowel disease (ulcerative colitis and Crohn's disease),  
CC gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated  
CC skin diseases (such as bullous skin disease, erythema multiforme and  
CC psoriasis), allergic diseases (such as asthma, allergic rhinitis,  
CC atopic dermatitis, food hypersensitivity and urticaria), immunologic  
CC diseases of the lung and transplantation associated diseases (such  
CC as graft rejection and graft-versus-host disease) (all claimed).  
CC Claimed methods of diagnosing these disorders comprise detecting  
CC the level of expression of the PRO gene. Also claimed are a method  
CC of identifying a compound capable of inhibiting the expression or  
CC activity of the PRO polypeptide, vectors, host cells, antibodies  
CC and a method of stimulating the proliferation of T-lymphocytes  
CC using PRO826.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
XX  
Alignment Scores:  
Pred. No.: 7 266-88 Length: 415  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
XX  
US-10-059-395-142 (1-99) x AAAF30059 (1-415)  
XX  
QY 1 MethylsileProValLeuProAlaValLeuLeuSerLeuValLeuHisSerAla 20  
Db 13 ATGAAGATCCCGGCTCTTCCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTG 72  
QY 21 GlnGlyAlaThrLeuGlyGlyProGlnGlnGlnSerThrIleGlnAsnTrpAlaSerArg 40  
Db 73 CAGGAGACACCCCTGGTGGTCTGAGAGAGAAACACCATGAGAAATTATCGCACGA 132  
QY 41 ProGlnAlaPheAsnThrProPheLeuAsnIleAspLysLeuSerAlaPheLysAla 60  
Db 133 CCGAGAGCCCTTAAACACCCGCTCTGAAACATGACAAATTCGATCGCTTAAAGCT 192  
QY 61 AspGlnPheLeuAsnTrpHisAlaLeuPheGlnSerIleLysArgLysLeuProPheLeu 80  
Db 193 GATGAGTTCCTGGAATCGAGAGCCCTTTGAGTCTATCAAAAGAACTCTTCCCTC 252  
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
Db 253 AACTGGATGCTTCTTCTTAAGCTGAAGAGACTGAGAGCGCAACTCGATGCCAG 309  
XX  
RESULT 5  
AAAF4164  
ID AAAF4164 standard; cDNA; 415 BP.  
XX  
AC AAAF4164;  
XX  
XX 02-APR-2001 (first entry)  
XX  
XX Human PRO826 (UNQ467) nucleotide sequence SEQ ID NO:200.  
XX  
XX Human; secreted and transmembrane protein; PRO; cytosstatic;  
KM cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
KM diagnostic assay; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200073454-A1.  
XX  
XX 07-DEC-2000.  
XX  
XX 30-MAR-2000; 2000MO-US08439.  
XX  
XX 02-JUN-1999; 99WO-US12252.  
XX 23-JUN-1999; 99US-0141037.  
XX 07-JUL-1999; 99US-0143048.  
XX 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.  
PR 28-JUL-1999; 99US-0146222.  
PR 17-AUG-1999; 99US-0149396.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 08-OCT-1999; 99US-0158663.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
  
(GETH ) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
PI Ferrara N, Fong S, Gerber H, Gertlsen ME, Goddard A, Godowski PJ,  
PI Grimaldi CU, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z,  
XX WPI: 2001-032160/04.  
DR P-PSDB; AAB65204.

PT PRO polynucleotides used to produce polypeptide used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -

XX Claim 2; Fig 128; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytosolic activity. The PRO proteins  
CC can be used for targeted delivery of bioactive molecules, such as  
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridization probes, in  
CC chromosomal, and gene mapping, and in the generation of anti-sense RNA  
CC and DNA. They may also be used to produce transgenic animals which are  
CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridization probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.

XX Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

XX Alignment Scores:

XX Pred. No.: 7,266-88 Length: 415  
XX Score: 99.00 Matches: 99  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 100.00% Indels: 0  
XX Ds: 22 Gaps: 0

US-10-059-395-142 (1-99) x AAF44164 (1-415)

OY 1 MetLysileProValleuProAlaValleuLeuSerLeuLeuValleuHisSerAla 20  
DB 13 ATGAAGATCCCGCTCTTCTCCGATGGCTCTCTCTCTCTCTCTCTCTCTCTCTGCC 72  
OY 21 GInGlyAlaThrLeuGlyGlyProGluGluGluGluSerThrIleGluAsnTyrLaseArg 40  
DB 73 CAGGAGACCAACCTCGGTGTGTCTCTAGGAGAAAGAACACCATTTAGATTCGTCACGA 132

OY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
DB 133 CCCGAGGCTTTAAACACCCCGTCTCTGACATCAACAAATTCGATCTGCTTTAAGGCT 192  
OY 61 AspGluPheLeuAsnThrPheAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
DB 193 GATGAGTCTCGAATCGGACGCGCTCTTGTAGCTATCAAAAGGAAATCTCTTCTCTC 252  
OY 81 AsnTPAAPAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
DB 253 AACTGGATGCTTCTCTTCAAGCTGAAGACTGAGAGCGCAACTCTCTGATGCCAG 309

RESULT 6

AACTG7491  
ID AACG7491 standard; cDNA; 415 BP.

AACTG7491;  
AC AACG7491;  
XX 28-FEB-2001 (first entry)

DT 28-FEB-2001 (first entry)

DE Human angiogenesis-associated protein PRO826 cDNA, SEQ ID NO:157.

XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
XX cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
XX angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
XX myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
XX Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
XX Alzheimer's disease; Huntington's disease; stroke; drug screening;  
XX gene therapy; transgenic animal; ss.

XX Homo sapiens.

XX MO200053753-A2.

XX 14-SEP-2000.

XX 05-JAN-2000; 2000WO-US00219.

XX 08-MAR-1999; 99WO-US05028.  
XX 12-MAR-1999; 99US-0123957.  
XX 14-MAY-1999; 99US-0134287.  
XX 02-JUN-1999; 99WO-US12252.  
XX 23-JUN-1999; 99US-0141037.  
XX 20-JUL-1999; 99US-0144758.  
XX 26-JUL-1999; 99US-0145698.  
XX 01-SEP-1999; 99WO-US20111.  
XX 08-SEP-1999; 99WO-US20594.  
XX 15-SEP-1999; 99WO-US21090.  
XX 15-SEP-1999; 99WO-US21547.  
XX 05-OCT-1999; 99WO-US23089.  
XX 30-NOV-1999; 99WO-US28313.  
XX 30-NOV-1999; 99WO-US28409.  
XX 02-DEC-1999; 99WO-US28564.  
XX 02-DEC-1999; 99WO-US28565.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Piltti RM, Watanabe CK, Williams PM, Wood WI;

DR WPI: 2001-090793/10.  
DR P-PSDB; AAB53094.

XX New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -

XX Claim 58; Fig 61; 293pp; English.

XX The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097) and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells

comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO protein, agonists or antagonists of a PRO protein, and compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or PRO agonist or antagonist; a retroviral gene therapy vector comprising a PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, osteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential therapeutic agents. The present sequence represents a cDNA encoding a PRO protein of the invention.

Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

## Alignment Scores:

|                        |          |               |     |
|------------------------|----------|---------------|-----|
| Pred. No.:             | 7,26e-88 | Length:       | 415 |
| Score:                 | 99.00    | Matches:      | 99  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 22       | Gaps:         | 0   |

US-10-059-395-142 (1-99) x AAC97491 (1-415)

```
QY      1 MetLysIleProValIleuProAlaValIleuSerLeuValIleuHisSerAla 20
DB      13 ATGAAGATCCCGGTCCTCTCCGCGTGGTCTCTCTCTCTGTCACCTGCC 72
QY      21 GInGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTrpAlaSerArg 40
DB      73 CAGGAGCCACCCCTGGTGGTCTCTGAGGAAAGCACCATGAGATTATGCTCAGCA 132
QY      41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60
DB      133 CCCGAGGCGCTTTAAACCCCGCTCTGAAACATGACAAATTGCGATCGCTTAAAGCT 192
QY      61 AspGluPheLeuAsnTrpHisAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80
DB      193 GATGAGTCTCTGAACCTGGACGCGCTCTTGAAGTATCAAAAGAACTCTTCTC 252
QY      81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99
DB      253 AACTGGATGCTTCTTCTTAAGCTGAAGAGAGGAGGCAACTCTGATGCCAG 309
```

## RESULT 7

ABL95626  
ID ABL95626 standard; cDNA, 415 BP.

XX ABL95626;

XX 19-JUL-2002 (first entry)

DE Human angiogenesis related cDNA PRO826 SEQ ID NO: 131.

KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;

KW cardiant; cyrostatic; antiangiogenic; hypotensive; vulneryary;  
KM antiarteriosclerotic; gene; ss.

XX Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 28-JUL-2000; 2000US-220664P.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-0643657.

XX 23-AUG-2000; 2000WO-US23522.

XX 24-AUG-2000; 2000WO-US23328.

XX 07-SEP-2000; 2000US-230978P.

XX 15-SEP-2000; 2000US-000000P.

XX 18-SEP-2000; 2000US-0664610.

XX 18-SEP-2000; 2000US-0665350.

XX 24-OCT-2000; 2000US-242922P.

XX 08-NOV-2000; 2000US-0709238.

XX 08-NOV-2000; 2000WO-US30952.

XX 10-NOV-2000; 2000WO-US30873.

XX 01-DEC-2000; 2000WO-US32678.

XX 20-DEC-2000; 2000US-0747259.

XX 20-DEC-2000; 2000WO-US34956.

XX 22-JAN-2001; 2001US-0767609.

XX 28-FEB-2001; 2001US-0796498.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2001; 2001WO-US06666.

XX 09-MAR-2001; 2001US-0802706.

XX 14-MAR-2001; 2001US-0806889.

XX 22-MAR-2001; 2001US-0816744.

XX 05-APR-2001; 2001US-0828366.

XX 10-MAY-2001; 2001US-0854208.

XX 10-MAY-2001; 2001US-0854280.

XX 25-MAY-2001; 2001US-0866028.

XX 25-MAY-2001; 2001US-0866034.

XX 30-MAY-2001; 2001US-0870574.

XX 01-JUN-2001; 2001WO-US17443.

XX 20-JUN-2001; 2001WO-US19692.

XX 28-JUN-2001; 2001WO-US00000.

XX (GETH ) GENENTECH INC.

PA (BAKE) BAKER K P.

PA (FERR) FERRARA N.

PA (GERB) GERBER H.

PA (GERR) GERRITSEN M E.

PA (GODD) GODDARD A.

PA (GODO) GODOWSKI P J.

PA (GURN) GURNEY A L.

PA (HILL) HILLAN K J.

PA (MARS) MARSTERS S A.

PA (PANU) PAN J.

PA (PAON) PAONI N F.

PA (STER) STERHAN J F.

PA (WATA) WATANABE C K.

PA (WILL) WILLIAMS P M.

PA (WOOD) WOOD W I.

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,

PI Stephan UF, Watanabe CK, Williams PM, Wood WI, Ye W,

XX WPI; 2002-171999/22.

XX P-PSDB; ABB95488.



PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX  
 PS Claim 1; Fig 131; 567bp; English.  
 CC  
 CC The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a coding sequence of the invention.  
 CC  
 XX  
 SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 7,266-88 Length: 415  
 Score: 99.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0  
 US-10-059-395-142 (1-99) x ABL95626 (1-415)  
 QY 1 MetLysIleProValIleuProAlaValIleuLeuSerLeuLeuValIleuHisSerAla 20  
 DB 13 ATGAAGATCCCGGTCTCTCTCCGTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTGCC 72  
 QY 21 GInGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTyraLaseArg 40  
 DB 73 CAGGAGCCACCCCTGGTGGTCTCTGAGGAGAAACACCATTTAGATATGCGTACAGA 132  
 QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspIleLeuArgSerAlaPheLeuAla 60  
 DB 133 CCGGAGGCTTTAAACACCCGTTCTCTGAAACATGCAAAATTGCGATGCGTTTAAAGGCT 192  
 QY 61 AspGluPheLeuAsnThrPheIleAlaLeuPheGluSerIleLeuArgLysLeuProPheLeu 80  
 DB 133 GATGAGTTCCTGAATGAGACCCCTCTTGTAGCTATCAAAAGAACTCTTCTCTC 252  
 QY 81 AsnTPAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
 DB 253 AACTGGATGACCTTCTCTTAAGCTGAAGACTGAGAGGCAACTCTGATGCCAG 309  
 RESULT 8  
 ABL95626  
 ID ABL95626 standard; DNA; 415 BP.  
 AC ABL95626;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE cDNA encoding human Pro peptide #11.  
 XX  
 KW Human; ss; gene; PRO; secreted protein; transmembrane protein;  
 XX genetic disorder; tumour; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200224888-A2.  
 PD  
 XX  
 PD 28-MAR-2002.  
 XX  
 PF 29-AUG-2001; 2001WO-US27099.  
 XX  
 PR 01-SEP-2000; 2000US-229896P.  
 PR 05-SEP-2000; 2000US-230621P.  
 PR 22-SEP-2000; 2000US-235147P.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 12-JAN-2001; 2001US-261878P.

PR 16-JAN-2001; 2001US-261910P.  
 PR 16-JAN-2001; 2001US-261939P.  
 PR 16-JAN-2001; 2001US-262150P.  
 PR 25-JAN-2001; 2001US-264395P.  
 PR 02-FEB-2001; 2001US-265421P.  
 PR 09-FEB-2001; 2001US-267623P.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 09-MAR-2001; 2001US-274399P.  
 PR 03-APR-2001; 2001US-280982P.  
 PR 04-APR-2001; 2001US-282129P.  
 PR 04-APR-2001; 2001US-282199P.  
 PR 09-MAY-2001; 2001US-290589P.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US19692.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 XX  
 XX (GERTH ) GENENTECH INC.  
 XX  
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,  
 PI Gunney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
 PI Fong S;  
 XX  
 DR WPI; 2002-362426/39.  
 DR P-PSDB; ABG34040.  
 XX  
 PT New PRO polypeptides and polynucleotides encoding the polypeptides,  
 PT useful in gene therapy, chromosome identification, tissue typing, or  
 PT for genetic analysis of individuals with genetic disorders -  
 XX  
 PS Claim 2; Figure 21; 218bp; English.  
 XX  
 CC This invention relates to the cDNA and protein sequences of novel  
 CC secreted and transmembrane polypeptides PRO polypeptides. The  
 CC invention also comprises a method for producing the proteins of the  
 CC invention by recombinant means and antibodies specific for the protein  
 CC of the invention. The antibody may be used for detecting the PRO  
 CC proteins of the invention and may be used to modify their activity.  
 CC polynucleotides may be used as hybridisation probes for a cDNA library  
 CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
 CC construct hybridisation probes for mapping the gene which encodes that  
 CC PRO and for genetic analysis of individuals with genetic disorders, in  
 CC assays to identify other proteins or molecules involved in binding  
 CC reaction, to generate transgenic animals or knock-out animals which  
 CC in turn are useful in the development and screening of therapeutically  
 CC useful reagents, for chromosome identification, and tissue typing. The  
 CC PRO polypeptides are useful in gene therapy, and as molecular weight  
 CC markers for protein electrophoresis purposes. The sequences may  
 CC also be used to detect overexpression on PRO polypeptides in cancerous  
 CC tumours and for screening for differentially expressed genes using  
 CC microarray technology. The present sequence represents a cDNA encoding  
 CC a human PRO protein of the invention.  
 XX  
 SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 7,266-88 Length: 415  
 Score: 99.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0  
 US-10-059-395-142 (1-99) x ABL95626 (1-415)  
 QY 1 MetLysIleProValIleuProAlaValIleuLeuSerLeuLeuValIleuHisSerAla 20  
 DB 13 ATGAAGATCCCGGTCTCTCTCCGTGTCCTCTCTCTCTCTCTCTCTCTCTCTCTGCC 72  
 QY 21 GInGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAsnTyraLaseArg 40  
 DB 73 CAGGAGCCACCCCTGGTGGTCTCTGAGGAGAAACACCATTTAGATATGCGTACAGA 132



DE CDNA encoding human PRO protein, Seq ID No 145.  
 XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
 KW pericyte cell proliferation; chondrocyte cell proliferation;  
 KW tumour necrosis factor-alpha; gene; ss.  
 XX Homo sapiens.  
 OS  
 PN WO200208288-A2.  
 XX  
 PD 31-JAN-2002.  
 XX  
 PF 29-JUN-2001; 2001WO-US21066.  
 XX  
 PR 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220585P.  
 PR 25-JUL-2000; 2000US-220605P.  
 PR 25-JUL-2000; 2000US-220607P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220638P.  
 PR 25-JUL-2000; 2000US-220664P.  
 PR 25-JUL-2000; 2000US-220666P.  
 PR 26-JUL-2000; 2000US-220893P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23528.  
 PR 15-SEP-2000; 2000US-000000P.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 28-NOV-2000; 2000US-253646P.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001WO-US17092.  
 XX  
 PA (GENENTECH INC.  
 XX  
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
 DR P-PSDB; A083664.  
 DR  
 DR MPI; 2002-172001/22.  
 XX  
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,  
 PT useful for treating a PRO related disorder and for diagnosing tumours  
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
 PT tumour or liver tumour -  
 XX  
 PS Claim 2; Figure 145; 359pp; English.  
 XX  
 CC The invention relates to one hundred and twenty two nucleic acids  
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
 CC agonists and antagonists are useful for treating a PRO related disorder.  
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
 CC liver tumour. The PRO polypeptides are useful for stimulating the  
 CC proliferation of, or gene expression, in pericyte cells, for stimulating  
 CC the proliferation or differentiation of chondrocyte cells, for  
 CC stimulating the release of tumour necrosis factor-alpha from human blood,  
 CC for stimulating or inhibiting the proliferation of normal human dermal  
 CC fibroblast cells. The PRO polypeptide may also be used as molecular  
 CC weight markers and for tissue typing. The PRO nucleic acids have  
 CC applications in molecular biology, including use as hybridisation probes,  
 CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human  
 CC PRO protein coding sequences of the invention.  
 XX  
 SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
 Alignment Scores: 7.26e-88 Length: 415  
 Pred. No.:

Score: 99.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0  
 US-10-059-395-142 (1-99) x ABK33608 (1-415)  
 QY 1 MetlysiLeProValIeuProAlaValIeuLeuSerLeuValIeuHisSerAla 20  
 DB 13 ATGAAGATCCCGGCTCTTCTCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTG 72  
 QY 21 GInGIyAlaThrLeuGIyGIyProGIuGIuIuSerThrIIeGIyAsnTyAlaSerArg 40  
 DB 73 CAGGAGCCACCCCTGGTGTCTCTGAGGAAGAACCATTCGAAATTAATCGTCACGA 132  
 QY 41 ProGIuAlaPheAsnThrProPheLeuAsnIIeAlaPheLeuArgSerAlaPheIyAla 60  
 DB 133 CCGAGGCGCTTTAAACCCCGTCTCGAACAATCGAATTCGATCGCTTTAAGGCT 192  
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 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes cell stimulation;  
 KW retinal disorder; retinitis pigmentosa; kidney disorder;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
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AC 22-APR-2003 (first entry)
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KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disease;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.
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PR 10-AUG-1998; 98US-095816P.  
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PR 17-AUG-1998; 98US-096768P.  
PR 17-AUG-1998; 98US-096773P.  
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PR 17-AUG-1998; 98US-096894P.  
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PR 23-JUN-1999; 99US-141037P.  
PR 07-JUL-1999; 99US-143048P.

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US-10-059-395-142 (1-99) x ABX77843 (1-415)

QY 1 MettVilLeProValleuProAlaValleuSerLeuValleuHisSerAla 20



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 09:36:04 ; Search time 264 Seconds

(without alignments)  
1235.509 Million cell updates/sec

Title: US-10-059-395-142

Sequence: 1 MKIPVLPAVLLSLVLSA.....LNWDAPFKLGRSATPPAQ 99

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2190069 seqs, 1647345023 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4373282

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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## ALIGNMENTS

RESULT 1  
US-09-989-722-200  
Sequence 200, Application US/09989722  
Patent No. US20020072067A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desmoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
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| 19 | PRIOR FILING DATE: 1998-06-25        |            |
| 20 | PRIOR APPLICATION NUMBER: 60/0906955 |            |
| 21 | PRIOR FILING DATE: 1998-06-25        |            |
| 22 | PRIOR APPLICATION NUMBER: 60/0906566 |            |
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| 24 | PRIOR APPLICATION NUMBER: 60/0908622 |            |
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| 29 | PRIOR FILING DATE: 1998-07-01        |            |
| 30 | PRIOR APPLICATION NUMBER: 60/0914787 |            |
| 31 | PRIOR FILING DATE: 1998-07-02        |            |
| 32 | PRIOR APPLICATION NUMBER: 60/0915444 |            |
| 33 | PRIOR FILING DATE: 1998-07-01        |            |
| 34 | PRIOR APPLICATION NUMBER: 60/0915159 |            |
| 35 | PRIOR FILING DATE: 1998-07-02        |            |
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| 39 | PRIOR FILING DATE: 1998-07-02        |            |
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| 42 | PRIOR APPLICATION NUMBER: 60/0919822 |            |
| 43 | PRIOR FILING DATE: 1998-07-07        |            |
| 44 | PRIOR APPLICATION NUMBER: 60/0921822 |            |
| 45 | PRIOR FILING DATE: 1998-07-09        |            |

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| Score:                 | 99.00    |
| Percent Similarity:    | 100.00%  |
| Best Local Similarity: | 100.00%  |
| Query Match:           | 100.00%  |
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| Indels:                | 0        |
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US-10-059-395-142 (1-99) X US-09-989-723-200 (1-415)

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| QY | 1   | MetVst1aProValLeuProAlaValValLeuLeuSerLeuLeuValLeuHisSerAla   | 20  |
| Db | 13  | ATMAAGATCCCGGCTCTCTCGCCGAGTGCTCTCTCCCTCGAGTCTCACTCTGCC        | 72  |
| QY | 21  | GIING1ValAthrLeuGIvGIYProGIuGIuGIuSerThrIIegIuAsnTYraIaSerArg | 40  |
| Db | 73  | CAGGAGGCCACCTGGGTGTGTCTTAGAGAAAGAACCACTTAGAGATTAGCGCTACGA     | 123 |
| QY | 41  | ProGIuAlaIphAsnThrProPheLeuAsnIIeAspYsLeuArgSerAlaPheYsAla    | 60  |
| Db | 133 | CCCGAGGCGCTTTAAACACCCCTTCTCGAACATCGCAATATGGCATCTGCGTTTAAAGCT  | 192 |
| QY | 61  | AspGIuPheLeuAsnTrpH1aIaLeuPheGIuSerIIeLYsArgYsLeuProPheLeu    | 80  |
| Db | 193 | GATGAGTCTCGAACTGAGCGACCCCTCTTAGAGTCTATCAAAAGAAACTCTCTTCTCTC   | 253 |
| QY | 81  | AsnTrpAspAlaPheProYsLeuYsGIYLeuArgSerAlaThrProAspAlaGln       | 99  |

Db 253 AACTGGATGCGCTTCTTAAGCTGAAGACTAGAGAGCCCACTCTATGCCAG 309  
RESULT 3  
US-09-989-279-200  
Sequence 200, Application US/09989279  
Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Rong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gruney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C56  
CURRENT APPLICATION NUMBER: US/09/989,279  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
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PRIOR APPLICATION NUMBER: 60/090254



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| 2  | PRIOR APPLICATION NUMBER: 60/090343 |
| 3  | PRIOR FILING DATE: 1998-06-23       |
| 4  | PRIOR APPLICATION NUMBER: 60/090355 |
| 5  | PRIOR FILING DATE: 1998-06-23       |
| 6  | PRIOR APPLICATION NUMBER: 60/090429 |
| 7  | PRIOR FILING DATE: 1998-06-24       |
| 8  | PRIOR APPLICATION NUMBER: 60/090431 |
| 9  | PRIOR FILING DATE: 1998-06-24       |
| 10 | PRIOR APPLICATION NUMBER: 60/090435 |
| 11 | PRIOR FILING DATE: 1998-06-24       |
| 12 | PRIOR APPLICATION NUMBER: 60/090444 |
| 13 | PRIOR FILING DATE: 1998-06-24       |
| 14 | PRIOR APPLICATION NUMBER: 60/090445 |
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| 17 | PRIOR FILING DATE: 1998-06-24       |
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| 25 | PRIOR FILING DATE: 1998-06-24       |
| 26 | PRIOR APPLICATION NUMBER: 60/090676 |
| 27 | PRIOR FILING DATE: 1998-06-25       |
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| 30 | PRIOR APPLICATION NUMBER: 60/090680 |
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| 38 | PRIOR APPLICATION NUMBER: 60/090862 |
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| 40 | PRIOR APPLICATION NUMBER: 60/090863 |
| 41 | PRIOR FILING DATE: 1998-06-26       |
| 42 | PRIOR APPLICATION NUMBER: 60/091360 |
| 43 | PRIOR FILING DATE: 1998-07-01       |
| 44 | PRIOR APPLICATION NUMBER: 60/091478 |
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| 46 | PRIOR APPLICATION NUMBER: 60/091544 |
| 47 | PRIOR FILING DATE: 1998-07-01       |
| 48 | PRIOR APPLICATION NUMBER: 60/091519 |
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| 52 | PRIOR APPLICATION NUMBER: 60/091633 |
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| 55 | PRIOR FILING DATE: 1998-07-07       |
| 56 | PRIOR APPLICATION NUMBER: 60/091982 |
| 57 | PRIOR FILING DATE: 1998-07-07       |
| 58 | PRIOR APPLICATION NUMBER: 60/092182 |
| 59 | PRIOR FILING DATE: 1998-07-09       |

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| Pred. No.:             | 5, 22e-92 |
| Score:                 | 99.00     |
| Percent Similarity:    | 100.00%   |
| Best Local Similarity: | 100.00%   |
| Query Match:           | 100.00%   |
| DB:                    | 9         |
| Gaps:                  | 0         |
| Matches:               | 99        |
| Conservative:          | 0         |
| Mismatches:            | 0         |
| Indels:                | 0         |
| Gaps:                  | 0         |

US-10-059-395-142 (1-99) x US-09-989-279-200 (1-415)

Dy  
1 MetVSIleProValIeuProAlaValIleuSerIeuValIeuHisSerAla 20

Dd  
13 ATGAAGATCCCGGCTCTTCCTGCCTGTGGTCTCTCCTCCTCGTGCTCACTCTGCC 72

|    |     |  |     |
|----|-----|--|-----|
| QY | 21  | GI <sup>1</sup> GL <sup>1</sup> VAL <sup>1</sup> ThrLeuGI <sup>1</sup> GL <sup>1</sup> ProGI <sup>1</sup> uGI <sup>1</sup> uSerThr <sup>1</sup> LeGI <sup>1</sup> uAn <sup>1</sup> Y <sup>1</sup> Val <sup>1</sup> As <sup>1</sup> Arg <sup>1</sup>  | 40  |
| Db | 73  | CAGGAGGACCCCTGGGTGTCTCTAGGAGAGAGACCATTTAGAAATTATGCTCAGCA   | 132 |
| QY | 41  | ProGI <sup>1</sup> uAl <sup>1</sup> A <sup>1</sup> PheAsn <sup>1</sup> Th <sup>1</sup> ProPheLeuAn <sup>1</sup> LeAs <sup>1</sup> uY <sup>1</sup> Leu <sup>1</sup> Arg <sup>1</sup> ser <sup>1</sup> Ala <sup>1</sup> Phe <sup>1</sup> Le <sup>1</sup> Val <sup>1</sup>  | 60  |
| Db | 133 | CCGAGAGCCTTTAAACCCCGTTCTGTGAACATCGCAAAATTGGCATCTGGGTTTAAAGCT   | 192 |
| QY | 61  | AspGI <sup>1</sup> uPheLeuAsn <sup>1</sup> Trp <sup>1</sup> His <sup>1</sup> Ala <sup>1</sup> LeuPheGI <sup>1</sup> uSer <sup>1</sup> Ile <sup>1</sup> Y <sup>1</sup> Val <sup>1</sup> Gly <sup>1</sup> Leu <sup>1</sup> ProPhe <sup>1</sup> Leu <sup>1</sup>  | 80  |
| Db | 193 | GAGAAATTCCTAACTGAGCAGCCCTCTTTGAGCTCATCAAAAGAAACCTCTCTTCCTC   | 252 |
| QY | 81  | Asn <sup>1</sup> Trp <sup>1</sup> Asp <sup>1</sup> Ala <sup>1</sup> Phe <sup>1</sup> Pro <sup>1</sup> Y <sup>1</sup> Leu <sup>1</sup> uY <sup>1</sup> GI <sup>1</sup> Leu <sup>1</sup> Arg <sup>1</sup> ser <sup>1</sup> Ala <sup>1</sup> Trp <sup>1</sup> Pro <sup>1</sup> Asp <sup>1</sup> Ala <sup>1</sup> Gln <sup>1</sup> | 99  |
| Db | 253 | AAC <sup>1</sup> TGGAGATCCCTTTCTTAAGCTGAAGAGACTGAGAGACGCACTCTCGAATGGCCAG   | 309 |

RESULT 4  
US-09-989-727-200  
; Sequence 200, Application US/09989727  
; Patent No. US2002007497A1  
; GENERAL INFORMATION:

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuclei  
 TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2730PIC65  
 CURRENT APPLICATION NUMBER: US/09/989,727  
 CURRENT FILING DATE: 2001-11-19  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/065186  
 PRIOR FILING DATE: 1997-11-12  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066770  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/075945  
 PRIOR FILING DATE: 1998-02-25  
 PRIOR APPLICATION NUMBER: 60/078910  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/083322  
 PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/087106  
 PRIOR FILING DATE: 1998-05-28  
 PRIOR APPLICATION NUMBER: 60/087607  
 PRIOR FILING DATE: 1998-06-02

[illegible]



[illegible]

APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC57  
CURRENT APPLICATION NUMBER: US/09/989,732  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

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DB: 10 Gaps: 0

US-10-059-395-142 (1-99) x US-09-989-732-200 (1-415)

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QY 21 GInGlyAlaThrLeuGlyGlyProGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 40  
DB 73 CAGGAGCCACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 132  
QY 41 ProGlyAlaPheAsnThrProPheLeuAsnIleAspLeuLeuArgSerAlaPheLeuVala 60  
DB 133 CCGGAGGCTTTACGCCCGCTTCTGAAACATCGACAAATTGCGATTCGCTTTAAGGCT 192  
QY 61 AppGlyPheLeuAsnTrpHisAlaLeuPheGlySerIleLeuArgSerAlaPheLeuVala 80  
DB 193 GATGAGTTCCTCAACGAGCGACCCCTTTGAGTCTATCAAAAGAACTTCCTTCCCTC 252  
QY 81 AsnTPAspAlaPheProLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 99  
DB 253 AACTGGATGCTCTTCTTAAGCTGAAGAGCTGAGAGCGCAACTCTGATGCCAG 309

RESULT 7  
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Sequence 200, Application US/09991073  
Patent No. US20020127576A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C15  
CURRENT APPLICATION NUMBER: US/09/991,073  
CURRENT FILING DATE: 2001-11-14  
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PRIOR FILING DATE: 1997-06-16  
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| 43 | PRIOR APPLICATION NUMBER: 60/091982-82 |
| 44 | PRIOR FILING DATE: 1998-07-07          |
| 45 | PRIOR APPLICATION NUMBER: 60/092182-82 |
| 46 | PRIOR FILING DATE: 1998-07-09          |

US-10-059-395-142 (1-99) x US-09-991-073-200 (1-415)

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| Db | 73  | CAGGAGGCCACCTGGGTGTCTGAGGAAAGAACCATTTGAGAAATTTATGCGTCACGA      | 132 |
| Qy | 41  | ProGluAlaPheAsnThrProPheIleuAsnIleAspTyrIleuArgSerAlaPheValAla | 60  |
| Db | 133 | CCCGAAGGCTTTAAACCCCGTCTCTGAACATCGCAATATGCAATCTGCGTTTAAAGCT     | 192 |
| Qy | 61  | AspGluPheLeuAsnTrpHisAlaLeuPheGInuSerIleTyrArgTyrLeuProPheLeu  | 80  |
| Db | 193 | GATGAGTTCCTGAACAGGACGCCCTCTTTGAGTCTATCAAAAGAAACCTCTCTCTC       | 252 |
| Qy | 81  | AsnTrpAspAlaPheProTyrLeuTyrGlyLeuArgSerAlaThrProAspAlaGln      | 99  |
| Db | 253 | AACGTGGAAATGCTTTCTTAAGCTGAAGAAAGATCGAAGCAACTCTCGAATGCCAG       | 309 |

RESULT 8  
US-09-990-442-200  
Sequence 200, Application US/09990442  
Patent No. US20020132252A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C8  
CURRENT APPLICATION NUMBER: US/09/990,442  
CURRENT FILING DATE: 2001-11-14  
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PRIOR FILING DATE: 1998-06-22  
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PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23







Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
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Query Match: 100.00% Indels: 0  
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Db 73 CAGGAGGCACCCCTGGTGGTCTTGAAGAAACACCATTTAGCAATTAAGCTCACGA 132  
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RESULT 10  
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Patent No. US2002013075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlesen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Klavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pat, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC25  
CURRENT APPLICATION NUMBER: US/09/993,604  
CURRENT FILING DATE: 2001-11-14  
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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Alignment Scores:

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US-10-059-395-142 (1-99) x US-09-993-604-200 (1-415)

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Db 193 GATGAGTTCTCGTAATGGAGAGCCCTCTTTGAGTCTATCAAAAGAAACTTCTTCTCTC 252
QY 81 AsnTPAspAlaPheProIysLeuIysGIyLeuArgSerAlaThrProAspAlaGln 99
Db 253 AACTGGATGCGCTTCTTAAGCTGAAGAGACTGAGAGAGGCACTCTGATGCCAG 309

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RESULT 11

US-09-990-456-200

Sequence 200, Application US/09990456

Patent No. US20020137890A1

GENERAL INFORMATION:

APPLICANT: Aehkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Matanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

[illegible]



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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

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Db 193 GATAGTCTCTGAACCTGACGACCCCTTGAAGTCATCAAAAGAAACTTCTTCTCTC 252  
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; Sequence 200, Application US/09992598

Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Thmas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C20  
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PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

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Qy 21 GlnGlyAlaThrLeuGlyGlyProGlnGlnGlnSerThrIleGlnAsnTyAlaSerArg 40  
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Qy 41 ProGlnAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLeuAla 60

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RESULT 14  
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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
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TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

FILE REFERENCE: P2730P1C6  
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PRIOR APPLICATION NUMBER: 60/091626  
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PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 5.22e-92 Length: 415  
Score: 99.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0



PRIOR APPLICATION NUMBER: 60/0916533  
 PRIOR FILING DATE: 1996-07-02  
 PRIOR APPLICATION NUMBER: 60/0919787  
 PRIOR FILING DATE: 1996-07-07  
 PRIOR APPLICATION NUMBER: 60/0919822  
 PRIOR FILING DATE: 1996-07-07  
 PRIOR APPLICATION NUMBER: 60/0921822  
 PRIOR FILING DATE: 1996-07-09

|                        |          |                 |
|------------------------|----------|-----------------|
| Pred. No.:             | 5,22e-92 | 415             |
| Score:                 | 99.00    | 99              |
| Percent Similarity:    | 100.00%  | Conservative: 0 |
| Best Local Similarity: | 100.00%  | Mismatches: 0   |
| Query Match:           | 100.00%  | Indels: 0       |
| DB:                    | 10       | Gaps: 0         |

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| QY | 1   | MeLys11eProVal1IleuPro1AlaVal1IleuSer1LeuVal1LeuH1Ser1A | 20  |
| Db | 13  | ARGAARATCCGGTCTTCTCGCGTGGTGTCTCTCCCTCTGGTGTCTC          | 72  |
| QY | 21  | GIINGLYALeTh1LeuGLYGLYProGIuGIuSerThr1IleGIuEnTYALAs    | 40  |
| Db | 73  | CAGGGAGCACCCCTGGGTGTCTCTAGAAGAAAGACATTTGAATTAAG         | 133 |
| QY | 41  | ProGIuALePheAsnTh1ProPheLeuAsn1IleAsp1LysLeuAGSer1A     | 60  |
| Db | 133 | CCCGAGGCTTTTAAACCCCGTTCTGTGAACATCGACAAATTGGCAT          | 193 |
| QY | 61  | AspGIuPheLeuAsn1TrpH1sAlaLeuPheGIuSer1IleYsARGLYsLeu    | 80  |
| Db | 193 | GATGAGTTCTCAACTGGGACGCCCTCTTTGAGTCTATCAAAAGAACT         | 253 |
| QY | 81  | Asn1TrpAspALePheProLys1LeuYsGLYLeuAGSer1ATrPAspALeG     | 99  |
| Db | 253 | AATCGGAATGCTTTTCTTAAGCTGAAGAGACTGAAGACGCAACTCTG         | 309 |

Search completed: November 28, 2003, 10:58:01  
Job time : 266 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 05:59:39 ; Search time 48 Seconds

(without alignments)  
327.374 Million cell updates/sec

Title: US-10-059-395-142

Perfect score: 510

Sequence: 1 MKIPLPAVVLSTLVLSA.....LWDAFPKLGKRSATPPAQ 99

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_19Jun03:\*

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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*

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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 510   | 100.0       | 99     | 20 | AAW67828    |
| 2          | 510   | 100.0       | 99     | 21 | AAV66681    |
| 3          | 510   | 100.0       | 99     | 22 | AAV66681    |
| 4          | 510   | 100.0       | 99     | 22 | AAV66681    |
| 5          | 510   | 100.0       | 99     | 22 | AAV66681    |
| 6          | 510   | 100.0       | 99     | 22 | AAV66681    |
| 7          | 510   | 100.0       | 99     | 22 | AAV66681    |
| 8          | 510   | 100.0       | 99     | 22 | AAV66681    |
| 9          | 510   | 100.0       | 99     | 23 | ABG34040    |

|    |       |       |      |    |          |                    |
|----|-------|-------|------|----|----------|--------------------|
| 10 | 510   | 100.0 | 99   | 23 | ABW4882  | Human PRO826 prote |
| 11 | 510   | 100.0 | 99   | 23 | AAU83664 | Human PRO protein, |
| 12 | 510   | 100.0 | 99   | 23 | AAU81964 | Human PRO826, Hom  |
| 13 | 510   | 100.0 | 99   | 24 | ABU59097 | Novel human secret |
| 14 | 510   | 100.0 | 99   | 24 | ABU59244 | Human secreted/cra |
| 15 | 510   | 100.0 | 99   | 24 | ABU59393 | Novel human secret |
| 16 | 510   | 100.0 | 99   | 24 | ABU60528 | Human secreted/cra |
| 17 | 510   | 100.0 | 99   | 24 | ABU58019 | Human PRO polypept |
| 18 | 510   | 100.0 | 99   | 24 | ABU58950 | Human secreted/cra |
| 19 | 510   | 100.0 | 99   | 24 | ABU13910 | Human PRO polypept |
| 20 | 510   | 100.0 | 99   | 24 | ABU10865 | Human PRO polypept |
| 21 | 421   | 82.5  | 85   | 23 | ABP69587 | Human polypeptide  |
| 22 | 278   | 54.5  | 96   | 23 | ABP69587 | Human polypeptide  |
| 23 | 255.5 | 50.1  | 88   | 23 | ABP72393 | Human polypeptide  |
| 24 | 77.5  | 15.2  | 1544 | 22 | ABW69002 | Murine protein iso |
| 25 | 72.5  | 14.2  | 500  | 21 | AAV40462 | Drosophila melanog |
| 26 | 72.5  | 14.2  | 505  | 21 | AAV40461 | Arabidopsis thalia |
| 27 | 72.5  | 14.2  | 612  | 21 | AAV40460 | Arabidopsis thalia |
| 28 | 72.5  | 14.2  | 629  | 21 | AAV31693 | Arabidopsis thalia |
| 29 | 72.5  | 14.2  | 634  | 21 | AAV31692 | Arabidopsis thalia |
| 30 | 72.5  | 14.2  | 741  | 21 | AAV31691 | Arabidopsis thalia |
| 31 | 71    | 13.9  | 749  | 21 | AAV52606 | Arabidopsis thalia |
| 32 | 71    | 13.9  | 758  | 21 | AAV51789 | Arabidopsis thalia |
| 33 | 71    | 13.9  | 842  | 21 | AAV52605 | Arabidopsis thalia |
| 34 | 71    | 13.9  | 851  | 21 | AAV51788 | Arabidopsis thalia |
| 35 | 71    | 13.9  | 876  | 21 | AAV52604 | Arabidopsis thalia |
| 36 | 71    | 13.9  | 885  | 21 | AAV51787 | Arabidopsis thalia |
| 37 | 70.5  | 13.8  | 731  | 22 | AAV95828 | Human protein sequ |
| 38 | 69.5  | 13.6  | 116  | 22 | AAV94219 | Human reproductive |
| 39 | 69.5  | 13.6  | 230  | 20 | AAV60056 | Human endometrium  |
| 40 | 69.5  | 13.6  | 479  | 21 | AAV50941 | Human adult skin c |
| 41 | 68.5  | 13.4  | 96   | 22 | AAV60384 | Human foetal prote |
| 42 | 68.5  | 13.4  | 601  | 22 | ABW66854 | Drosophila melanog |
| 43 | 66.5  | 13.0  | 531  | 22 | ABW66846 | C. pneumoniae prot |
| 44 | 66.5  | 13.0  | 692  | 20 | AAV35548 |                    |
| 45 | 65.5  | 12.8  | 361  | 24 | ABU11576 | Human MDT polypep  |

#### ALIGNMENTS

|          |   |
|----------|---|
| RESULT 1 |   |
| ID       | AAW67828 standard; Protein, 99 AA.  |
| XX       | AAW67828;   |
| XX       |   |
| DT       | 25-MAR-1999 (first entry)   |
| XX       |   |
| DE       | Human secreted protein encoded by gene 22 clone HFEAR41.                      |
| XX       |   |
| KW       | Human; secreted protein; fusion protein; gene therapy; protein therapy;       |
| KW       | diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;     |
| KW       | developmental abnormality; foetal deficiency; blood; allergy; renal;          |
| KW       | immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;         |
| KW       | inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;         |
| KW       | cognitive disorder; schizophrenia; prostate; obesity; osteoarthritis; thymus; |
| KW       | osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;       |
| KW       | endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.        |
| XX       |   |
| OS       | Homo sapiens.   |
| XX       |   |
| PN       | WO9842738-A1.   |
| XX       |   |
| PD       | 01-OCT-1998.  |
| XX       |   |
| PF       | 19-MAR-1998; 98WO-US05311.  |
| XX       |   |
| PR       | 30-MAY-1997; 97US-0050937.  |
| PR       | 21-MAR-1997; 97US-0041276.  |
| PR       | 21-MAR-1997; 97US-0041277.  |
| PR       | 21-MAR-1997; 97US-0041281.  |
| PR       | 21-MAR-1997; 97US-0042344.  |

| KW  | KM  | KX            | XX           | OS           | PN           | PN            | XX | PD | PF | XX |
|---|---|---------------|--------------|--------------|--------------|---------------|----|----|----|----|
| Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand | pharmaceutical; receptor immunoadhesin; gene mapping. | Homo sapiens. | MO963088-AZ. | 09-DEC-1999. | 02-JUN-1999; | 99WO-US12252. |    |    |    |    |
| PR  | 02-JUN-1998;  | 98US-0087607. |              |              |              |               |    |    |    |    |
| PR  | 02-JUN-1998;  | 98US-0087609. |              |              |              |               |    |    |    |    |
| PR  | 02-JUN-1998;  | 98US-0087759. |              |              |              |               |    |    |    |    |
| PR  | 03-JUN-1998;  | 98US-0087827. |              |              |              |               |    |    |    |    |
| PR  | 04-JUN-1998;  | 98US-0088621. |              |              |              |               |    |    |    |    |
| PR  | 04-JUN-1998;  | 98US-0088625. |              |              |              |               |    |    |    |    |
| PR  | 04-JUN-1998;  | 98US-0088628. |              |              |              |               |    |    |    |    |
| PR  | 04-JUN-1998;  | 98US-0088629. |              |              |              |               |    |    |    |    |
| PR  | 04-JUN-1998;  | 98US-0088630. |              |              |              |               |    |    |    |    |
| PR  | 04-JUN-1998;  | 98US-0088633. |              |              |              |               |    |    |    |    |
| PR  | 04-JUN-1998;  | 98US-0088626. |              |              |              |               |    |    |    |    |
| PR  | 05-JUN-1998;  | 98US-0088167. |              |              |              |               |    |    |    |    |
| PR  | 05-JUN-1998;  | 98US-0088202. |              |              |              |               |    |    |    |    |
| PR  | 05-JUN-1998;  | 98US-0088212. |              |              |              |               |    |    |    |    |
| PR  | 05-JUN-1998;  | 98US-0088217. |              |              |              |               |    |    |    |    |
| PR  | 09-JUN-1998;  | 98US-0088655. |              |              |              |               |    |    |    |    |
| PR  | 10-JUN-1998;  | 98US-0088622. |              |              |              |               |    |    |    |    |
| PR  | 10-JUN-1998;  | 98US-0088730. |              |              |              |               |    |    |    |    |
| PR  | 10-JUN-1998;  | 98US-0088734. |              |              |              |               |    |    |    |    |
| PR  | 10-JUN-1998;  | 98US-0088740. |              |              |              |               |    |    |    |    |
| PR  | 10-JUN-1998;  | 98US-0088741. |              |              |              |               |    |    |    |    |
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| PR  | 10-JUN-1998;  | 98US-0088810. |              |              |              |               |    |    |    |    |
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| PR  | 11-JUN-1998;  | 98US-0088861. |              |              |              |               |    |    |    |    |
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| PR  | 11-JUN-1998;  | 98US-0088876. |              |              |              |               |    |    |    |    |
| PR  | 12-JUN-1998;  | 98US-0089090. |              |              |              |               |    |    |    |    |
| PR  | 12-JUN-1998;  | 98US-0089105. |              |              |              |               |    |    |    |    |
| PR  | 16-JUN-1998;  | 98US-0089440. |              |              |              |               |    |    |    |    |
| PR  | 16-JUN-1998;  | 98US-0089512. |              |              |              |               |    |    |    |    |
| PR  | 16-JUN-1998;  | 98US-0089514. |              |              |              |               |    |    |    |    |
| PR  | 17-JUN-1998;  | 98US-0089532. |              |              |              |               |    |    |    |    |
| PR  | 17-JUN-1998;  | 98US-0089538. |              |              |              |               |    |    |    |    |
| PR  | 17-JUN-1998;  | 98US-0089598. |              |              |              |               |    |    |    |    |
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| PR  | 17-JUN-1998;  | 98US-0089600. |              |              |              |               |    |    |    |    |
| PR  | 17-JUN-1998;  | 98US-0089603. |              |              |              |               |    |    |    |    |
| PR  | 18-JUN-1998;  | 98US-0089801. |              |              |              |               |    |    |    |    |
| PR  | 18-JUN-1998;  | 98US-0089807. |              |              |              |               |    |    |    |    |
| PR  | 18-JUN-1998;  | 98US-0089908. |              |              |              |               |    |    |    |    |
| PR  | 19-JUN-1998;  | 98US-0089947. |              |              |              |               |    |    |    |    |
| PR  | 19-JUN-1998;  | 98US-0089948. |              |              |              |               |    |    |    |    |
| PR  | 19-JUN-1998;  | 98US-0089952. |              |              |              |               |    |    |    |    |
| PR  | 22-JUN-1998;  | 98US-0090246. |              |              |              |               |    |    |    |    |
| PR  | 22-JUN-1998;  | 98US-0090252. |              |              |              |               |    |    |    |    |
| PR  | 22-JUN-1998;  | 98US-0090254. |              |              |              |               |    |    |    |    |
| PR  | 23-JUN-1998;  | 98US-0090349. |              |              |              |               |    |    |    |    |
| PR  | 23-JUN-1998;  | 98US-0090     |              |              |              |               |    |    |    |    |

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PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
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PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091360.
PR 02-JUL-1998; 98US-0091478.
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PR 02-JUL-1998; 98US-0091528.
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PR 02-JUL-1998; 98US-0091546.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
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PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
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PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
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PR 17-AUG-1998; 98US-0096897.
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PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 24-AUG-1998; 98US-0097951.
PR 24-AUG-1998; 98US-0097952.
PR 24-AUG-1998; 98US-0097954.
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PR 24-AUG-1998; 98US-0097971.
PR 24-AUG-1998; 98US-0097974.
PR 24-AUG-1998; 98US-0097978.
PR 24-AUG-1998; 98US-0097979.
PR 24-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.

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PR 12-JAN-1999; 99US-0115565.
XX (GETH ) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
XX Wood WI, Yuan J;
XX WPI, 2000-072883/06.
XX N-PSDB; AA265018.
XX Membrane-bound proteins and related nucleotide sequences -
PT Claim 12; Fig 129; 822pp; English.
PS
XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX sequences have homology with proteins including LDL receptors, TIR
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences
XX will also be useful for the preparation of PRO polypeptides, especially
XX by recombinant techniques.
XX
SQ Sequence 99 AA;
Query Match 100.0%; Score 510; DB 21; Length 99;
Best Local Similarity 100.0%; Pred. No. 4.6e-57;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKIPVLPAVVLISLVLSAQCATTGPEESTIENYASRPAPFNTPLINDKLSAFKA 60
DB 1 MKIPVLPAVVLISLVLSAQCATTGPEESTIENYASRPAPFNTPLINDKLSAFKA 60
QY 61 DEFLNWHALFESIKRKRLPFLNWDAPPKLGKRSATPDAG 99
DB 61 DEFLNWHALFESIKRKRLPFLNWDAPPKLGKRSATPDAG 99
QY 61 DEFLNWHALFESIKRKRLPFLNWDAPPKLGKRSATPDAG 99
DB 61 DEFLNWHALFESIKRKRLPFLNWDAPPKLGKRSATPDAG 99
RESULT 3
AAB20117
ID AAB20117 standard; Protein; 99 AA.
XX
AC AAB20117;
XX
XX 30-APR-2001 (first entry)
DT
XX
XX Human immunostimulant PRO826.
DE
XX
XX PRO826; UNQ467; human; immune disease; autoimmune disease;
XX antineumatic; antiarthritic; antiinflammatory; antianaemic;
XX immunosuppressive; antithyroid; antidiabetic; neuroprotective;
XX hepatotropic; virucide; dermatological; antipsoptic;
XX antiaesthetic; antiallergic; immunostimulant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..22 /label= Signal_peptide
FT 23..99 /label= Mature_protein
FT /label= Mature_protein
FT Modified-site 22..28 /note= "N-myristoylation site"
FT Modified-site 90..96 /note= "N-myristoylation site"
FT /note= "N-myristoylation site"
FT 16..48 /note= "homology to peroxidase"
FT

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XX PN WO200105972-A1.  
 XX PD 25-JAN-2001.  
 XX PF 15-MAR-2000; 2000WO-US06884.  
 XX PR 20-JUL-1999; 99US-0144758.  
 XX (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godwaski PJ, Gurney AL,  
 XX Hillan KJ, Mark MR, Marscers SA, Pilti RM, Tumas D, Watanabe CK,  
 XX Wood WI;  
 XX WPI, 2001-103149/11.  
 XX N-PEDB; AAF30059.  
 XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
 XX diagnosing and treating immune-related disorders, such as multiple  
 XX sclerosis, rheumatoid arthritis and diabetes -  
 XX  
 XX PS Claim 20; Fig 20; 127pp; English.  
 XX  
 XX The present sequence is that of novel human immunomodulator PRO826  
 XX (UNQ467), as deduced from cDNA (see AAF30059) isolated from a pi  
 XX database screening. PRO826 has a mol.wt. of 11 kDa and a pI of  
 XX 7.47. The invention provides polynucleotides (see AAF30050-62)  
 XX encoding novel human PRO proteins (see AAB20108-20) including PRO826.  
 XX Claimed compositions comprising these proteins or their agonists  
 XX are useful for increasing infiltration of inflammatory cells into  
 XX a tissue of a mammal, stimulating or enhancing an immune  
 XX response, or increasing the proliferation of T-lymphocytes in a  
 XX mammal in response to an antigen. Claimed compositions comprising  
 XX a PRO polypeptide or its antagonist have the opposite effect. A  
 XX claimed method for treating an immune related disorder, such as a T  
 XX cell disorder, involves administering a PRO polypeptide, an agonist  
 XX antibody or an antagonist antibody. The disorder is selected from  
 XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 XX juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,  
 XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 XX vasculitis, sarcoidosis, autoimmune hemolytic anaemia, autoimmune  
 XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated  
 XX renal disease, demyelinated diseases (such as multiple sclerosis),  
 XX autoimmune chronic active hepatitis, primary biliary cirrhosis,  
 XX granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel  
 XX disease (ulcerative colitis and Crohn's disease), gluten-sensitive  
 XX enteropathy, Whipple's disease, (auto)immune-mediated skin diseases  
 XX (such as bullous skin disease, erythema multiforme and psoriasis),  
 XX allergic diseases (such as asthma, allergic rhinitis, atopic  
 XX dermatitis, food hypersensitivity and urticaria), immunologic  
 XX diseases of the lung and transplantation associated diseases (such  
 XX as graft rejection and graft-versus-host disease) (all claimed).  
 XX Claimed methods of diagnosing these disorders comprise detecting  
 XX the level of expression of the PRO gene. Also claimed are a method  
 XX of identifying a compound capable of inhibiting the expression or  
 XX activity of the PRO polypeptide, vectors, host cells, antibodies,  
 XX and a method of stimulating the proliferation of T lymphocytes  
 XX using PRO826.  
 XX  
 XX SQ Sequence 99 AA;  
 XX  
 XX Query Match 100.0%; Score 510; DB 22; Length 99;  
 XX Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
 XX Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 MKPIPLPAVVLISLVSAQATIGGPEESTIENYSRPAFTPTINDIKLSARFA 60  
 XX DB 1 MKPIPLPAVVLISLVSAQATIGGPEESTIENYSRPAFTPTINDIKLSARFA 60  
 XX QY 61 DEFLNMHALFESIKRKLPIPLNDAPPKLGLRSATPDQA 99  
 XX DB 61 DEFLNMHALFESIKRKLPIPLNDAPPKLGLRSATPDQA 99

RESULT 4  
 AAB65204  
 ID AAB65204 standard; Protein; 99 AA.  
 XX AC AAB65204;  
 XX DT 02-APR-2001 (first entry)  
 XX DE Human PRO826 (UNQ467) protein sequence SEQ ID NO:201.  
 XX KW Human; secreted and transmembrane protein; PRO; cytosolic;  
 XX cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
 XX diagnostic assay.  
 XX OS Homo sapiens.  
 XX PN WO200073454-A1.  
 XX PD 07-DEC-2000.  
 XX PF 30-MAR-2000; 2000WO-US08439.  
 XX PR 02-JUN-1999; 99WO-US12252.  
 XX PR 23-JUN-1999; 99US-0141037.  
 XX PR 07-JUL-1999; 99US-0143048.  
 XX PR 20-JUL-1999; 99US-0144758.  
 XX PR 26-JUL-1999; 99US-0145698.  
 XX PR 28-JUL-1999; 99US-0146222.  
 XX PR 17-AUG-1999; 99US-0149396.  
 XX PR 15-SEP-1999; 99WO-US21090.  
 XX PR 15-SEP-1999; 99WO-US21547.  
 XX PR 08-OCT-1999; 99US-0158663.  
 XX PR 30-NOV-1999; 99WO-US28213.  
 XX PR 01-DEC-1999; 99WO-US28301.  
 XX PR 16-DEC-1999; 99WO-US30095.  
 XX PR 20-DEC-1999; 99WO-US30911.  
 XX PR 05-JAN-2000; 2000WO-US00219.  
 XX PR 06-JAN-2000; 2000WO-US00376.  
 XX PR 11-FEB-2000; 2000WO-US03565.  
 XX PR 18-FEB-2000; 2000WO-US04341.  
 XX PR 22-FEB-2000; 2000WO-US04414.  
 XX PR 24-FEB-2000; 2000WO-US04914.  
 XX PR 02-MAR-2000; 2000WO-US05004.  
 XX PR 15-MAR-2000; 2000WO-US05841.  
 XX PR 20-MAR-2000; 2000WO-US06884.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Borstein D, Desnoyers L, Eaton DL;  
 XX Perrera N, Fong S, Garber H, Gerritsen ME, Goddard A, Godwaski PJ;  
 XX Grimaudo CJ, Gurney AL, Kljavin IO, Napier MA, Pan J, Paoni NF;  
 XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 XX Zhang Z;  
 XX WPI; 2001-032160/04.  
 XX N-PEDB; AAF4164.  
 XX PRO polynucleotides used to produce polypeptides used to target  
 XX bioactive molecules such as toxins, radiolabels or antibodies, to  
 XX specific cells, to cause targeted cell death -  
 XX  
 XX PS Claim 12; Fig 129; 935pp; English.  
 XX  
 XX The present invention describes human secreted and transmembrane PRO  
 XX proteins. The PRO proteins have cytostatic activity. The PRO proteins  
 XX can be used for targeted delivery of bioactive molecules, such as  
 XX toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
 XX sequences, and their fragments, can be used as hybridisation probes, in  
 XX chromosomal and gene mapping, and in the generation of anti-sense RNA  
 XX and DNA. They may also be used to produce transgenic animals which are



used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

Sequence 99 AA;

Query Match 100.0%; Score 510; DB 22; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPVAVLLSLVLSAQAATLGGPEBSSTIENVASRPEAFNTPLNIDKLSAFKA 60  
DB 1 MKIPVLPVAVLLSLVLSAQAATLGGPEBSSTIENVASRPEAFNTPLNIDKLSAFKA 60  
QY 61 DEFLNWHALFESIKRKLPLNWDAPFKLKGRLSATPDQ 99  
DB 61 DEFLNWHALFESIKRKLPLNWDAPFKLKGRLSATPDQ 99

# RESULT 5

AAB50916 standard; Protein; 99 AA.

XX AAB50916;

DT 21-MAR-2001 (first entry)

DE Human PRO826 protein.

XX Human; PRO; antiinflammatory; dermatological; antiarthritic;  
XX antirheumatic; cardiant; antihaemic; immunosuppressive; antithyroid;  
XX antidiabetic; nocrotic; neuroprotective; hepatocytic; virucide;  
XX antiallergic; antiaesthetic; immune related disorder;  
XX hepatobiliary disease; autoimmune disease; allergy.

OS Homo sapiens.

XX WO200073452-A2.

PD 07-DEC-2000.

PF 02-JUN-2000; 2000MO-US15264.

XX 02-JUN-1999; 99MO-US12252.

XX 20-JUL-1999; 99US-0144732.

XX 28-JUL-1999; 99US-0144758.

XX 01-SEP-1999; 99MO-US20111.

XX 15-SEP-1999; 99MO-US21547.

XX 29-OCT-1999; 99US-0162506.

XX 30-NOV-1999; 99MO-US28313.

XX 01-DEC-1999; 99MO-US28313.

XX 09-DEC-1999; 99US-0170262.

XX 20-DEC-1999; 99MO-US30911.

XX 05-JAN-2000; 2000MO-US00219.

XX 11-FEB-2000; 2000MO-US03565.

XX 18-FEB-2000; 2000MO-US04341.

XX 22-FEB-2000; 2000MO-US04342.

XX 14-FEB-2000; 2000MO-US04914.

XX 15-MAR-2000; 2000MO-US06884.

XX 20-MAR-2000; 2000MO-US07377.

XX 21-MAR-2000; 2000MO-US07532.

XX 30-MAR-2000; 2000MO-US08439.

XX 17-MAY-2000; 2000MO-US13705.

XX 22-MAY-2000; 2000MO-US14042.

PA (GENE) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;

XX Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;

XX Wood W;

XX MPI: 2001-025253/03.

XX N-PSDB; AAC91475.

PT Thirty three nucleic acids encoding PRO polypeptides which are useful

XX in the diagnosis and treatment of immune related disorders, e.g.

XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

XX thyroiditis and diabetes mellitus -

XX Claim 58; Fig 30; 218pp; English.

XX The present sequence is one of thirty three novel PRO polypeptides.

XX The PRO polypeptides, anti-PRO antibodies, agonists and

XX antagonists are useful for treating and diagnosing immune related

XX disorders such as systemic lupus erythematosus, rheumatoid arthritis,

XX osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,

XX systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's

XX syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

XX anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,

XX immune-mediated renal disease, demyelinating diseases of the central

XX and peripheral nervous systems (such as multiple sclerosis, idiopathic

XX demyelinating polynuropathy or Guillain-Barre syndrome, and chronic

XX inflammatory demyelinating polynuropathy), hepatobiliary diseases

XX (such as infectious, autoimmune chronic active hepatitis, primary

XX biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),

XX inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's

XX disease, autoimmune or immune-mediated skin diseases (such as bullous

XX skin diseases, erythema multiforme, contact dermatitis, psoriasis),

XX allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,

XX food hypersensitivity and urticaria), immunological diseases of the

XX lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis

XX and hypersensitivity pneumonitis), transplantation associated diseases

XX including graft rejection and graft-versus-host diseases.

XX Sequence 99 AA;

XX Query Match 100.0%; Score 510; DB 22; Length 99;

XX Best Local Similarity 100.0%; Pred. No. 4.6e-57;

XX Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPVAVLLSLVLSAQAATLGGPEBSSTIENVASRPEAFNTPLNIDKLSAFKA 60  
DB 1 MKIPVLPVAVLLSLVLSAQAATLGGPEBSSTIENVASRPEAFNTPLNIDKLSAFKA 60

QY 61 DEFLNWHALFESIKRKLPLNWDAPFKLKGRLSATPDQ 99

DB 61 DEFLNWHALFESIKRKLPLNWDAPFKLKGRLSATPDQ 99

# RESULT 6

AAB53094 standard; Protein; 99 AA.

XX AAB53094;

DT 28-FEB-2001 (first entry)

DE Human angiogenesis-associated protein PRO826, SEQ ID NO:158.

XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;

XX cardiac hypertrophy; cardiovascular disorder; endothelial disorder;

XX angiogenic disorder; atherosclerosis; osteoporosis; hypertension;

XX myocardial infarction; diabetic retinopathy; rheumatoid arthritis;

XX Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;

XX Alzheimer's disease; Huntington's disease; stroke; drug screening;

XX gene therapy; transgenic animal.

XX Homo sapiens.

XX WO20053753-A2.  
 XX 14-SEP-2000.  
 XX 05-JAN-2000; 2000WO-US00219.  
 XX 08-MAR-1999; 99WO-US05028.  
 XX 12-MAR-1999; 99US-0123957.  
 XX 14-MAY-1999; 99US-0134287.  
 XX 02-JUN-1999; 99WO-US12252.  
 XX 23-JUN-1999; 99US-0141037.  
 XX 20-JUL-1999; 99US-0144758.  
 XX 26-JUL-1999; 99US-0145698.  
 XX 01-SEP-1999; 99WO-US20111.  
 XX 08-SEP-1999; 99WO-US20594.  
 XX 15-SEP-1999; 99WO-US21090.  
 XX 15-SEP-1999; 99WO-US21547.  
 XX 05-OCT-1999; 99WO-US23089.  
 XX 30-NOV-1999; 99WO-US28313.  
 XX 30-NOV-1999; 99WO-US28409.  
 XX 02-DEC-1999; 99WO-US28564.  
 XX 02-DEC-1999; 99WO-US28565.  
 XX (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
 PI Godowski RJ, Gurney AT, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
 PI Paoni NF, Picti RM, Watanabe CK, Williams PM, Wood WJ;  
 DR WPI: 2001-090793/10.  
 DR N-PSDB; AAC97491.  
 XX New isolated nucleic acid for producing a PRO polypeptide, analyzing  
 PT genetic disorders and treating cardiovascular, endothelial or  
 PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
 XX Claim 69; Fig 62; 293pp; English.  
 XX The invention relates to novel human angiogenesis-associated proteins  
 CC designated PRO proteins (AA53064-B53097), and to nucleic acids encoding  
 CC PRO proteins. The invention also relates to vectors and host cells  
 CC comprising a PRO nucleic acid, the recombinant production of a PRO  
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
 CC compounds which inhibit the expression of a PRO gene. The invention  
 CC additionally encompasses methods of identifying modulators of PRO  
 CC expression or activity; diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
 CC mutations in a PRO gene, or the expression level of a PRO gene within a  
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
 CC administration of a PRO protein, or an agonist or antagonist thereof.  
 CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
 CC agonists and PRO antagonists may be used as therapeutic agents to treat  
 CC cardiovascular, endothelial or angiogenic disorders, such as  
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
 CC disease, or stroke. PRO nucleic acids are additionally useful in the  
 CC recombinant production of PRO proteins, as hybridization probes to  
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
 CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
 CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
 CC animals useful for the development and screening of potential  
 CC therapeutic agents. The present sequence represents a PRO protein of the  
 CC invention.  
 CC Sequence 99 AA;

Query Match 100.0%; Score 510; DB 22; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 MKIPVLPAVVLISLVTHSAQATLGGPEESTIENTYASRPENATPFLINDKRSAPKA 60  
 Db 1 MKIPVLPAVVLISLVTHSAQATLGGPEESTIENTYASRPENATPFLINDKRSAPKA 60  
 Oy 61 DEFLNMAHLPFESIRKLPFLNMDAPFKLKGSRATPPAQ 99  
 Db 61 DEFLNMAHLPFESIRKLPFLNMDAPFKLKGSRATPPAQ 99  
 RESULT 7  
 ID ABP69586 standard; Protein; 99 AA.  
 AC ABP69586;  
 AC 20-JAN-2003 (first entry)  
 DT 20-JAN-2003 (first entry)  
 DE Human polypeptide SEQ ID NO 1633.  
 XX Human; genome mapping; gene therapy; food supplement; virus; fungus;  
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;  
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;  
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
 KW arthritis; cytostatic; immunomodulator; neotropic; neuroprotective;  
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
 KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
 KW antiarthritic.  
 XX Homo sapiens.  
 OS  
 XX WO200270539-A2.  
 PD 12-SEP-2002.  
 PF 05-MAR-2002; 2002WO-US05095.  
 PR 05-MAR-2001; 2001US-0799451.  
 XX (HYSE-) HYSEQ INC.  
 XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
 PI Wehrman T, Wang J, Wang D, Drmanac RT;  
 DR WPI: 2002-759812/82.  
 DR N-PSDB; ABZ11803.  
 XX New polynucleotides comprising sequences assembled from expressed  
 PT sequence tags (ESTs), useful for treating cell-proliferative, or  
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or  
 PT platelet or coagulation disorders -  
 XX Claim 9; SEQ ID NO 1633; 1012pp + Sequence Listing; English.  
 XX The invention relates to an isolated polynucleotide (I) comprising a  
 CC nucleotide sequence selected from any of 948 sequences  
 CC (ABZ11119-ABZ12066) or their mature protein coding portion, active domain  
 CC coding protein or complementary sequences. The polynucleotides are useful  
 CC for identifying expressed genes or for physical mapping of human genome.  
 CC The encoded polypeptides (ABP68902-ABP69849) are useful as molecular  
 CC weight markers, as a food supplement, for generating antibodies, in  
 CC medical imaging, screening and diagnostic assays and for treating  
 CC cell-proliferative disorders (cancer), neurodegenerative diseases  
 CC (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple  
 CC sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid  
 CC disorders, platelet or coagulation disorders, wound, burns, incision,  
 CC ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,  
 CC parasitic), arthritis, etc.  
 CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 99 AA;

Query Match 100.0%; Score 510; DB 23; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPVAVVLSLVLSAQAATGCGPEESTIENVASRPAFTPTPLNIDKLSAFKA 60  
 DB 1 MKIPVLPVAVVLSLVLSAQAATGCGPEESTIENVASRPAFTPTPLNIDKLSAFKA 60  
 QY 61 DEFLNMHALFESIKRKLPLNWDAPPKLGLRSATPDQ 99  
 DB 61 DEFLNMHALFESIKRKLPLNWDAPPKLGLRSATPDQ 99

## RESULT 8

ABB95488  
 ID ABB95488 standard; Protein; 99 AA.

XX ABB95488;

DT 19-JUL-2002 (first entry)

DE Human angiogenesis related protein PRO826 SEQ ID NO: 132.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW carliant; cytosolic; antiangiogenic; hypotensive; vulnerary;  
 KW antarteriosclerotic.

XX Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

PF 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 28-JUL-2000; 2000WO-US20710.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-0643657.

XX 23-AUG-2000; 2000WO-US23322.

XX 07-SEP-2000; 2000WO-US23328.

XX 15-SEP-2000; 2000US-230978P.

XX 18-SEP-2000; 2000US-0664610.

XX 18-SEP-2000; 2000US-0665350.

XX 24-OCT-2000; 2000US-242922P.

XX 08-NOV-2000; 2000US-0709238.

XX 08-NOV-2000; 2000WO-US30952.

XX 10-NOV-2000; 2000WO-US30873.

XX 01-DEC-2000; 2000WO-US32678.

XX 20-DEC-2000; 2000WO-US34956.

XX 22-JAN-2001; 2001US-0767609.

XX 28-FEB-2001; 2001US-0796498.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2001; 2001WO-US06666.

XX 09-MAR-2001; 2001US-0802706.

XX 14-MAR-2001; 2001US-0808689.

XX 22-MAR-2001; 2001US-0816744.

XX 05-APR-2001; 2001US-0828366.

XX 10-MAY-2001; 2001US-0854208.

XX 10-MAY-2001; 2001US-0854280.

XX 25-MAY-2001; 2001US-0866028.

XX 25-MAY-2001; 2001US-0866034.

XX 25-MAY-2001; 2001WO-US17092.

PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 28-JUN-2001; 2001WO-US00000.

XX (GETH) GENENTECH INC.

PA (BAKE) BAKER K P.

PA (FERR) FERRARA N.

PA (GERB) GERBER H.

PA (GERR) GERRTSEN M E.

PA (GODD) GODDARD A.

PA (GODD) GODDARD A.

PA (GURN) GURNEY A L.

PA (HILL) HILLAN K J.

PA (MARS) MARSTERS S A.

PA (PANJ) PAN J.

PA (PAON) PAONI N F.

PA (STEP) STEPHAN J F.

PA (WATA) WATANABE C K.

PA (WILL) WILLIAMS P M.

PA (WOOD) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Paoni NF,

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-171999/22.

DR N-PSDB; AB195626.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial

PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 11; Fig 132; 567pp; English.

PS The present invention provides the protein and coding sequences of human

XX PRO proteins. These are useful for treating or diagnosing a

CC cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound

CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 99 AA;

Query Match 100.0%; Score 510; DB 23; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPVAVVLSLVLSAQAATGCGPEESTIENVASRPAFTPTPLNIDKLSAFKA 60  
 DB 1 MKIPVLPVAVVLSLVLSAQAATGCGPEESTIENVASRPAFTPTPLNIDKLSAFKA 60  
 QY 61 DEFLNMHALFESIKRKLPLNWDAPPKLGLRSATPDQ 99  
 DB 61 DEFLNMHALFESIKRKLPLNWDAPPKLGLRSATPDQ 99

## RESULT 9

ABB34040  
 ID ABB34040 standard; Protein; 99 AA.

XX ABB34040;

DT 15-JUL-2002 (first entry)

DE Human Pro peptide #11.

XX Human; PRO; secreted protein; transmembrane protein;

XX genetic disorder; tumour; cancer.

OS Homo sapiens.  
 XX MO200224888-A2.  
 XX  
 PD 28-MAR-2002.  
 XX  
 PF 29-AUG-2001; 2001WO-US27099.  
 XX  
 PR 01-SEP-2000; 2000US-229896P.  
 PR 05-SEP-2000; 2000US-230621P.  
 PR 22-SEP-2000; 2000US-235147P.  
 PR 10-NOV-2000; 2000WO-US310873.  
 PR 12-JAN-2001; 2001US-261878P.  
 PR 16-JAN-2001; 2001US-261910P.  
 PR 16-JAN-2001; 2001US-261939P.  
 PR 16-JAN-2001; 2001US-262150P.  
 PR 25-JAN-2001; 2001US-264395P.  
 PR 02-FEB-2001; 2001US-266421P.  
 PR 09-FEB-2001; 2001US-267623P.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 09-MAR-2001; 2001US-274399P.  
 PR 03-APR-2001; 2001US-280982P.  
 PR 04-APR-2001; 2001US-282129P.  
 PR 04-APR-2001; 2001US-282199P.  
 PR 09-MAY-2001; 2001US-290589P.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
 PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
 PI Fong S;  
 XX  
 DR WPI; 2002-362426/39.  
 XX  
 N-PSDB; ABR69971.  
 XX  
 PT New PRO polypeptides and polynucleotides encoding the polypeptides,  
 PT useful in gene therapy, chromosome identification, tissue typing, or  
 PT for genetic analysis of individuals with genetic disorders -  
 XX  
 XX Claim 11; Figure 22; 218pp; English.  
 PS  
 PS  
 PS  
 CC This invention relates to the cDNA and protein sequences of novel  
 CC secreted and transmembrane polypeptides PRO polypeptides. The  
 CC invention also comprises a method for producing the proteins of the  
 CC invention by recombinant means and antibodies specific for the protein  
 CC of the invention. The antibody may be used for detecting the PRO  
 CC polypeptides and may be used to modify their activity.  
 CC polynucleotides may be used as hybridisation probes for a cDNA library  
 CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
 CC construct hybridisation probes for mapping the gene which encodes that  
 CC PRO and for genetic analysis of individuals with genetic disorders, in  
 CC assays to identify other proteins or molecules involved in binding  
 CC reaction, to generate transgenic animals or knock-out animals which in  
 CC turn are useful in the development and screening of therapeutically  
 CC useful reagents, for chromosome identification, and tissue typing. The  
 CC PRO polypeptides are useful in gene therapy, and as molecular weight  
 CC markers for protein electrophoresis purposes. The sequences may  
 CC also be used to detect overexpression on PRO polypeptides in cancerous  
 CC tumours and for screening for differentially expressed genes using  
 CC microarray technology. The present sequence represents a human PRO  
 CC protein of the invention.  
 XX  
 SQ Sequence 99 AA;  
 Query Match 100.0%; Score 510; DB 23; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 4,66-57;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKIPVLPAVLLSLVLSAQAATLGGPEEESTIENYASRPEAFNTPFLNIDKLSAFKA 60  
 Db 1 MKIPVLPAVLLSLVLSAQAATLGGPEEESTIENYASRPEAFNTPFLNIDKLSAFKA 60  
 Qy 61 DEFLNHALFESIRKLPFLNMDAFPCLKGLRSNTPPAQ 99  
 Db 61 DEFLNHALFESIRKLPFLNMDAFPCLKGLRSNTPPAQ 99  
 RESULT 10  
 ABB84882  
 ID ABB84882 standard; Protein; 99 AA.  
 XX  
 AC ABB84882;  
 XX  
 DT 16-MAY-2002 (first entry)  
 XX  
 DB Human PRO826 protein sequence SEQ ID NO:122.  
 XX  
 KW Human; angiogenesis; cardiast; cytostatic; antiangiogenic; hypotensive;  
 KW vunerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; gene mapping.  
 XX  
 OS Homo sapiens.  
 XX  
 XX MO200200690-A2.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 20-JUN-2001; 2001WO-US19692.  
 XX  
 PR 23-JUN-2000; 2000US-213637P.  
 PR 20-JUL-2000; 2000US-219566P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220664P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 02-AUG-2000; 2000US-222695P.  
 PR 17-AUG-2000; 2000US-0643657.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 18-SEP-2000; 2000US-0665360.  
 PR 24-OCT-2000; 2000US-242922P.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-DEC-2000; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 XX  
 PA (GETH ) GENENTECH INC.

XX Baker KP, Ferrera N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF, Stephan JF, Watanabe CK, Williams PM, Wood WT, Ye W, WPI: 2002-090516/12.  
 DR N-PSDB; ABL88137.  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -  
 PS Claim 11; Fig 132; 565pp; English.  
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABL884817 to ABL885003. The PRO proteins and polynucleotides have cardiant, cyostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.  
 XX Sequence 99 AA;  
 SQ  
 Query Match 100.0%; Score 510; DB 23; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKIPVLPVAVLLSLVLSAQAATLGGPEESTIENTYASRPAFTPTPLNTDKLSAFKA 60  
 DB 1 MKIPVLPVAVLLSLVLSAQAATLGGPEESTIENTYASRPAFTPTPLNTDKLSAFKA 60  
 QY 61 DEFLNWHALFESIKRKLPLNWDAPPKLKGLSATPDAQ 99  
 DB 61 DEFLNWHALFESIKRKLPLNWDAPPKLKGLSATPDAQ 99  
 RESULT 11  
 ID AUB83664 standard; Protein; 99 AA.  
 AC AUB83664;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE Human PRO protein, Seq ID No 146.  
 XX  
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200208288-A2.  
 XX  
 PD 31-JAN-2002.  
 XX  
 PF 29-JUN-2001; 2001WO-US21066.  
 XX  
 PR 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220585P.  
 PR 25-JUL-2000; 2000US-220605P.  
 PR 25-JUL-2000; 2000US-220607P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220638P.

PR 25-JUL-2000; 2000US-220664P.  
 PR 25-JUL-2000; 2000US-220666P.  
 PR 26-JUL-2000; 2000US-220893P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 15-SEP-2000; 2000WO-000000P.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 28-NOV-2000; 2000US-253646P.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001WO-US17092.  
 XX  
 XX (GENTECH ) GENENTECH INC.  
 PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT; WPI: 2002-172001/22.  
 DR N-PSDB; ABLK33608.  
 XX  
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour -  
 PT  
 PS Claim 11; Figure 146; 359pp; English.  
 XX  
 CC The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the release of tumour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AUB83592-AUB83713 represent human PRO protein sequences of the invention.  
 CC  
 CC  
 CC  
 XX  
 XX Sequence 99 AA;  
 SQ  
 Query Match 100.0%; Score 510; DB 23; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKIPVLPVAVLLSLVLSAQAATLGGPEESTIENTYASRPAFTPTPLNTDKLSAFKA 60  
 DB 1 MKIPVLPVAVLLSLVLSAQAATLGGPEESTIENTYASRPAFTPTPLNTDKLSAFKA 60  
 QY 61 DEFLNWHALFESIKRKLPLNWDAPPKLKGLSATPDAQ 99  
 DB 61 DEFLNWHALFESIKRKLPLNWDAPPKLKGLSATPDAQ 99  
 RESULT 12  
 ID AUB81964 standard; Protein; 99 AA.  
 AC AUB81964;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Human PRO826.  
 XX

KW Human, PRO; antiinflammatory; ophthalmological; vasotropic;  
KW retinal cell injury; ocular disease; retinitis pigmentosa;  
KW macular degeneration; retinal detachment; retinal tear; retinopathy;  
KW retinal degenerative disease; macular hole; degenerative myopia;  
KW acute retinal necrosis syndrome; traumatic choriorretinopathy;  
KW Putzcher's retinopathy; oedema; ischaemic condition;  
KW retinal vision occlusion; collagen vascular disease;  
KW thrombocytopenic purpura; uveitis; retinal vasculitis; Bales disease;  
KW systemic lupus erythematosus; environmental trauma.  
XX  
OS Homo sapiens.  
XX  
PN WO200109327-A2.  
XX  
PD 08-FEB-2001.  
XX  
PF 28-JUL-2000; 2000WO-US20710.  
XX  
PR 28-JUL-1999; 99US-146222P.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
XX  
PA (GENE) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;  
PI Kljavin IU, Lafleur M, Mark MR, Marsters SA, Pittl RM;  
PI Watanabe CK, Wood WT;  
XX  
DR WPI: 2002-130120/17.  
XX  
N-PsDB: ABR28600.  
XX  
PT Promoting survival of retinal cells, or delaying or preventing retinal  
cell injury or death, by contacting retinal cells with PRO175, 220,  
PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132  
PT polypeptide -  
XX  
PS Claim 44; Fig 25; 152pp; English.  
XX  
CC The invention relates to promoting the survival of retinal cells, or  
delaying or preventing retinal cell injury or death, by contacting the  
CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
CC PRO243, PRO306, PRO346, PRO322, PRO336, PRO943, PRO840, PRO828, PRO826,  
CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
CC encoding the PRO proteins, a vector comprising the nucleic acid, a host  
CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
CC useful for promoting survival of retinal cells (retinal neurons such as  
CC retinal ganglion cells, displaced retinal ganglion cells, amacrine  
CC cells, displaced amacrine cells, horizontal neurons or bipolar neurons,  
CC rod photoreceptors, or supportive cells such as Muller cells or pigment  
CC epithelial cells), or delaying or preventing retinal cell injury or  
CC death caused by ocular disease (which is or is associated with  
CC retinitis pigmentosa, macular degeneration, retinal detachment, retinal  
CC tear, retinopathy, retinal degenerative disease, macular hole,  
CC degenerative myopia, acute retinal necrosis syndrome, traumatic  
CC choriorretinopathy or contusion, Putzcher's retinopathy, oedema, an  
CC ischaemic condition, central or branch retinal vision occlusion,  
CC collagen vascular disease, thrombocytopenic purpura, uveitis, retinal  
CC vasculitis, occlusion associated with Bales disease or systemic lupus  
CC erythematosus), retinal injury or environmental trauma. The retinal  
CC cell injury or death is delayed or prevented by substantially not

CC causing angiogenesis or mitogenesis. The present sequence represents  
CC a PRO protein.  
XX  
SQ Sequence 99 AA;  
Query Match 100.0%; Score 510; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4,6e-57;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MKIPVLPAVVLLSLVLSAOGATIGGPEESTTENYASPEAFNPFLINDKLSAFKA 60  
Db 1 MKIPVLPAVVLLSLVLSAOGATIGGPEESTTENYASPEAFNPFLINDKLSAFKA 60  
Qy 61 DEFLNHALFESIRKRLPLINMDAFPKLIGLRATPDQAQ 99  
Db 61 DEFLNHALFESIRKRLPLINMDAFPKLIGLRATPDQAQ 99  
RESULT 13  
ABU59097  
ID ABU59097 standard; Protein; 99 AA.  
XX  
AC ABU59097;  
XX  
DT 28-APR-2003 (first entry)  
XX  
DE Novel human secreted or transmembrane protein PRO826.  
XX  
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.  
XX  
OS Homo sapiens.  
XX  
PN US2002132252-A1.  
XX  
PD 19-SEP-2002.  
XX  
PF 14-NOV-2001; 2001US-0990442.  
XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 16-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 11-FEB-2000; 2000WO-US00376.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.

PR 30-MAR-2000; 2000MO-US08439.  
 PR 15-MAY-2000; 2000MO-US13358.  
 PR 17-MAY-2000; 2000MO-US13705.  
 PR 22-MAY-2000; 2000MO-US14042.  
 PR 30-MAY-2000; 2000MO-US14941.  
 PR 02-JUN-2000; 2000MO-US15264.  
 PR 28-JUL-2000; 2000MO-US20710.  
 PR 11-AUG-2000; 2000MO-US22031.  
 PR 23-AUG-2000; 2000MO-US23522.  
 PR 24-AUG-2000; 2000MO-US23328.  
 PR 08-NOV-2000; 2000MO-US30952.  
 PR 01-DEC-2000; 2000MO-US32678.  
 PR 28-FEB-2001; 2001MO-US06520.  
 PR 01-JUN-2001; 2001MO-US17800.  
 PR 20-JUN-2001; 2001MO-US19992.  
 PR 29-JUN-2001; 2001MO-US21066.  
 PR 09-JUL-2001; 2001MO-US21735.  
 PR 16-JUN-1997; 97US-049787P.  
 PR 17-OCT-1997; 97US-062250P.  
 PR 12-NOV-1997; 97US-065186P.  
 PR 13-NOV-1997; 97US-065311P.  
 PR 24-NOV-1997; 97US-066710P.  
 PR 25-FEB-1998; 98US-075945P.  
 PR 20-MAR-1998; 98US-078910P.  
 PR 28-APR-1998; 98US-083322P.  
 PR 07-MAY-1998; 98US-084600P.  
 PR 28-MAY-1998; 98US-087106P.  
 PR 02-JUN-1998; 98US-087607P.  
 PR 02-JUN-1998; 98US-087609P.  
 PR 03-JUN-1998; 98US-087759P.  
 PR 03-JUN-1998; 98US-087837P.  
 PR 04-JUN-1998; 98US-088021P.  
 PR 04-JUN-1998; 98US-088025P.  
 PR 04-JUN-1998; 98US-088026P.  
 PR 04-JUN-1998; 98US-088028P.  
 PR 04-JUN-1998; 98US-088029P.  
 PR 04-JUN-1998; 98US-088030P.  
 PR 04-JUN-1998; 98US-088033P.  
 PR 04-JUN-1998; 98US-088326P.  
 PR 05-JUN-1998; 98US-088157P.  
 PR 05-JUN-1998; 98US-088202P.  
 PR 05-JUN-1998; 98US-088212P.  
 PR 05-JUN-1998; 98US-088217P.  
 PR 09-JUN-1998; 98US-088655P.  
 PR 10-JUN-1998; 98US-088744P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088742P.  
 PR 10-JUN-1998; 98US-088810P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 11-JUN-1998; 98US-088826P.  
 PR 11-JUN-1998; 98US-088858P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088867P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089440P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 17-JUN-1998; 98US-089532P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089598P.  
 PR 17-JUN-1998; 98US-089599P.  
 PR 17-JUN-1998; 98US-089600P.  
 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.

(GETH ) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers L, Eaton DJ,  
 XX Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers L, Eaton DJ,  
 PI Ferreira N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF,

PI Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM, Wood WT,  
 PI Zhang Z;  
 XX WPI; 2003-247083/24.  
 DR N-PSDB; ABX80254.  
 XX

PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 PT are therapeutically useful for enhancing immune response and in cancer  
 PT treatments

PS Claim 12; Fig 129; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1134 and PRO136  
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
 CC useful for treating cancerous tumours. PRO812 inhibits vascular  
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 CC cells and is thus useful for inhibiting endothelial cell growth in  
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
 CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorder associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or redifferentiation of chondrocytes in culture and  
 CC are thus useful for treating sports injuries, and arthritis. This  
 CC is the amino acid sequence of a novel human PRO protein.

SO Sequence 99 AA;

Query Match 100.0%; Score 510; DB 24; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-57;  
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 61 DEFLNMHALFESIKRKLPFLNMDAPFKKGLRSATPDQ 99  
 DB 61 DEFLNMHALFESIKRKLPFLNMDAPFKKGLRSATPDQ 99

RESULT 14  
 ABUS9244  
 ID ABUS9244 standard; Protein; 99 AA.

XX ABUS9244;

DT 22-APR-2003 (first entry)

DE Human secreted/transmembrane protein, #78.

XX Human, PRO, secreted; transmembrane; pharmaceutical;  
 KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
 KW gene therapy; tumour-associated antigenic target; TAT; ADAPT;  
 KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.

OS Homo sapiens.  
XX US2003027162-A1.  
XX  
PD 06-FEB-2003.  
XX  
FF 15-NOV-2001; 2001US-0997428.  
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PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
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PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
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PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
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PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
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PR 28-FEB-2001; 2001WO-US06520.  
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PR 16-SEP-1998; 98US-100634P.  
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Query Match 100.0%; Score 510; DB 24; Length 99;  
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Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKIPVLPVAVLISLVHSAQATLGGPEESTIENYASRPEAFNTPFINTIDLRSAFRA 60  
QY 61 DEFLNMHALFESIKRKLPLFNMDAFPKLGKRSATPDAQ 99  
DB 61 DEFLNMHALFESIKRKLPLFNMDAFPKLGKRSATPDAQ 99

RESULT 15  
ABUS9393  
ID ABUS9393 standard; Protein; 99 AA.  
XX ABUS9393;  
XX

DT 22-APR-2003 (first entry)  
XX  
XX Novel human secreted or transmembrane protein PRO819.  
DE  
XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KM cardiac insufficiency disorder; cancer; tumour; immune response;  
KM adrenal cortical capillary endothelial growth; c-fos induction;  
KM vascular endothelial growth factor inhibition; VEGF inhibition;  
KM endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KM retinal neurons cell survival; rod photoreceptor cell survival;  
KM retinal disorder; retinitis pigmentosa; kidney disorder;  
KM mammalian kidney mesangial cell proliferation; Berger disease;

KM dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.  
XX Homo sapiens.  
OS  
XX US2003027985-A1.  
PN  
XX  
PD 06-FEB-2003.  
XX  
PF 14-NOV-2001; 2001US-0990562.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
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PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
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PR 30-NOV-1999; 99WO-US28313.  
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PR 20-DEC-1999; 99WO-US00219.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
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PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
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PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
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PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
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Query Match 100.0%; Score 510; DB 24; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4, 6e-57;  
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Db 61 DEFLNMTALFESIRKXLPFLNWDAPFKLKGIRSATPDQAQ 99

Search completed: November 28, 2003, 07:55:09  
Job time : 50 secs



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| 2  | PRIOR FILING DATE: 1997-11-12       |
| 3  | PRIOR APPLICATION NUMBER: 60/065311 |
| 4  | PRIOR FILING DATE: 1997-11-13       |
| 5  | PRIOR APPLICATION NUMBER: 60/066770 |
| 6  | PRIOR FILING DATE: 1997-11-24       |
| 7  | PRIOR APPLICATION NUMBER: 60/075945 |
| 8  | PRIOR FILING DATE: 1998-02-25       |
| 9  | PRIOR APPLICATION NUMBER: 60/078910 |
| 10 | PRIOR FILING DATE: 1998-03-20       |
| 11 | PRIOR APPLICATION NUMBER: 60/083322 |
| 12 | PRIOR FILING DATE: 1998-04-28       |
| 13 | PRIOR APPLICATION NUMBER: 60/084600 |
| 14 | PRIOR FILING DATE: 1998-05-07       |
| 15 | PRIOR APPLICATION NUMBER: 60/087106 |
| 16 | PRIOR FILING DATE: 1998-05-28       |
| 17 | PRIOR APPLICATION NUMBER: 60/087607 |
| 18 | PRIOR FILING DATE: 1998-06-02       |
| 19 | PRIOR APPLICATION NUMBER: 60/087609 |
| 20 | PRIOR FILING DATE: 1998-06-02       |
| 21 | PRIOR APPLICATION NUMBER: 60/087759 |
| 22 | PRIOR FILING DATE: 1998-06-02       |
| 23 | PRIOR APPLICATION NUMBER: 60/087827 |
| 24 | PRIOR FILING DATE: 1998-06-03       |
| 25 | PRIOR APPLICATION NUMBER: 60/088021 |
| 26 | PRIOR FILING DATE: 1998-06-04       |
| 27 | PRIOR APPLICATION NUMBER: 60/088025 |
| 28 | PRIOR FILING DATE: 1998-06-04       |
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| 30 | PRIOR FILING DATE: 1998-06-04       |
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| 70 | PRIOR FILING DATE: 1998-06-12       |
| 71 | PRIOR APPLICATION NUMBER: 60/089440 |
| 72 | PRIOR FILING DATE: 1998-06-16       |
| 73 | PRIOR APPLICATION NUMBER: 60/089512 |

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PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 510; DB 9; Length 99;  
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Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 2

US-09-989-723-201  
Sequence 201, Application US/09989723  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P162  
CURRENT APPLICATION NUMBER: US/09/989, 723  
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;; PRIOR FILING DATE: 1998-07-02  
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;; PRIOR APPLICATION NUMBER: 60/091633  
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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 510; DB 9; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1,4e-55; Indels 0; Gaps 0;  
Matches 99; Conservative 0; Mismatches 0;

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Db 1 MKIPVLPAVVLLSLVLSAAGATLGGPEESTETENTYASRPEAFNTPLNIDKLSAFA 60

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Db 61 DEFLNWHALFESIKRKLPFLNWDAPPKLKGIRSATPDQ 99

RESULT 3  
US-09-989-279-201  
; Sequence 201, Application US/09989279  
; Patent No. US20020072496A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gottlieb, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tunes, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PLC56  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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3 PRIOR APPLICATION NUMBER: 60/078910  
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Query Match 100.0%; Score 510; DB 9; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1,4e-55;  
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Patent No. US20020072497A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PLC65  
CURRENT APPLICATION NUMBER: US/09/989,727  
PRIOR FILING DATE: 2001-11-19  
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PRIOR APPLICATION NUMBER: 60/091633
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 510; DB 9; Length 99;
Best Local Similarity 100.0%; Pred. No. 1,4e-55;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps

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RESULT 5
US-09-989-731-201
Sequence 201, Application US/09989731
Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Wary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kjaevan, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OR INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C70
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28

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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C57  
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; PRIOR FILING DATE: 2001-11-19  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982

PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09  
Query Match 100.0%; Score 510; DB 10; Length 99;  
Best local similarity 100.0%; Pred. No. 1, 4e-55;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MKIPVLPVVLSTLVHSAQATLGGPEESTENTYASREAPNTPLNTDKLSAFKA 60  
Qy 61 DEFNWHALFESIRKLPFLNMDAFPKLKGSRATPDQAQ 99  
61 DEFNWHALFESIRKLPFLNMDAFPKLKGSRATPDQAQ 99  
Db 61 DEFNWHALFESIRKLPFLNMDAFPKLKGSRATPDQAQ 99  
RESULT 7  
US-09-991-073-201  
Sequence 201, Application US/09991073  
Patent No. US20020127576A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kljavin, Mary A.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C15  
CURRENT APPLICATION NUMBER: US/09/991,073  
CURRENT FILING DATE: 2001-11-14  
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PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02



Query Match 100.0%; Score 510; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1,4e-55;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKIPVLPAVVLISLVLVHSAQAGATGPEESTTENVASREAFVNTPLNTDKLSAFKA 60  
Db 1 MKIPVLPAVVLISLVLVHSAQAGATGPEESTTENVASREAFVNTPLNTDKLSAFKA 60

Qy 61 DEFNMWALFESIKRKLPELWMDAPPKLKGHSATPDQ 99  
Db 61 DEFNMWALFESIKRKLPELWMDAPPKLKGHSATPDQ 99

RESULT 8  
US-09-990-442-201  
Sequence 201: Application US/09990442  
Patent No. US20020132252A1

GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deemeyer, Luc  
APPLICANT: Batton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C8  
CURRENT FILING DATE: US/09/990,442  
PRIOR APPLICATION NUMBER: 2001-11-14  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 510; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1,4e-55;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MKIPVLPVAVLLSLVLSHAQATLGGPEESTIENYASRPAFAFNTPLINDKLSAFRA 60  
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DB 61 DEFLNHALFESIKRRLPLNWDAPFKLKGASATPDAQ 99

RESULT 9  
US-09-991-163-201  
Sequence 201, Application US/09991163  
Patent No. US20020132253A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
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APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C17  
CURRENT APPLICATION NUMBER: US/09/991,163  
PRIOR FILING DATE: 2001-11-14  
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PRIOR FILING DATE: 1997-06-16  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 510; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1,4e-55;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10  
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Sequence 201, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Godowski, Paul J.  
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APPLICANT: Grimey, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C25  
CURRENT APPLICATION NUMBER: US/09/993,604  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 510; DB 10; Length 99;

Best Local Similarity 100.0%; Pred No. 1,4e-55;  
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RESULT 11  
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Sequence 201, Application US/09990456  
Patent No. US20020137890A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bocstein, David  
APPLICANT: Deenoyers, Inc  
APPLICANT: Falcon, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltseu, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Napier, Mary A.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Collin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OR INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC22  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 510; DB 10; Length 99;  
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Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12  
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Sequence 201. Application US/09989721  
Patent No. US20020142961A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C55  
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 510; DB 10; Length 99;  
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RESULT 13

US-09-992-598-201  
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Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
Baker, Kevin P.  
Botstein, David  
Desnovers, Luc  
Eaton, Dan L.  
Fertara, Napoleone  
Fong, Sherman  
Gerber, Hanspeter  
Gerritsen, Mary E.  
Godard, Audrey  
Godowski, Paul J.  
Grimaldi, J. Christopher  
Gurney, Austin L.  
Kjavin, Ivar J.  
Napier, Mary A.  
Pan, James  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Stewart, Timothy A.  
Tumas, Daniel  
Watanabe, Colin K.  
Williams, P. Mickey  
Wood, William I.  
Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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FILE REFERENCE: P2730PIC20  
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/ PRIOR FILING DATE: 1997-10-02
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/ SOFTWARE: PatentIn Ver. 2.0
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/ ORGANISM: Homo sapiens
/ US-09-984-245-142

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/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desmoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gertlson, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Kjaavin, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2730PIC66
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/ PRIOR FILING DATE: 2001-11-20
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Query Match 100.0%; Score 510; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1,4e-55;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIPVLPVNTLSLVHSAQATLGGPBEESTIENTVSRREARTPTPLNTDKLSAFKA 60  
DB 1 MKIPVLPVNTLSLVHSAQATLGGPBEESTIENTVSRREARTPTPLNTDKLSAFKA 60  
QY 61 DEFLNWHALFESIRKLPFLNWDAPPKLGGRSATPDQ 99  
|||||



Db 61 DEFLNWHALFESIKRKLFINMDAPPKLGKLSATPDAQ 99

Search completed: November 29, 2003, 08:03:02  
Job time : 319 secs



|    |    |   |
|----|----|---|
| XX | PN | MO2000073452-A2.  |
| XX | PD | 07-DEC-2000.  |
| XX | PF | 02-JUN-2000; 2000MO-US15264.  |
| XX | PR | 02-JUN-1999; 99MO-US12252.  |
| PR | PR | 20-JUL-1999; 99US-0144733.  |
| PR | PR | 20-JUL-1999; 99US-0144758.  |
| PR | PR | 28-JUL-1999; 99US-0146222.  |
| PR | PR | 01-SEP-1999; 99MO-US20111.  |
| PR | PR | 15-SEP-1999; 99MO-US21090.  |
| PR | PR | 15-SEP-1999; 99MO-US21547.  |
| PR | PR | 29-OCT-1999; 99US-0162506.  |
| PR | PR | 30-NOV-1999; 99MO-US28313.  |
| PR | PR | 01-DEC-1999; 99MO-US28634.  |
| PR | PR | 09-DEC-1999; 99US-0170262.  |
| PR | PR | 20-DEC-1999; 99MO-US30911.  |
| PR | PR | 05-JAN-2000; 2000MO-US00219.  |
| PR | PR | 06-JAN-2000; 2000MO-US00376.  |
| PR | PR | 11-FEB-2000; 2000MO-US03565.  |
| PR | PR | 18-FEB-2000; 2000MO-US04341.  |
| PR | PR | 18-FEB-2000; 2000MO-US04342.  |
| PR | PR | 22-FEB-2000; 2000MO-US04414.  |
| PR | PR | 24-FEB-2000; 2000MO-US04914.  |
| PR | PR | 15-MAR-2000; 2000MO-US06884.  |
| PR | PR | 20-MAR-2000; 2000MO-US07377.  |
| PR | PR | 21-MAR-2000; 2000MO-US07532.  |
| PR | PR | 30-MAR-2000; 2000MO-US08439.  |
| PR | PR | 17-MAY-2000; 2000MO-US13705.  |
| PR | PR | 22-MAY-2000; 2000MO-US14042.  |
| XX | PA | (GENTH ) GENENTECH INC.   |
| XX | PI | Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AT,          |
| PI | PI | Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tamas D, Watanabe CK,          |
| PI | PI | Wood WI;  |
| XX | DR | WPI; 2001-025253/03.  |
| XX | PT | P-PSDB; AAB50916.   |
| XX | PT | Thirty three nucleic acids encoding PRO polypeptides which are useful       |
| XX | PT | in the diagnosis and treatment of immune related disorders, e.g.            |
| XX | PT | systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,         |
| XX | PT | thyroiditis and diabetes mellitus -   |
| XX | PS | Claim 48; Fig 29; 218pp; English.   |
| XX | XX |   |
| CC | CC | The present sequence is one of thirty three nucleic acids encoding PRO      |
| CC | CC | polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and       |
| CC | CC | antagonists are useful for treating and diagnosing immune related           |
| CC | CC | disorders such as systemic lupus erythematosus, rheumatoid arthritis,       |
| CC | CC | osteoarthritis, juvenile chronic arthritis, spondyloarthritis,              |
| CC | CC | systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's           |
| CC | CC | syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic           |
| CC | CC | anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,       |
| CC | CC | immune-mediated renal disease, demyelinating diseases of the central        |
| CC | CC | and peripheral nervous systems (such as multiple sclerosis, idiopathic      |
| CC | CC | demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic        |
| CC | CC | inflammatory demyelinating polyneuropathy), hepatobiliary diseases          |
| CC | CC | (such as infections, autoimmune chronic active hepatitis, primary           |
| CC | CC | biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),     |
| CC | CC | inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's      |
| CC | CC | disease, autoimmune or immune-mediated skin diseases (such as bullous       |
| CC | CC | skin diseases, erythema multiforme, contact dermatitis, psoriasis),         |
| CC | CC | allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,     |
| CC | CC | food hypersensitivity and urticaria), immunological diseases of the         |
| CC | CC | lung (such as eosinophilic pneumonia), idiopathic pulmonary fibrosis        |
| CC | CC | and hypersensitivity pneumonitis), transplant rejection associated diseases |
| CC | CC | including graft rejection and graft-versus-host disease.                    |
| XX | XX |   |
| XX | XX | Sequence 414BP; 98 A; 126 C; 92 G; 98 T; 0 other;                           |

| Alignment Scores:                           |              | Pred. No.:   | 1-576-60 | Length: | 414 |
|---|--------------|--|----------|---------|-----|
| Score:                                      | 510.00       | Matches:   | 99       |         |     |
| Percent Similarity:                         | 100.00%      | Mismatches:  | 0        |         |     |
| Best Local Similarity:                      | 100.00%      | Indels:  | 0        |         |     |
| Query Match:                                | 100.00%      | Gaps:  | 0        |         |     |
| DB:   | 22           |  |          |         |     |
| US-10-059-395-142 (1-99) x AAC91475 (1-414) |              |  |          |         |     |
| QY  | 1            | MethyliseprovallleuproalvalvalleuleuSerleuValleuHisSerAla              | 20       |         |     |
| Db  | 13           | ATGAAGATCCCGATCCCTTCCTGCGTGGGCTCCTCCTCGTGGTCCATCTGCC                   | 72       |         |     |
| QY  | 21           | GlNGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAenTYrAlaSerArg           | 40       |         |     |
| Db  | 73           | CAGGAGGACCACTGGGGTGTCTTAGAAGAAAGCAACATGGAATTAAAGCTCAG                  | 132      |         |     |
| QY  | 41           | ProGluAlaPheAsnThrProPheLeuAsnIleAspLYsLeuAGSerAlaPheLYsAla            | 60       |         |     |
| Db  | 133          | CCGAGAGCTTTAAACACCCCGTCTCTGAACATCAAAATTGCCATCTGCCTTAAAGCT              | 192      |         |     |
| QY  | 61           | AspGluPheLeuAsnTYrPheAlaLeuPheGluSerIleLYsArgLYsLeuProPheLeu           | 80       |         |     |
| Db  | 193          | GATGAGTCTCTGAACATGAGCAGCGCTCTTGGAGTCTCAAAAGAAACCTCTTCCTC               | 252      |         |     |
| QY  | 81           | AsnTYrAspAlaPheProLYsLeuLYsGlyLeuArgSerAlaThrProAspAlaGln              | 99       |         |     |
| Db  | 253          | AACGTGAATGCCCTTCTCTTAAGCTGAAGAACTGAGAGAGCGCAACTCTGATGCCAG              | 309      |         |     |
| RESULT 2                                    |              |  |          |         |     |
| ID  | ABK28600     | standard; cDNA; 414 BP.  |          |         |     |
| XX  | AC           | ABK28600;  |          |         |     |
| XX  | DT           | 09-APR-2002 (first entry)  |          |         |     |
| XX  | DE           | Human DNAs7694-1341 encoding PRO826.                                   |          |         |     |
| KW  |              | Human; ss; gene; PRO; antiinflammatory; ophthalmological; vasotropic;  |          |         |     |
| KW  |              | retinal cell injury; ocular disease; retinitis pigmentosa;             |          |         |     |
| KW  |              | macular degeneration; retinal detachment; retinal tear; retinopathy;   |          |         |     |
| KW  |              | retinal degenerative disease; macular hole; degenerative myopia;       |          |         |     |
| KW  |              | acute retinal necrosis syndrome; traumatic chorioretinopathy;          |          |         |     |
| KW  |              | Purtscher's retinopathy; oedema; ischaemic condition;                  |          |         |     |
| KW  |              | retinal vision occlusion; collagen vascular disease;                   |          |         |     |
| KW  |              | thrombocytopaenic purpura; uveitis; retinal vasculitis; Pales disease; |          |         |     |
| XX  |              | systemic lupus erythematosus; environmental trauma.                    |          |         |     |
| XX  | OS           | Homo sapiens.  |          |         |     |
| XX  | PN           | W0200109327-A2.  |          |         |     |
| XX  | PD           | 08-FEB-2001.   |          |         |     |
| XX  | PF           | 28-JUL-2000; 2000MC-US20710.   |          |         |     |
| XX  |              |  |          |         |     |
| XX  |              |  |          |         |     |
| PR  | 13-SEP-1999; | 99US-146222P.  |          |         |     |
| PR  | 15-SEP-1999; | 99MO-US20944.  |          |         |     |
| PR  | 29-NOV-1999; | 99MO-US21090.  |          |         |     |
| PR  | 30-NOV-1999; | 99MO-US28214.  |          |         |     |
| PR  | 01-DEC-1999; | 99MO-US28313.  |          |         |     |
| PR  | 05-JAN-2000; | 2000MC-US00219.  |          |         |     |
| PR  | 06-JAN-2000; | 2000MC-US00376.  |          |         |     |
| PR  | 11-FEB-2000; | 2000MC-US03565.  |          |         |     |
| PR  | 18-FEB-2000; | 2000MC-US04341.  |          |         |     |
| PR  | 22-FEB-2000; | 2000MC-US04414.  |          |         |     |
| PR  | 24-FEB-2000; | 2000MC-US05004.  |          |         |     |
| PR  | 02-MAR-2000; | 2000MC-US05841.  |          |         |     |
| PR  | 15-MAR-2000; | 2000MC-US06884.  |          |         |     |

PR 30-MAR-2000; 2000MO-US08439.  
PR 17-MAY-2000; 2000MO-US13705.  
XX  
XX (GETH ) GENENTECH INC.  
PI Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL,  
PI Kljavin IJ, Lafleur M, Mark MR, Masters SA, Pletti RM,  
PI Matanabe CK, Wood WI;  
XX  
DR WPI; 2002-130120/17.  
DR P-PSDB; AA081964.  
XX  
XX Promoting survival of retinal cells, or delaying or preventing retinal  
PT cell injury or death, by contacting retinal cells with PRO175 220,  
PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132  
PT polypeptide -  
XX  
XX Claim 33; Fig 24; 152pp; English.  
XX  
XX The invention relates to promoting the survival of retinal cells, or  
CC delaying or preventing retinal cell injury or death, by contacting the  
CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
CC PRO243, PRO306, PRO346, PRO322, PRO356, PRO943, PRO840, PRO828, PRO826,  
CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
CC encoding the PRO proteins, a vector comprising the nucleic acid, a host  
CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
CC useful for promoting survival of retinal cells (retinal neurons such as  
CC retinal ganglion cells, displaced retinal ganglion cells, amacrine  
CC cells, displaced amacrine cells, horizontal neurons or bipolar neurons,  
CC rod photoreceptors, or supportive cells such as Muller cells or pigment  
CC epithelial cells), or delaying or preventing retinal cell injury or  
CC death caused by ocular disease (which is or is associated with  
CC retinitis pigmentosa, macular degeneration, retinal detachment, retinal  
CC tear, retinopathy, retinal degenerative disease, macular hole,  
CC degenerative myopia, acute retinal necrosis syndrome, traumatic  
CC chorioretinopathy or concussion, Purtscher's retinopathy, edema, an  
CC ischaemic condition, central or branch retinal vision occlusion,  
CC collagen vascular disease, thrombocytopenic purpura, uveitis, retinal  
CC vasculitis, occlusion associated with Hales disease or systemic lupus  
CC erythematosus), retinal injury or environmental trauma. The retinal  
CC cell injury or death is delayed or prevented by substantially not  
CC causing angiogenesis or mitogenesis. The present sequence is a cDNA  
CC encoding a PRO protein.  
XX  
XX  
SQ Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 1,57e-60 Length: 414  
Score: 510.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
  
US-10-059-395-142 (1-99) x ABK28600 (1-414)  
QY 1 MetLelIleProValIeuProAlaValIleuLeuSerIeuValIeuHisSerAla 20  
DB 13 ATGAAAGTCCCGGATCTCTCTGCGGAGTGTCTCTCTCCCTCGGCGCCACTGCGC 72  
QY 21 GlnGlyAlaThrIeuGlyGlyProGluGluGlySerThrIleGluIleuValIleuSerArg 40  
DB 73 CAGGAGCCACCTGGTGTCTCTGAGAGAAAGCAACCAATTGAGATCGGTCTACGA 132  
QY 41 ProGluAlaIleuLeuThrProPheLeuAsnIleAspIleuLeuArgSerAlaPheLeuAla 60  
DB 133 CCGAGAGCCCTTTAAACCCCGCTTCGAAACATGACAAATTTGAGATCGGTCTTAAGGCT 192  
QY 61 AspGluPheLeuLeuThrPheIleuLeuPheGluSerIleuValIleuValIleuProPheLeu 80  
DB 193 GATGAGTCTCTGAACTGGACGCGCTCTTTGAGCTATCAAAAGAAACTCTCTTCTCCTC 252  
QY 81 AsnTrpAspAlaIleuPheProIleuValIleuValIleuArgSerAlaThrProAspAlaGln 99

DB 253 AACTGGAGTCCCTTCTCTTAAGCTGAAGAGCTGAGAGCGCAACTCTCTATGCCCCAG 309  
RESULT 3  
ID AAZ65018 standard; cDNA; 415 BP.  
XX  
XX AAZ65018;  
AC  
XX  
XX 05-APR-2000 (first entry)  
XX  
XX Membrane-bound protein PRO826 encoding cDNA.  
XX  
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
XX pharmaceutical; receptor immunoadhesin; gene mapping; ss.  
XX  
XX Homo sapiens.  
XX  
XX MO9963086-A2.  
XX  
XX 09-DEC-1999.  
XX  
XX 02-JUN-1999; 99MO-US12252.  
XX  
XX 02-JUN-1998; 98US-0087607.  
XX 02-JUN-1998; 98US-0087609.  
XX 02-JUN-1998; 98US-0087759.  
XX 03-JUN-1998; 98US-0087827.  
XX 04-JUN-1998; 98US-0088021.  
XX 04-JUN-1998; 98US-0088025.  
XX 04-JUN-1998; 98US-0088028.  
XX 04-JUN-1998; 98US-0088029.  
XX 04-JUN-1998; 98US-0088030.  
XX 04-JUN-1998; 98US-0088033.  
XX 04-JUN-1998; 98US-0088326.  
XX 05-JUN-1998; 98US-0088167.  
XX 05-JUN-1998; 98US-0088202.  
XX 05-JUN-1998; 98US-0088212.  
XX 05-JUN-1998; 98US-0088217.  
XX 09-JUN-1998; 98US-0088655.  
XX 10-JUN-1998; 98US-0088722.  
XX 10-JUN-1998; 98US-0088730.  
XX 10-JUN-1998; 98US-0088734.  
XX 10-JUN-1998; 98US-0088738.  
XX 10-JUN-1998; 98US-0088740.  
XX 10-JUN-1998; 98US-0088741.  
XX 10-JUN-1998; 98US-0088742.  
XX 10-JUN-1998; 98US-0088810.  
XX 10-JUN-1998; 98US-0088811.  
XX 10-JUN-1998; 98US-0088824.  
XX 10-JUN-1998; 98US-0088825.  
XX 10-JUN-1998; 98US-0088826.  
XX 11-JUN-1998; 98US-0088858.  
XX 11-JUN-1998; 98US-0088861.  
XX 11-JUN-1998; 98US-0088863.  
XX 11-JUN-1998; 98US-0088866.  
XX 11-JUN-1998; 98US-0088876.  
XX 12-JUN-1998; 98US-0089090.  
XX 12-JUN-1998; 98US-0089105.  
XX 16-JUN-1998; 98US-0089440.  
XX 16-JUN-1998; 98US-0089512.  
XX 16-JUN-1998; 98US-0089514.  
XX 17-JUN-1998; 98US-0089532.  
XX 17-JUN-1998; 98US-0089538.  
XX 17-JUN-1998; 98US-0089598.  
XX 17-JUN-1998; 98US-0089599.  
XX 17-JUN-1998; 98US-0089600.  
XX 17-JUN-1998; 98US-0089653.  
XX 18-JUN-1998; 98US-0089801.  
XX 18-JUN-1998; 98US-0089807.  
XX 18-JUN-1998; 98US-0089908.  
XX 19-JUN-1998; 98US-0089947.  
XX 19-JUN-1998; 98US-0089948.  
XX 19-JUN-1998; 98US-0089952.

PR 22-JUN-1998; 98US-0090246.  
 PR 22-JUN-1998; 98US-0090252.  
 PR 22-JUN-1998; 98US-0090254.  
 PR 23-JUN-1998; 98US-0090349.  
 PR 23-JUN-1998; 98US-0090355.  
 PR 24-JUN-1998; 98US-0090429.  
 PR 24-JUN-1998; 98US-0090431.  
 PR 24-JUN-1998; 98US-0090435.  
 PR 24-JUN-1998; 98US-0090444.  
 PR 24-JUN-1998; 98US-0090445.  
 PR 24-JUN-1998; 98US-0090461.  
 PR 24-JUN-1998; 98US-0090472.  
 PR 24-JUN-1998; 98US-0090535.  
 PR 24-JUN-1998; 98US-0090538.  
 PR 24-JUN-1998; 98US-0090540.  
 PR 24-JUN-1998; 98US-0090557.  
 PR 25-JUN-1998; 98US-0090676.  
 PR 25-JUN-1998; 98US-0090678.  
 PR 25-JUN-1998; 98US-0090688.  
 PR 25-JUN-1998; 98US-0090690.  
 PR 25-JUN-1998; 98US-0090691.  
 PR 25-JUN-1998; 98US-0090694.  
 PR 25-JUN-1998; 98US-0090695.  
 PR 25-JUN-1998; 98US-0090696.  
 PR 26-JUN-1998; 98US-0090862.  
 PR 26-JUN-1998; 98US-0090863.  
 PR 01-JUL-1998; 98US-0091358.  
 PR 01-JUL-1998; 98US-0091544.  
 PR 01-JUL-1998; 98US-0091546.  
 PR 02-JUL-1998; 98US-0091478.  
 PR 02-JUL-1998; 98US-0091486.  
 PR 02-JUL-1998; 98US-0091519.  
 PR 02-JUL-1998; 98US-0091626.  
 PR 02-JUL-1998; 98US-0091628.  
 PR 02-JUL-1998; 98US-0091633.  
 PR 02-JUL-1998; 98US-0091646.  
 PR 02-JUL-1998; 98US-0091673.  
 PR 07-JUL-1998; 98US-0091978.  
 PR 07-JUL-1998; 98US-0091982.  
 PR 09-JUL-1998; 98US-0092182.  
 PR 10-JUL-1998; 98US-0092472.  
 PR 20-JUL-1998; 98US-0093339.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 04-AUG-1998; 98US-0095282.  
 PR 04-AUG-1998; 98US-0095285.  
 PR 04-AUG-1998; 98US-0095301.  
 PR 04-AUG-1998; 98US-0095302.  
 PR 04-AUG-1998; 98US-0095318.  
 PR 04-AUG-1998; 98US-0095321.  
 PR 04-AUG-1998; 98US-0095325.  
 PR 10-AUG-1998; 98US-0095316.  
 PR 10-AUG-1998; 98US-0095329.  
 PR 10-AUG-1998; 98US-0096012.  
 PR 11-AUG-1998; 98US-0096143.  
 PR 11-AUG-1998; 98US-0096146.  
 PR 12-AUG-1998; 98US-0096329.  
 PR 17-AUG-1998; 98US-0096757.  
 PR 17-AUG-1998; 98US-0096766.  
 PR 17-AUG-1998; 98US-0096768.  
 PR 17-AUG-1998; 98US-0096773.  
 PR 17-AUG-1998; 98US-0096791.  
 PR 17-AUG-1998; 98US-0096867.  
 PR 17-AUG-1998; 98US-0096891.  
 PR 17-AUG-1998; 98US-0096894.  
 PR 17-AUG-1998; 98US-0096895.  
 PR 17-AUG-1998; 98US-0096897.  
 PR 18-AUG-1998; 98US-0096849.  
 PR 18-AUG-1998; 98US-0096930.  
 PR 18-AUG-1998; 98US-0096939.  
 PR 18-AUG-1998; 98US-0096960.  
 PR 18-AUG-1998; 98US-0097022.  
 PR 19-AUG-1998; 98US-0097141.  
 PR 20-AUG-1998; 98US-0097218.

PR 24-AUG-1998; 98US-0097661.  
 PR 26-AUG-1998; 98US-0097951.  
 PR 26-AUG-1998; 98US-0097952.  
 PR 26-AUG-1998; 98US-0097954.  
 PR 26-AUG-1998; 98US-0097955.  
 PR 26-AUG-1998; 98US-0097971.  
 PR 26-AUG-1998; 98US-0097974.  
 PR 26-AUG-1998; 98US-0097978.  
 PR 26-AUG-1998; 98US-0097979.  
 PR 26-AUG-1998; 98US-0097986.  
 PR 31-AUG-1998; 98US-0098014.  
 PR 16-SEP-1998; 98US-0098525.  
 PR 12-JAN-1999; 98US-0115565.  
 XX  
 PA (GENTH ) GENENTECH INC.  
 PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 PI Wood WI, Yuan J;  
 XX  
 DR WPI, 2000-072883/06.  
 DR P-PSDB; AAY66681.  
 XX  
 PT Membrane-bound proteins and related nucleotide sequences -  
 XX  
 PS Claim 2; Fig 128; 822pp; English.  
 XX  
 CC The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LbL receptors, TIR  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
 CC will also be useful for the preparation of PRO polypeptides, especially  
 CC by recombinant techniques.  
 XX  
 SQ Sequence 415 BP, 99 A, 126 C, 92 G, 98 T, 0 other;  
 Alignment Scores:  
 Pred. No.: 1,58e-60 Length: 415  
 Score: 510.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0  
 US-10-059-395-142 (1-99) x AAZ65018 (1-415)  
 QY 1 MetLysIleProValLeuProAlaValLeuSerLeuLeuValLeuHisSerAla 20  
 DB 13 ATGAAGATCCCGGCTCTTCCTGCGGTGCTCTCTCCCTCGGTGCTCCACTGCGC 72  
 QY 21 GlnGlyAlaThrLeuGlyGlyProGlnGlnGlnSerThrIleGluAenTYAlaSerArg 40  
 DB 73 CAGGAGCCACCTGGGAGGCTCTGAGGAAAGACACCATTTGAAATTAATGCTGACGA 132  
 QY 41 ProGlnAlaPheAenThrProPheLeuAsnIleAspLeuArgSerAlaPheLysAla 60  
 DB 133 CCCGAGGCTTTAACCCCGCTTCTGAAACATTCGACATTCGCGTTAAAGGCT 192  
 QY 61 AspGlnPheLeuAenThrPheAlaLeuPheGlnSerIleLysArgLysLeuProPheLeu 80  
 DB 193 GATGAGTTCCTGAATCGACAGCCCTCTTGAAGCTATCAAAAGAACTTCCTTCTC 252  
 QY 81 AenTPAaPAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
 DB 253 AACTGGATGCCCTTCTTAAGCTGAAAGACTGAGAGCGCAACTCTCGATGCCAG 309

RESULT 4  
AA30059  
ID AAF30059 standard; cDNA, 415 BP.  
XX  
AC AAF30059;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Human cDNA encoding PRO826.  
XX  
XX PRO826; UNQ467; human; immune disease; autoimmune disease;  
XX antirheumatic; antirheumatic; antirheumatic; antirheumatic;  
XX immunosuppressive; antihypertensive; antidiabetic; neuroprotective;  
XX hepatocarcinoma; virucide; dermatological; antiproliferative;  
XX antitubercular; antiallergic; immunostimulant; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 13..312  
FT /tag= a  
FT sig\_peptide 13..78  
FT /tag= b  
FT mat\_peptide 79..309  
FT /tag= c  
XX  
XX MO200105972-A1.  
XX  
XX 25-JAN-2001.  
XX  
XX 15-MAR-2000; 2000MO-US06884.  
XX  
XX 20-JUL-1999; 99US-0144758.  
XX  
XX (GENE) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
XX Hillan KJ, Mark MR, Masters SA, Pitti RM, Tumas D, Watanabe CK;  
XX Wood WJ;  
XX WPI; 2001-103149/11.  
XX P-PSDB; AAB20117.  
XX  
XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
XX diagnosing and treating immune-related disorders, such as multiple  
XX sclerosis, rheumatoid arthritis and diabetes -  
XX  
XX Claim 21; Fig 19; 127pp; English.  
XX  
XX The present sequence is that of cDNA clone DN57694-1341 (ATCC 203017)  
XX encoding novel human immunomodulator protein PRO826 (UNQ467) (see  
XX AAB20117). The clone was isolated following a database search by  
XX applying a signal sequence algorithm. The predicted protein has a  
XX mol. wt. of 11 kDa and a pI of 7.47. The invention provides  
XX polynucleotides (see AAF30050-62) encoding novel human PRO proteins  
XX (see AAB20108-20) including PRO826. Claimed compositions  
XX comprising these proteins or their agonists are useful for increasing  
XX infiltration of inflammatory cells into a tissue of a mammal,  
XX stimulating or enhancing an immune response in a mammal,  
XX increasing the proliferation of T-lymphocytes in a mammal in response  
XX to an antigen. Claimed compositions comprising the PRO polypeptide  
XX or its antagonist have the opposite effect. A claimed method for  
XX treating an immune related disorder, such as a T cell disorder,  
XX involves administering the PRO polypeptide, an agonist antibody or  
XX an antagonist antibody. The disorder is selected from systemic  
XX lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
XX juvenile chronic arthritis, spondyloarthritis, systemic  
XX sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome,  
XX systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia,  
XX autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
XX immune-mediated renal disease, demyelinated diseases (such as  
XX multiple sclerosis), autoimmune chronic active hepatitis, primary

biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
CC inflammatory bowel disease (ulcerative colitis and Crohn's disease),  
CC gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated  
CC skin diseases (such as bullous skin disease, erythema multiforme and  
CC psoriasis), allergic diseases (such as asthma, allergic rhinitis,  
CC atopic dermatitis, food hypersensitivity and urticaria), immunologic  
CC diseases of the lung and transplantation associated diseases (such  
CC as graft rejection and graft-versus-host disease) (all claimed).  
CC Claimed methods of diagnosing these disorders comprise detecting  
CC the level of expression of the PRO gene. Also claimed are a method  
CC of identifying a compound capable of inhibiting the expression or  
CC activity of the PRO polypeptide, vectors, host cells, antibodies  
CC and a method of stimulating the proliferation of T-lymphocytes  
CC using PRO826.  
XX  
XX SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 1,586-60 Length: 415  
XX Score: 510.00 Matches: 99  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 100.00% Indels: 0  
XX DB: 22 Gaps: 0  
XX  
XX US-10-059-395-142 (1-99) x AAF30059 (1-415)  
XX  
XX QY 1 MetLysIleProValLeuProAlaValLeuLeuSerLeuValLeuHisSerAla 20  
XX Db 13 ATGAAGATCCCGGCTCTTCCTGCGCTGCTCCCTCTCTGCTGCTCACTGCTC 72  
XX QY 21 GlnGlyAlaThrLeuGlyGlyProGlnGlnGlnSerThrIleGlnAsnTyrAlaSerArg 40  
XX Db 73 CAGGAGGACACCCCTGGTGGTCTGAGAGAGAAACACCATTTGAGATTATCGTCACGA 132  
XX QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
XX Db 133 CCGAGGCGCTTTAACACCCCGTCTGTAACATGCAATTCGATCGCTTAAGGCT 192  
XX QY 61 AspGluPheLeuAsnThrIleAlaLeuPheGlnSerIleLysArgLysLeuProPheLeu 80  
XX Db 193 GATGAGTTCCTGAACATGACGACGCCCTCTTGAATCTATCAAAAGAACTCTTCTC 252  
XX QY 81 AsnTyrAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
XX Db 253 AACTGGATGCTTCTTCTTAAGCTGAAGAGACGAGACGCAACTCGATGCCAG 309  
XX  
XX RESULT 5  
XX AAF44164  
XX ID AAF44164 standard; cDNA, 415 BP.  
XX  
XX AC AAF44164;  
XX  
XX DT 02-APR-2001 (first entry)  
XX  
XX DE Human PRO826 (UNQ467) nucleotide sequence SEQ ID NO:200.  
XX  
XX KW Human; secreted and transmembrane protein; PRO; cytoskeletal;  
XX cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
XX diagnostic assay; ss.  
XX  
XX OS Homo sapiens.  
XX  
XX WO200073454-A1.  
XX  
XX PD 07-DEC-2000.  
XX  
XX PF 30-MAR-2000; 2000MO-US08439.  
XX  
XX PR 02-JUN-1999; 99MO-US12252.  
XX PR 23-JUN-1999; 99US-0141037.  
XX PR 07-JUL-1999; 99US-0143048.  
XX PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 17-AUG-1999; 99US-0149396.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 08-OCT-1999; 99US-0158663.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US30095.  
 PR 16-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US00219.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.

(GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 PI Ferrara N, Fong S, Gerber H, Gertlissen ME, Goddard A, Godowski PJ,  
 PI Girmaldi CJ, Gurney AL, Kijavini IU, Napier MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT,  
 PI Zhang Z;

DR WPI, 2001-032160/04.  
 DR P-PSDB; AAB55204.

PT PRO polynucleotides used to produce polypeptides used to target  
 PT bioactive molecules such as toxins, radiolabels or antibodies, to  
 PT specific cells, to cause targeted cell death -

XX Claim 2, Fig 128; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO  
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
 CC can be used for targeted delivery of bioactive molecules, such as  
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
 CC and DNA. They may also be used to produce transgenic animals which are  
 CC used to develop and screen therapeutically useful reagents. The PRO  
 CC nucleotide and protein sequence can be used for tissue typing and in  
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:  
 Pred. No.: 1.58e-60 Length: 415  
 Score: 510.00 Matches: 99  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US-10-059-395-142 (1-99) x AAF44164 (1-415)

QY 1 MetLVEIIIPProValIeuProAlaValIValIleuSerIeuValIleuHISerAla 20  
 DB 13 ATGAAGATCCCGATCTTCCTCGCGTGGTCTCTCTCCCTCGTGTCTCCACCTCTGCTC 72  
 QY 21 GINGLYAlaThrIeuGLyGLyProGIuGIuGIuSerThrIleGIuValnTYzAlaSerArg 40  
 DB 73 CAGGAGCACCCTGGTGGTGTCTCTGAGAAAGACACCATTTAGAAATTATGCTACCA 132

QY 41 ProGIuIaIaPheAsnThrProPheIeuAsnIlaAspLySleuArgSerAlaPheLYAla 60  
 DB 133 CCGAGGCGCTTTAAACCCCGTTCCTTAACATGACAAATTTGCGATCTGGCTTTAAAGCT 192  
 QY 61 AspGIuIaIeUaAntTPhISAlaIeUPheGIuSerIleLYsArgLYleuProPheIeu 80  
 DB 193 GATGAGTTCCTGAACCTGGACAGCCCTCTTGAGCTCTTCAAAAGGAACCTTCCTTCCTC 252  
 QY 81 AsnTrpAlaPhePhePolYsLeuLYeGIYleuArgSerAlaThrProAspAlaGln 99  
 DB 253 AACTGGATGCTTTTCTTAAGCTTAAGACTGAAGAGCGCACTCTGATGCCAG 309

RESULT 6

AAC97491  
 ID AAC97491 standard; cDNA, 415 BP.

XX AAC97491;

DT 28-FEB-2001 (first entry)

DE Human angiogenesis-associated protein PRO826 cDNA, SEQ ID NO:157.

XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
 KW gene therapy; transgenic animal; ss.

XX Homo sapiens.

XX WC200053753-A2.

XX 14-SEP-2000.

PD 05-JAN-2000; 2000WO-US00219.

XX 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WT;

DR WPI, 2001-090793/10.  
 DR P-PSDB; AAB53094.

PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
 PT genetic disorders and treating cardiovascular, endothelial or  
 PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
 XX Claim 58; Fig 61; 293pp; English.

CC The invention relates to novel human angiogenesis-associated proteins  
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
 CC PRO proteins. The invention also relates to vectors and host cells

comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO protein, agonists or antagonists of a PRO protein, and compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; creating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or PRO agonist or antagonist; a retroviral gene therapy vector comprising a PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, osteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential therapeutic agents. The present sequence represents a cDNA encoding a PRO protein of the invention.

Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

## Alignment Scores:

|                        |         |               |         |     |
|------------------------|---------|---------------|---------|-----|
| Pred. No.:             | 1       | 58e-60        | Length: | 415 |
| Score:                 | 510.00  | Matches:      | 99      |     |
| Percent Similarity:    | 100.00% | Conservative: | 0       |     |
| Best Local Similarity: | 100.00% | Mismatches:   | 0       |     |
| Query Match:           | 100.00% | Indels:       | 0       |     |
| DB:                    | 22      | Gaps:         | 0       |     |

US-10-059-395-142 (1-99) x AAC97491 (1-415)

QY 1 MetIysIleProValIleuProAlaValIleuLeuSerLeuValIleuHisSerAla 20  
Db 13 ATGAAGATCCCGTCTTCTCTGCGGATGCTCTCTCTCTCTGATGCTCCACTGTGCC 72  
QY 21 GInGInAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAntyAlaSerArg 40  
Db 73 CAGGGAGCCACCTGGGTGCTCTGAGGAAGAACCACTGAGATTATATGCTCAGCA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspIleuArgSerAlaPheIysAla 60  
Db 133 CCGAGAGCCTTAAACCCCGTCTGACATGACAAATGGATCGATTAAAGGCT 192  
QY 61 AspGluPheLeuAsnThrPheIleAlaLeuPheGluSerIleIysArgIysLeuProPheLeu 80  
Db 193 GATGAGTCTCTGAACGGACGCGCTTGTGACTCATCAAAAGAAACTCTTCTCTC 252  
QY 81 AsnTrpAspAlaPheProIysLeuIysGlyIleuArgSerAlaThrProAspAlaGln 99  
Db 253 AACTGGAGATGCCCTTCTTAAGTGAAGAGACTGAGAGCGCACTCCTGATGCCAG 309

## RESULT 7

ABL95626  
ID ABL95626 standard; cDNA; 415 BP.

AC ABL95626;

DT 19-JUL-2002 (first entry)

DE Human angiogenesis related cDNA PRO826 SEQ ID NO: 131.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;

KW Cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;  
KM antiarteriosclerotic; gene; ss.

XX Homo sapiens.

XX MO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 28-JUL-2000; 2000WO-US20710.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-0643657.

XX 23-AUG-2000; 2000WO-US23522.

XX 24-AUG-2000; 2000WO-US23328.

XX 07-SEP-2000; 2000US-230978P.

XX 15-SEP-2000; 2000US-000000P.

XX 18-SEP-2000; 2000US-0664610.

XX 24-OCT-2000; 2000US-0665350.

XX 08-NOV-2000; 2000US-0709238.

XX 08-NOV-2000; 2000WO-US30952.

XX 10-NOV-2000; 2000WO-US30873.

XX 01-DEC-2000; 2000WO-US32678.

XX 20-DEC-2000; 2000WO-US34956.

XX 22-JAN-2001; 2001US-0767609.

XX 28-FEB-2001; 2001US-0796498.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2001; 2001WO-US06666.

XX 09-MAR-2001; 2001US-0802706.

XX 14-MAR-2001; 2001US-0808689.

XX 22-MAR-2001; 2001US-0816744.

XX 05-APR-2001; 2001US-0828366.

XX 10-MAY-2001; 2001US-0854208.

XX 10-MAY-2001; 2001US-0854280.

XX 25-MAY-2001; 2001US-0866028.

XX 25-MAY-2001; 2001US-0866034.

XX 30-MAY-2001; 2001WO-US17092.

XX 30-MAY-2001; 2001US-0870574.

XX 01-JUN-2001; 2001WO-US17443.

XX 20-JUN-2001; 2001WO-US17800.

XX 28-JUN-2001; 2001WO-US19692.

XX (GERT) GENENTECH INC.

PA (BAKE) BAKER K P.

PA (FERR) FERRARA N.

PA (GERB) GERBER H.

PA (GERR) GERRITSEN M E.

PA (GODD) GODDARD A.

PA (GODO) GODOWSKI P J.

PA (GURN) GURNEY A L.

PA (HILL) HILLAN K J.

PA (MARS) MARSTERS S A.

PA (PANJ) PAN J.

PA (PAON) PAONI N F.

PA (STEP) STEPHAN J F.

PA (WATA) WATANABE C K.

PA (WILL) WILLIAMS P W.

PA (WOOD) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF, Watanabe CK, Williams PW, Wood WJ, Ye W, WPI; 2002-171999/22.

DR F-PSDB; ABB95488.

XX



One hundred and eighty seven nucleic acids encoding PRO polypeptides useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -

CC The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hypertrophy, cirrhosis, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a coding sequence of the invention.  
CC

**5Q** Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

### Alignment Scores:

|                        |         |               |     |
|------------------------|---------|---------------|-----|
| Pred. No.:             | 1.5e+00 | Length:       | 415 |
| Score:                 | 510.00  | Matches:      | 99  |
| Percent Similarity:    | 100.00% | Conservative: | 0   |
| Best Local Similarity: | 100.00% | Mismatches:   | 0   |
| Query Match:           | 100.00% | Indels:       | 0   |
| DB:                    | 24      | Gaps:         | 0   |

US-10-059-395-142 (1-99) X ABL95626 (1-415)

|          |   |
|----------|---|
| Qy       | Metcys11erProVal1eupProAla1Val1LeuLeuSerLeuLeuValLeuH1SerAla 20       |
| Db       | 13 ATGAGAGTCCGGATCTCTCTCCGCGAGGAGCTCTCTCTCCCTCTGAGTCTCACTCGCC 72      |
| Qy       | 21 G1NG1YAlaThrLeuG1yG1yProG1uG1uG1uSerThr11eG1uAsnTYrAlaSerArg 40    |
| Db       | 73 CAGGAGCCACCCCTGGGTGGTCTCTGAGGAAGAAGACACCATTTGAAGATTATGCGTCACGA 132 |
| Qy       | 41 ProG1uAlaIleAsnThrProPheLeuAsn11eApLYLeuArgSerAlaPheLYsa1a 60      |
| Db       | 133 CCGAGGCGCTTTAAACCCCGCTTCCCTGGAACATCGACAAATTCGATCTGCGTTTAAGGCT 192 |
| Qy       | 61 AspG1uPheLeuAsnTrpH1sa1aLeuPheG1uSer11eLYsaLYLeuProPheLeu 80       |
| Db       | 193 GATGAGTTCCTGAACCTGGACGCGCCCTTGTAGTCTATCTAAAGAACTTCCTTCTCTC 252    |
| Qy       | 81 AsnTrpAspAlaPheProLYLeuLYsG1YLeuArgSerAlaThrProAspAlaG1n 99        |
| Db       | 253 AACTGGATGCTCTTCTCTTAAGCTGAAGAAGACTGAAGAGCGCACTCGATGCCAG 309       |
| RESULT 8 |   |
| ABK69971 |   |
| ID       | ABK69971 standard; DNA; 415 BP.                                       |
| AC       | ABK69971;   |
| XX       | 15-JUL-2002 (first entry)   |
| DT       | cdNA encoding human Pro peptide #11.                                  |
| DE       | Human; ss; gene; PRO; secreted protein; transmembrane protein;        |
| KW       | genetic disorder; tumour; cancer.                                     |
| KW       | Homo sapiens.   |
| XX       | WO200224888-A2.   |
| FN       | 28-MAR-2002.  |
| PD       | 29-AUG-2001; 2001WO-US27099.  |
| PF       | 01-SEP-2000; 2000US-229896P.  |
| PR       | 05-SEP-2000; 2000US-230621P.  |
| PR       | 22-SEP-2000; 2000US-225147P.  |
| PR       | 12-NOV-2000; 2000WO-US30873.  |
| PR       | 12-JAN-2001; 2001US-261878P.  |

PR 16-JAN-2001; 2001US-261910P.  
PR 16-JAN-2001; 2001US-261939P.  
PR 16-JAN-2001; 2001US-262150P.  
PR 25-JAN-2001; 2001US-264395P.  
PR 02-FEB-2001; 2001US-266421P.  
PR 09-FEB-2001; 2001US-267623P.  
PR 28-FEB-2001; 2001WO-US06550.  
PR 09-MAR-2001; 2001US-274393P.  
PR 03-APR-2001; 2001US-280982P.  
PR 04-APR-2001; 2001US-282123P.  
PR 04-APR-2001; 2001US-282199P.  
PR 09-MAY-2001; 2001US-290583P.  
PR 25-MAY-2001; 2001WO-US17052.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
XX  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.

PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S,

PT New PRO polypeptides and polynucleotides encoding the polypeptides,  
PT useful in gene therapy, chromosome identification, tissue typing, or  
PT for genetic analysis of individuals with genetic disorders -

PS Claim 2; Figure 21; 218pp; English

CC This invention relates to the cDNA and protein sequences of novel  
CC secreted and transmembrane polypeptides PRO polypeptides. The  
CC invention also comprises a method for producing the proteins of the  
CC invention by recombinant means and antibodies specific for the protein  
CC of the invention. The antibody may be used for detecting the PRO  
CC proteins of the invention and may be used to modify their activity.  
CC polynucleotides may be used as hybridisation probes for a cDNA library  
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
CC construct hybridisation probes for mapping the gene which encodes that  
CC PRO and for genetic analysis of individuals with genetic disorders, in  
CC assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knock-out animals which  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides are useful in gene therapy, and as molecular weight  
CC markers for protein electrophoresis purposes. The sequences may  
CC also be used to detect overexpression on PRO polypeptides in cancerous  
CC tumours and for screening for differentially expressed genes using  
CC microarray technology. The present sequence represents a cDNA encoding  
CC a human PRO protein of the invention.

**50** Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other.

**Alignment Scores:**

|                        |          |               |     |
|------------------------|----------|---------------|-----|
| Pred. No.:             | 1,586-60 | Length:       | 415 |
| Score:                 | 510.00   | Matches:      | 99  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 24       | Gaps:         | 0   |

US-10-059-395-142 (1-99) X ABK69971 (1-415)

Qy MetVsl15ProValLeuProAlaValValLeuLeuSerLeuValLeuH15SerA120  
Db 13 ATAAAGATCCGGCTCTCTCTCCGAGTGGCTCTCTCTCTCTGGTCTCACTCTGCC 72  
Qy 21 GInGValaThrLeuGlyValProGInGInGInSerThr11LeG1uSerTrpA15SerArg 40  
Db 73 CAGGAGGCCACCTCTGGTGGTCTCTAGAGAAAGAACACATTTGAGAAATTAAGCCTTCAGA 134



DE cDNA encoding human PRO protein, Seq ID No 145.  
 XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
 KW pericyte cell proliferation; chondrocyte cell proliferation;  
 KW tumour necrosis factor-alpha; gene; ss.  
 OS Homo sapiens.  
 XX MO200208288-A2.  
 XX  
 PD 31-JAN-2002.  
 XX  
 PF 29-JUN-2001; 2001WO-US21066.  
 XX  
 PR 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220585P.  
 PR 25-JUL-2000; 2000US-220605P.  
 PR 25-JUL-2000; 2000US-220607P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220638P.  
 PR 25-JUL-2000; 2000US-220664P.  
 PR 25-JUL-2000; 2000US-220666P.  
 PR 26-JUL-2000; 2000US-220893P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 15-SEP-2000; 2000WO-US0000P.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 28-NOV-2000; 2000US-253646P.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001WO-US17092.  
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 PA (GENTECH ) GENENTECH INC.  
 XX Baker KP, Deaneys L, Gerltzen MB, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT,  
 XX MPI; 2002-172001/22.  
 DR P-PBDB; AAU83664.  
 XX  
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,  
 PT useful for treating a PRO related disorder and for diagnosing tumours  
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
 PT tumour or liver tumour -  
 XX  
 XX Claim 2; Figure 145; 359pp; English.  
 PS  
 XX The invention relates to one hundred and twenty two nucleic acids  
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
 CC agonists and antagonists are useful for treating a PRO related disorder.  
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
 CC liver tumour. The PRO polypeptides are useful for stimulating the  
 CC proliferation of, or gene expression, in pericyte cells, for stimulating  
 CC the proliferation or differentiation of chondrocyte cells, for  
 CC stimulating the release of tumour necrosis factor-alpha from human blood,  
 CC for stimulating or inhibiting the proliferation of normal human dermal  
 CC fibroblast cells. The PRO polypeptide may also be used as molecular  
 CC weight markers and for tissue typing. The PRO nucleic acids have  
 CC applications in molecular biology, including use as hybridisation probes,  
 CC and in chromosome and gene mapping. ABK3535-ABK3657 represent human  
 CC PRO protein coding sequences of the invention.  
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 Pred. No.:

Score: 510.00 Matches: 99  
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 QY 21 GlnGlyAlaThrLeuGlyGlyProGluGluGluSerThrIleGluAenTyAlaSerArg 40  
 DB 73 CAGGAGCCACCCCTGGGTGTCTCGAGAAAGAACCAATTGAGATTATGCTCAGA 132  
 QY 41 ProGluAlaPheAenThrProPheLeuAenIleAspLysLeuArgSerAlaPheLysAla 60  
 DB 133 CCGAGGCTTTAAACACCCCTCTTCAATGACAAATTGCGATCTGCTTTAAGCT 192  
 QY 61 AspGluPheLeuAenThrPheIleAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80  
 DB 193 GATGAGTTCCTGAACCTGCAAGCCCTCTTGAAGTCTATCAAAAGAAACTCTTCTC 252  
 QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAlaPheAla 99  
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 ID ABK80255 standard; DNA, 415 BP.  
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 AC ABK80255;  
 XX  
 DT 28-APR-2003 (first entry)  
 XX  
 DE Novel human secreted or transmembrane protein PRO819 DNA.  
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 KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disorder;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002132252-A1.  
 XX  
 PD 19-SEP-2002.  
 XX  
 PF 14-NOV-2001; 2001US-0990442.  
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 PR 05-NOV-1997; 97WO-US20069.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
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 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
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 PR 20-DEC-1999; 99WO-US30911.  
 PR 06-JAN-2000; 2000WO-US00219.



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DT      22-APR-2003 (first entry)
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KW      Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;
KW      diagnostic; biosensor; bioreactor; tumour; therapeutic;
KW      gene therapy; tumour-associated antigenic target; TAT; ADEPT;
KW      antibody-dependent enzyme mediated prodrug therapy; cytostatic.
XX
OS      Homo sapiens.
XX
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PN      US2003027162-A1.
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PD      06-FEB-2003.
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PF      15-NOV-2001; 2001US-0997428.
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Length: 415  
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 Db 133 CCGAGGCGCTTTAAACCGCCGTTCTGAAACATGCAAAATGGAGTGGTTAAAGGCT 192

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 XX XX  
 KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibitor; VEGF inhibition;  
 KW retinal neurons cell survival; T-lymphocytes stimulation;  
 KW rectal disorder; rectitis pigmentosum; kidney disorder;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis; gene; de.  
 XX XX  
 OS Homo sapiens.  
 XX XX  
 PN US2003027985-A1.  
 PD 06-FEB-2003.  
 XX XX  
 PF 14-NOV-2001; 2001US-0990562.  
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US-10-059-395-142 (1-99) x ABX77843 (1-415)

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Search completed: November 28, 2003, 08:09:59  
Job time : 234 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 08:10:04 ; Search time 265 Seconds  
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1230.846 Million cell updates/sec

Title: US-10-059-395-142

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Searched: 2190069 segs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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| 38 | 510 | 100.0 | 415 | 11 | US-09-997-601-200 Sequence 200, App  |
| 39 | 510 | 100.0 | 415 | 11 | US-09-990-443-200 Sequence 200, App  |
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| 42 | 510 | 100.0 | 415 | 11 | US-09-989-763-200 Sequence 200, App  |
| 43 | 510 | 100.0 | 415 | 11 | US-09-989-799A-200 Sequence 200, App |
| 44 | 510 | 100.0 | 415 | 11 | US-09-997-349-200 Sequence 200, App  |
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#### ALIGNMENTS

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Sequence 200, Application US/09989722  
Patent No. US20020072067A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P27301PC63  
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 7.79e-67 Length: 415  
Score: 510.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x US-09-989-722-200 (1-415)

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QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLysLeuArgSerAlaPheLysAla 60  
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DB 193 GATGATTTCTGTAACCTGGCACCGCCCTTTGATCTATCAAAAGAAAGAACTCTTCCCTC 252  
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99  
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RESULT 2  
US-09-989-723-200  
; Sequence 200, Application US/09989723  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone

;; APPLICANT: Fong, Sherman  
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;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C62  
;; CURRENT FILING DATE: 2001-11-19  
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PRIOR FILING DATE: 1998-07-09

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Query Match: 100.00% Indels: 0  
Dels: 9 Gaps: 0

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RESULT 3  
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Sequence 200, Application US/09989279  
Patent No. US20020072496X1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Boctsein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C56  
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CURRENT FILING DATE: 2001-11-19  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 7,79e-67 Length: 415  
Score: 510.00 Matches: 99  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-059-395-142 (1-99) x US-09-989-279-200 (1-415)

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DB 73 CAGGAGCACACCCGGGTGGTCCGAGGAGGAGGACCACTTGAGATTGCTCAGCA 132  
QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspLeuArgSerAlaPheGlyAla 60  
DB 133 CCCAGGCGCTTTAACACCCCGTCTGACATGCAAAATTGCGATCTGGCGTTTAAGCT 192  
QY 61 AspGluPheLeuAsnTPH1sAlaLeuPheGluSerIleLeuArgGlyLeuProPheLeu 80  
DB 193 GATAGTTCCTGAATGACGAGCCCTTTGAGCTATCAAAAGGAAACTTCTTCTC 252  
QY 81 AsnTPAspAlaPheProLYSLeuLYSGLYLeuArgSerAlaThrProAspAlaGln 99  
DB 253 AACTGGATGCTTCTCTTAAGCTGAAGACTGAGAGCGGAACTCTGATGCCAG 309  
RESULT 4  
US-09-989-727-200  
Sequence 200, Application US/09989727  
Patent No. US20020072497A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Inc  
APPLICANT: Falcon, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P27301C65  
CURRENT APPLICATION NUMBER: US/09/989,727  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1997-11-12  
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[illegible]

PRIOR APPLICATION NUMBER: 60/089532



APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC57  
CURRENT APPLICATION NUMBER: US/09/989,732  
CURRENT FILING DATE: 2001-11-19  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

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US-10-059-395-142 (1-99) x US-09-991-073-200 (1-415)

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DB 133 CCCGAGGCTTTAAACACCCGCTTCGAAATTCGCAATTCGATCGCTTAAAGGCT 192  
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DB 193 GATGATCTCGAATCGACGCGCTTTGATGCTATCAAGAACTTCCTTCTC 252  
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DB 253 AACTGATGCTTTCTTAAGCTGAAGAGACTGAGGCGCACTCGATGCCAG 309

RESULT 8  
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Sequence 200, Application US/09990442  
Patent No. US20020132252A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC8  
CURRENT APPLICATION NUMBER: US/09/990,442  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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Score: 510.00 Matches: 99
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Query Match: 100.00% Indels: 0
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QY 21 GInGlyAlaThrLeuGlyIleProGluGluGluGluThrIleGluAsnTrpAlaSerArg 40
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DB 133 CCCAGAGCCTTTAAACACCCCTTCTCTGACATTCACAAATTCGATCTGCCTTTAAAGCT 192
QY 61 AspGluPheLeuAntThrPheIleAlaLeuPheGluSerIleLysArgLysLeuProPheLeu 80
DB 193 GATGAGTTCCTGAACGTGACAGCCCTCTTGAGTCTATCAAAAGAAACTTCCTTCTC 252
QY 81 AsnTrpAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 99
DB 253 AACTGGATGCTTCTTCTTAAGCTGAAGAGCTGAAGAGCGCAACTCTGATGCCAG 309

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Sequence 200: Application US/09991163
Patent No. US20020132253A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary B.
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: KJavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C17
CURRENT APPLICATION NUMBER: US/09/991,163
PRIOR FILING DATE: 2001-11-14
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Patent No. US20020137890A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same

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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

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 QY 81 AsnTrpAspAlaPheProGlyLeuArgSerAlaThrProAspAlaGln 99  
 DB 253 AACTGGATGCTTCTTAAGCTAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 309  
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Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Gertlson, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
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APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730P1C20  
CURRENT APPLICATION NUMBER: US/09/992,598  
CURRENT FILING DATE: 2001-11-14  
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QY 21 GInGyAlaThLeuGlyGlyProGluGluGluSerThrIleGluAsnTYAlaSerArg 40  
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QY 41 ProGluAlaPheAsnThrProPheLeuAsnIleAspIleuArgSerAlaPheIysAla 60

DB 133 CCCAGGCCCTTTAAACCCCGCTTCCTGAACATCGAATAATGCGATCGCTTAAGGCT 192  
QY 61 AspGluPheLeuAsnTPHISAlaLeuPheGluSerIleIysArgIleuProPheLeu 80  
DB 193 GATAGTTCCTGAACCTGACAGCCCTCTTGAAGTCATCAAGAAACCTCTTCTCTC 252  
QY 81 AsnTPAspAlaPheProLysLeuIleGlyLeuArgSerAlaThrProAspAlaGln 99  
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US-09-989-293A-200  
Sequence 200, Application US/09989293A  
Patent No. US20020177164A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C66  
CURRENT FILING DATE: US/09/989, 293A  
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[illegible][illegible]

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| Best Local Similarity: | 100.00%  |
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Search completed: November 28, 2003, 09:32:03  
Job time : 270 secs



PR 30-MAY-1997; 97US-0048069.  
PR 30-MAY-1997; 97US-0048094.  
PR 30-MAY-1997; 97US-0048095.  
PR 30-MAY-1997; 97US-0048096.  
PR 30-MAY-1997; 97US-0048099.  
PR 30-MAY-1997; 97US-0048131.  
PR 30-MAY-1997; 97US-0048135.  
PR 30-MAY-1997; 97US-0048154.  
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PR 30-MAY-1997; 97US-0048186.  
PR 30-MAY-1997; 97US-0048187.  
PR 30-MAY-1997; 97US-0048188.  
PR 30-MAY-1997; 97US-0048350.  
PR 30-MAY-1997; 97US-0048351.  
PR 30-MAY-1997; 97US-0048352.  
PR 30-MAY-1997; 97US-0048355.  
PR 05-AUG-1997; 97US-0054804.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Brewer LA, Duan R, Ebner R, Ferlie AM, Florence KA,  
PI Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;  
PI Rosen CA, Ruben SM, Shi Y, Young P;  
XX WPI; 1999-070066/06.  
XX N-PSDB; AAX00632.  
XX  
XX New isolated human genes and the secreted polypeptides they encode -  
PT useful for diagnosis and treatment of e.g. cancer, neurological  
PT disorders, immune diseases, inflammation or blood disorders  
XX  
XX Claim 11; Page 285; 385pp; English.  
XX  
XX This sequence represents a secreted human protein encoded by the gene  
CC clone detailed in the descriptor line. The gene can be used to generate  
CC fusion proteins by linking to the gene to a human immunoglobulin Fc  
CC portion (e.g. AAX00602) for increasing the stability of the fused  
CC protein as compared to the human protein only.  
CC The invention relates to 87 novel genes and their fragments (nucleic  
CC acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004)  
CC which are useful for preventing, treating or ameliorating medical  
CC conditions e.g. by protein or gene therapy. Also, pathological  
CC conditions can be diagnosed by determining the amount of the new  
CC polypeptides in a sample or by determining the presence of mutations in  
CC the new polynucleotides. Specific uses are described for each of the 87  
CC polynucleotides, based on which tissues they are most highly expressed in  
CC (see AAX00611 for described uses).  
XX  
XX Sequence 99 AA;  
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QY 61 KGLRSATPDAQ 71  
DB 89 KGLRSATPDAQ 99  
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AAY66681  
ID AAY66681 standard; protein; 99 AA.  
XX  
AC AAY66681;  
XX  
DT 05-APR-2000 (first entry)  
XX  
DE Membrane-bound protein PRO826.  
XX

KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIR ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping.  
XX  
OS Homo sapiens.  
XX W09963088-A2.  
EN  
XX  
PD 09-DEC-1999.  
XX  
PF 02-JUN-1999; 99WO-US12252.  
XX  
XX 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
PR 02-JUN-1998; 98US-0087759.  
PR 03-JUN-1998; 98US-0087827.  
PR 04-JUN-1998; 98US-0088021.  
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PR 05-JUN-1998; 98US-0088217.  
PR 05-JUN-1998; 98US-0088555.  
PR 09-JUN-1998; 98US-0088655.  
PR 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
PR 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
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PR 10-JUN-1998; 98US-0088826.  
PR 11-JUN-1998; 98US-0088828.  
PR 11-JUN-1998; 98US-0088858.  
PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
PR 12-JUN-1998; 98US-0089090.  
PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
PR 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089801.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.  
PR 19-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
PR 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090355.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090461.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.

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|  | PR                    | 24-JUN-1998;  | 98US-0090538. |
|  | XX                    | 24-JUN-1998;  | 98US-0090540. |
|  | PA                    | (GETH ) GENENTECH INC.  | 98US-0090557. |
|  | XX                    | Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;              | 98US-0090676. |
|  | PI                    | Wood WL, Yuan J;  | 98US-0090678. |
|  | XX                    | WPI; 2000-072883/06.  | 98US-0090680. |
|  | DR                    | N-Psdb; AAZ65018.   | 98US-0090681. |
|  | XX                    | Membrane-bound proteins and related nucleotide sequences -                | 98US-0090694. |
|  | PT                    | claim 12; Fig 129; 822pp; English.  | 98US-0090695. |
|  | PS                    | The invention provides membrane-bound PRO polypeptides and                | 98US-0090696. |
|  | XX                    | polynucleotides encoding them. The PRO sequences of the invention were    | 98US-0090697. |
|  | CC                    | identified based on extracellular domain homology screening. The PRO      | 98US-0090698. |
|  | CC                    | sequences have homology with proteins including LDL receptors, TIR        | 98US-0090699. |
|  | CC                    | ligands and various enzymes. The membrane-bound proteins and receptor     | 98US-0090700. |
|  | CC                    | molecules are useful as pharmaceutical and diagnostic agents. Receptor    | 98US-0090701. |
|  | CC                    | immunoadhesins, for instance, can be used as therapeutic agents to block  | 98US-0090702. |
|  | CC                    | receptor-ligand interactions. The membrane-bound proteins can also be     | 98US-0090703. |
|  | CC                    | employed for screening of potential peptide or small molecule inhibitors  | 98US-0090704. |
|  | CC                    | of the relevant receptor/ligand interaction. The PRO encoding sequences   | 98US-0090705. |
|  | CC                    | are useful as hybridization probes, in chromosome and gene mapping and in | 98US-0090706. |
|  | CC                    | the generation of antisense RNA and DNA. PRO nucleic acid sequences       | 98US-0090707. |
|  | CC                    | will also be useful for the preparation of PRO polypeptides, especially   | 98US-0090708. |
|  | SQ                    | by recombinant techniques.  | 98US-0090709. |
|  | XX                    | Sequence 99 AA;   | 98US-0090710. |
|  | Query Match           | 100.0%; Score 71; DB 21; Length 99;                                       | 98US-0090711. |
|  | Best Local Similarity | 100.0%; Pred. No. 1.6e-69;  | 98US-0090712. |
|  | Matches               | 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0                        | 98US-0090713. |
|  | QY                    | 1 EESSTINVASRPFAFTPLNIDKLSAKFADEFLNMHALFSSIRKKLPFLMWDAFPKL 60             | 98US-0090714. |
|  | DB                    | 29 EEESTINIASRPAFAFTPLNIDKLSAKFADEFLNMHALFSSIRKKLPFLMWDAFPKL 88           | 98US-0090715. |
|  | QY                    | 61 KGARSATPDQA 71   | 98US-0090716. |
|  | DB                    | 89 KGARSATPDQA 99   | 98US-0090717. |
|  | RESULT 3              |   |               |
|  | AAB20117              |   |               |
|  | ID                    | AAB20117 standard; Protein; 99 AA.  |               |
|  | AC                    | AAB20117;   |               |
|  | XX                    | 30-APR-2001 (first entry)   |               |
|  | DT                    |   |               |
|  | XX                    | Human immunostimulant PRO826.   |               |
|  | DE                    |   |               |
|  | XX                    | PRO826; UNQ467; human; immune disease; autoimmune disease;                |               |
|  | KW                    | anti-neumatic; anti-arthritis; anti-inflammatory; antianemic;             |               |
|  | KW                    | immunosuppressive; antithyroid; antidiabetic; neuroprotective;            |               |
|  | KW                    | hepatotropic; virucide; dermatological; antipsoriatic;                    |               |
|  | KW                    | antiallergic; immunostimulant.  |               |
|  | OS                    | Homo sapiens.   |               |
|  | XX                    |   |               |
|  | PH                    | Key   |               |
|  | FT                    | Peptide   |               |
|  | FT                    | /label= Signal_peptide  |               |
|  | FT                    | Protein   |               |
|  | FT                    | /label= Mature_protein  |               |
|  | FT                    | Modified-site   |               |
|  | FT                    | /note= "N-myristoylation site"  |               |
|  | FT                    | Modified-site   |               |
|  | FT                    | /note= "N-myristoylation site"  |               |
|  | FT                    | Region  |               |
|  | FT                    | /note= "homology to peroxidase"   |               |

XX MO200105972-A1.  
 XX 25-JAN-2001.  
 XX 15-MAR-2000; 2000MO-US06884.  
 XX 20-JUL-1999; 99US-0144758.  
 XX (GETH ) GENENTECH INC.  
 XX Aabkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
 PI Hillan KJ, Mark MR, Marsters SA, Pileri RM, Tumas D, Watanabe CK;  
 PI Wood WI;  
 XX WPI; 2001-103149/11.  
 DR N-PSDB; AAF30059.  
 XX  
 PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
 PT diagnosing and treating immune-related disorders, such as multiple  
 PT sclerosis, rheumatoid arthritis and diabetes -  
 XX  
 PS Claim 20; Fig 20; 127pp; English.  
 XX  
 CC The present sequence is that of novel human immunomodulator PRO826  
 CC (UNQ467), as deduced from cDNA (see AAF30059) isolated from a  
 CC database screening. PRO826 has a mol.wt. of 11 kDa and a pI of  
 CC 7.47. The invention provides polynucleotides (see AAF30050-62)  
 CC encoding novel human PRO proteins (see AAB20108-20) including PRO826.  
 CC Claimed compositions comprising these proteins or their agonists  
 CC are useful for increasing infiltration of inflammatory cells into  
 CC a tissue of a mammal, stimulating or enhancing an immune  
 CC response, or increasing the proliferation of T-lymphocytes in a  
 CC mammal in response to an antigen. Claimed compositions comprising  
 CC a PRO polypeptide or its antagonist have the opposite effect. A  
 CC claimed method for treating an immune related disorder, such as a T  
 CC cell disorder, involves administering a PRO polypeptide, an agonist  
 CC antibody or an antagonist antibody. The disorder is selected from  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated  
 CC renal disease, demyelinated diseases (such as multiple sclerosis),  
 CC autoimmune chronic active hepatitis, primary biliary cirrhosis,  
 CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel  
 CC disease (ulcerative colitis and Crohn's disease), gluten-sensitive  
 CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases  
 CC (such as bullous skin disease, erythema multiforme and psoriasis),  
 CC allergic diseases (such as asthma, allergic rhinitis, atopic  
 CC dermatitis, food hypersensitivity and urticaria), immunologic  
 CC diseases of the lung and transplantation associated diseases (such  
 CC as graft rejection and graft-versus-host disease) (all claimed).  
 CC Claimed methods of diagnosing these disorders comprise detecting  
 CC the level of expression of the PRO gene. Also claimed are a method  
 CC of identifying a compound capable of inhibiting the expression or  
 CC activity of the PRO polypeptide, vectors, host cells, antibodies,  
 CC and a method of stimulating the proliferation of T lymphocytes  
 CC using PRO826.  
 XX  
 SQ Sequence 99 AA;  
 Query Match 100.0%; Score 71; DB 22; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-59;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EESTINVSAPPAFTPTPLNTDKLSAPKADFLNMHLFESIKRKLPLINMDAPKL 60  
 DB 29 EESTINVSAPPAFTPTPLNTDKLSAPKADFLNMHLFESIKRKLPLINMDAPKL 88  
 QY 61 KGLRSATPDAQ 71  
 DB 89 KGLRSATPDAQ 99

RESULT 4  
 ID AAB65204  
 ID AAB65204 standard; Protein; 99 AA.  
 AC AAB65204;  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Human PRO826 (UNQ467) protein sequence SEQ ID NO:201.  
 XX  
 KW Human; secreted and transmembrane protein; PRO; cytosolic;  
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200073454-A1.  
 XX 07-DEC-2000.  
 PD  
 XX  
 PF 30-MAR-2000; 2000MO-US08439.  
 XX  
 PR 02-JUN-1999; 99MO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146322.  
 PR 17-AUG-1999; 99US-0149396.  
 PR 15-SEP-1999; 99MO-US21090.  
 PR 15-SEP-1999; 99MO-US21547.  
 PR 08-OCT-1999; 99US-0158663.  
 PR 30-NOV-1999; 99MO-US28313.  
 PR 01-DEC-1999; 99MO-US28301.  
 PR 16-DEC-1999; 99MO-US30095.  
 PR 20-DEC-1999; 99MO-US30911.  
 PR 05-JAN-2000; 2000MO-US00219.  
 PR 06-JAN-2000; 2000MO-US00376.  
 PR 11-FEB-2000; 2000MO-US03565.  
 PR 18-FEB-2000; 2000MO-US04341.  
 PR 22-FEB-2000; 2000MO-US04414.  
 PR 24-FEB-2000; 2000MO-US04914.  
 PR 24-FEB-2000; 2000MO-US05004.  
 PR 02-MAR-2000; 2000MO-US05841.  
 PR 15-MAR-2000; 2000MO-US06884.  
 PR 20-MAR-2000; 2000MO-US07377.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Aabkenazi AJ, Baker KP, Botstein D, Deaneviers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Gtimaldi CJ, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Piloni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX  
 DR WPI; 2001-032160/04.  
 DR N-PSDB; AAF44164.  
 XX  
 PT PRO polynucleotides used to produce polypeptides used to target  
 PT bioactive molecules such as toxins, radiolabels or antibodies, to  
 PT specific cells, to cause targeted cell death -  
 XX  
 PS Claim 12; Fig 129; 935pp; English.  
 XX  
 CC The present invention describes human secreted and transmembrane PRO  
 CC proteins. The PRO proteins have cytosolic activity. The PRO proteins  
 CC can be used for targeted delivery of bioactive molecules, such as  
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
 CC and DNA. They may also be used to produce transgenic animals which are



CC used to develop and screen therapeutically useful reagents. The PRO  
 CC nucleotide and protein sequence can be used for tissue typing and in  
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
 CC AAB65154 to AAB65500 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX Sequence 99 AA;

Query Match 100.0%; Score 71; DB 22; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPEAFNTPLNIDKLSAFKADDEFINMHALFESIKRKLPLINMDAPFRL 60  
 DB 29 EESTIENYASRPEAFNTPLNIDKLSAFKADDEFINMHALFESIKRKLPLINMDAPFRL 88  
 QY 61 KGLRSATPDAQ 71  
 DB 89 KGLRSATPDAQ 99

RESULT 5  
 ID AAB50916 standard; Protein; 99 AA.

AC AAB50916;  
 DT 21-MAR-2001 (first entry)  
 DE Human PRO826 protein.

KW Human; PRO; antiinflammatory; dermatological; antirheumatic;  
 KW antirheumatic; cardiantic; antihaemic; immunosuppressive; antihydroid;  
 KW antidiabetic; nocitropic; neuroprotective; hepatocytic; vitucide;  
 KW antiallergic; antiasthmatic; immune related disorder;  
 KW hepatobiliary disease; autoimmune disease; allergy.

OS Homo sapiens.

PN WO200073452-A2.

PD 07-DEC-2000.

PF 02-JUN-2000; 2000WO-US15264.

XX 02-JUN-1999; 99WO-US12252.  
 XX 20-JUL-1999; 99US-0144732.  
 XX 20-JUL-1999; 99US-0144758.  
 XX 28-JUL-1999; 99US-0146222.  
 XX 01-SEP-1999; 99WO-US20111.  
 XX 15-SEP-1999; 99WO-US21090.  
 XX 15-SEP-1999; 99WO-US21547.  
 XX 29-OCT-1999; 99US-0162506.  
 XX 30-NOV-1999; 99WO-US28313.  
 XX 01-DEC-1999; 99WO-US28634.  
 XX 09-DEC-1999; 99US-0170262.  
 XX 20-DEC-1999; 99WO-US30511.  
 XX 05-JAN-2000; 2000WO-US00219.  
 XX 06-JAN-2000; 2000WO-US00376.  
 XX 11-FEB-2000; 2000WO-US03565.  
 XX 18-FEB-2000; 2000WO-US04341.  
 XX 18-FEB-2000; 2000WO-US04342.  
 XX 22-FEB-2000; 2000WO-US04414.  
 XX 24-FEB-2000; 2000WO-US04814.  
 XX 15-MAR-2000; 2000WO-US06884.  
 XX 20-MAR-2000; 2000WO-US07377.  
 XX 21-MAR-2000; 2000WO-US07532.  
 XX 30-MAR-2000; 2000WO-US08339.  
 XX 17-MAY-2000; 2000WO-US13705.  
 XX 22-MAY-2000; 2000WO-US14042.

PA (GENTH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
 PI Wood WI;  
 DR WPI; 2001-025253/03.  
 DR N-PsDB; AAC91475.

PT Thirty three nucleic acids encoding PRO polypeptides which are useful  
 PT in the diagnosis and treatment of immune related disorders, e.g.  
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 PT thyroiditis and diabetes mellitus -

PS Claim 58; Fig 30; 218pp; English.

CC The present sequence is one of thirty three novel PRO polypeptides.  
 CC The PRO polypeptides, anti-PRO antibodies, agonists and  
 CC antagonists are useful for treating and diagnosing immune related  
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
 CC (such as infectious, autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
 CC food hypersensitivity and urticaria), immunological diseases of the  
 CC lung (such as eosinophilic pneumonia, idiopathic pulmonary fibrosis  
 CC and hypersensitivity pneumonitis), transplantation associated diseases  
 CC including graft rejection and graft-versus-host diseases.

XX SQ Sequence 99 AA;

Query Match 100.0%; Score 71; DB 22; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPEAFNTPLNIDKLSAFKADDEFINMHALFESIKRKLPLINMDAPFRL 60  
 DB 29 EESTIENYASRPEAFNTPLNIDKLSAFKADDEFINMHALFESIKRKLPLINMDAPFRL 88  
 QY 61 KGLRSATPDAQ 71  
 DB 89 KGLRSATPDAQ 99

RESULT 6

ID AAB53094 standard; Protein; 99 AA.

AC AAB53094;

DT 28-FEB-2001 (first entry)

DE Human angiogenesis-associated protein PRO826, SEQ ID NO:158.

XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
 XX cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
 XX angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
 XX myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
 XX Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
 XX Alzheimer's disease; Huntington's disease; stroke; drug screening;  
 XX gene therapy; transgenic animal.

OS Homo sapiens.

XX WO200053753-A2.  
 XX 14-SEP-2000.  
 XX  
 XX 05-JAN-2000; 2000WO-US00219.  
 XX  
 XX 08-MAR-1999; 99WO-US05028.  
 XX 12-MAR-1999; 99US-0123957.  
 XX 14-MAY-1999; 99US-0134287.  
 XX 23-JUN-1999; 99WO-US12252.  
 XX 20-JUL-1999; 99US-0141037.  
 XX 26-JUL-1999; 99US-0144758.  
 XX 01-SEP-1999; 99US-0145698.  
 XX 08-SEP-1999; 99WO-US20111.  
 XX 15-SEP-1999; 99WO-US20594.  
 XX 15-SEP-1999; 99WO-US21090.  
 XX 05-OCT-1999; 99WO-US23089.  
 XX 30-NOV-1999; 99WO-US28313.  
 XX 02-DEC-1999; 99WO-US28409.  
 XX 02-DEC-1999; 99WO-US28564.  
 XX 02-DEC-1999; 99WO-US28565.  
 XX  
 XX (GENTH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
 XX Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Masters SA,  
 XX Paoni NF, Pictti RM, Watanabe CK, Williams PM, Wood WI,  
 XX WPI: 2001-090793/10.  
 XX N-PSDB; AAC97491.  
 XX  
 XX New isolated nucleic acid for producing a PRO polypeptide, analyzing  
 XX genetic disorders and treating cardiovascular, endothelial or  
 XX angiogenic disorders, such as atherosclerosis, wounds or cancer -  
 XX  
 XX Claim 69; Fig 62; 293pp; English.  
 XX  
 XX The invention relates to novel human angiogenesis-associated proteins  
 XX designated PRO proteins (AA53064-B53097), and to nucleic acids encoding  
 XX PRO proteins. The invention also relates to vectors and host cells  
 XX comprising a PRO nucleic acid, the recombinant production of a PRO  
 XX protein, PRO antibodies specific for a PRO protein, fusion proteins  
 XX comprising a PRO protein, agonists or antagonists of a PRO protein, and  
 XX compounds which inhibit the expression of a PRO gene. The invention  
 XX additionally encompasses methods of identifying modulators of PRO  
 XX expression or activity; diagnosing a cardiovascular, endothelial or  
 XX angiogenic disorder, or a susceptibility to such a disorder by detecting  
 XX mutations in a PRO gene, or the expression level of a PRO gene within a  
 XX particular tissue; treating a cardiovascular, endothelial or angiogenic  
 XX disorder via the administration of a PRO protein, PRO nucleic acid, or  
 XX PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
 XX PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
 XX cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
 XX administration of a PRO protein, or an agonist or antagonist thereof.  
 XX PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
 XX agonists and PRO antagonists may be used as therapeutic agents to treat  
 XX cardiovascular, endothelial or angiogenic disorders, such as  
 XX atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
 XX diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
 XX endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
 XX disease, or stroke. PRO nucleic acids are additionally useful in the  
 XX recombinant production of PRO proteins, as hybridization probes to  
 XX screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
 XX to map genes encoding PRO proteins, to analyse genetic disorders, and in  
 XX gene therapy. PRO nucleic acids can also be used to produce transgenic  
 XX animals useful for the development and screening of potential  
 XX therapeutic agents. The present sequence represents a PRO protein of the  
 XX invention.  
 XX Sequence 99 AA;

Query Match 100.0%; Score 71; DB 22; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EESTETENTYASRPEAFNTPTFLINDKRSAPFADERTLMMHALLPESTIKRLLPFLNMDAPFRL 60  
 DB 29 EESTETENTYASRPEAFNTPTFLINDKRSAPFADERTLMMHALLPESTIKRLLPFLNMDAPFRL 88  
 QY 61 KGLRSATPDAQ 71  
 DB 89 KGLRSATPDAQ 99  
 RESULT 7  
 ABP69586  
 ID ABP69586 standard; Protein; 99 AA.  
 AC ABP69586;  
 XX  
 XX 20-JAN-2003 (first entry)  
 XX  
 XX Human polypeptide SEQ ID NO 1633.  
 DE  
 XX Human; genome mapping; gene therapy; food supplement; virus; fungus;  
 XX cell-proliferative disorder; neurodegenerative disease; bacterial;  
 XX Parkinson's disease; Alzheimer's disease; autoimmune disease;  
 XX multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
 XX arthritis; cytostatic; immunomodulator; neoplastic; neuroprotective;  
 XX antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
 XX haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;  
 XX antithrilltic.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200270539-A2.  
 XX 12-SEP-2002.  
 PD  
 XX  
 XX 05-MAR-2002; 2002WO-US05095.  
 PF  
 XX  
 XX 05-MAR-2001; 2001US-0799451.  
 PR  
 XX  
 XX (HUSE-) HUSEQ INC.  
 XX  
 XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
 XX Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
 XX Wehman T, Wang J, Wang D, Dmanac RT;  
 XX WPI: 2002-759812/82.  
 XX N-PSDB; AB211803.  
 DR  
 XX  
 XX New polynucleotides comprising sequences assembled from expressed  
 XX sequence tags (ESTs), useful for treating cell-proliferative,  
 XX neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or  
 XX platelet or coagulation disorders -  
 XX  
 XX Claim 9; SEQ ID NO 1633; 1012pp + Sequence Listing; English.  
 PS  
 XX The invention relates to an isolated polynucleotide (I) comprising a  
 XX nucleotide sequence selected from any of 948 sequences  
 XX (AB21119-AB212066) or their mature protein coding portion, active domain  
 XX coding protein or complementary sequences. The polynucleotides are useful  
 XX for identifying expressed genes or for physical mapping of human genome.  
 XX The encoded polypeptides (ABP68902-ABP68849) are useful as molecular  
 XX weight markers, as a food supplement, for generating antibodies, in  
 XX medical imaging, screening and diagnostic assays and for treating  
 XX cell-proliferative disorders (cancer), neurodegenerative diseases  
 XX (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple  
 XX sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid  
 XX disorders, platelet or coagulation disorders, wound, burns, incision,  
 XX ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,  
 XX parasitic), arthritis, etc.  
 CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPD  
 CC at ftp.wipd.int/pub/published\_pct\_sequences.

XX Sequence 99 AA;

Query Match 100.0%; Score 71; DB 23; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBEESTIENYASRPEAFNTPLINIDKLSAFKADDEFNWHALFESIKRKLPLNWDAPFPL 60  
 DB 29 EBEESTIENYASRPEAFNTPLINIDKLSAFKADDEFNWHALFESIKRKLPLNWDAPFPL 88

QY 61 KGLRSATPDQAQ 71  
 DB 89 KGLRSATPDQAQ 99

## RESULT 8

ABG34040  
 ID ABG34040 standard; Protein; 99 AA.

AC ABG34040;

DT 19-JUL-2002 (first entry)

XX Human angiogenesis related protein PRO826 SEQ ID NO: 132.

KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiac; cytoskeletal; antiangiogenic; hypotensive; vulnerary;  
 KW antiarteriosclerotic.

OS Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

PF 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 28-JUL-2000; 2000US-220664P.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-0643657.

XX 23-AUG-2000; 2000WO-US23322.

XX 07-SEP-2000; 2000US-230978P.

XX 15-SEP-2000; 2000US-000000P.

XX 18-SEP-2000; 2000US-0664610.

XX 24-OCT-2000; 2000US-242922P.

XX 08-NOV-2000; 2000US-0709238.

XX 10-NOV-2000; 2000WO-US30952.

XX 01-DEC-2000; 2000WO-US30873.

XX 20-DEC-2000; 2000US-0747259.

XX 22-DEC-2000; 2000WO-US34956.

XX 28-FEB-2001; 2001US-0767609.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2001; 2001WO-US06666.

XX 09-MAR-2001; 2001US-0802706.

XX 14-MAR-2001; 2001US-0806889.

XX 22-MAR-2001; 2001US-0816744.

XX 05-APR-2001; 2001US-0828366.

XX 10-MAY-2001; 2001US-0854208.

XX 10-MAY-2001; 2001US-0854280.

XX 25-MAY-2001; 2001US-0866028.

XX 25-MAY-2001; 2001US-0866034.

XX 25-MAY-2001; 2001WO-US17092.

PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 28-JUN-2001; 2001WO-US00000.

XX (GETH) GENENTECH INC.

PA (BAKE) BAKER K P.

PA (FERR) FERRARA N.

PA (GERB) GERBER H.

PA (GERR) GERRITSEN M E.

PA (GODD) GODDARD A.

PA (GODO) GODOWSKI P J.

PA (GURN) GURNEY A L.

PA (HILL) HILLAN K J.

PA (MARS) MASTERS S A.

PA (PANI) PAN J.

PA (PAON) PAONI N F.

PA (STEP) STEPHAN J F.

PA (WATA) WATANABE C K.

PA (WILL) WILLIAMS P M.

PA (WOOD) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,

PI Godowski PJ, Gurney AL, Hillan KJ, Masters SA, Pan J, Paoni NF,

PI Stephan JP, Watanabe CK, Williams PM, Wood WI, Ye W;

DR WPI; 2002-171999/22.

XX N-PSDB; ABL95626.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial

PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 11; Fig 132; 567pp; English.

XX The present invention provides the protein and coding sequences of human

XX PRO proteins. These are useful for treating or diagnosing a

XX cardiovascular, endothelial or angiogenic disorder, including cardiac

XX hypertrophy, trauma, cancer, age-related macular degeneration,

XX atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound

XX healing. The present sequence is a PRO protein of the invention.

XX Sequence 99 AA;

Query Match 100.0%; Score 71; DB 23; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBEESTIENYASRPEAFNTPLINIDKLSAFKADDEFNWHALFESIKRKLPLNWDAPFPL 60  
 DB 29 EBEESTIENYASRPEAFNTPLINIDKLSAFKADDEFNWHALFESIKRKLPLNWDAPFPL 88

QY 61 KGLRSATPDQAQ 71  
 DB 89 KGLRSATPDQAQ 99

## RESULT 9

ABG34040  
 ID ABG34040 standard; Protein; 99 AA.

AC ABG34040;

DT 15-JUL-2002 (first entry)

XX Human Pro peptide #11.

XX Human; PRO; secreted protein; transmembrane protein;

XX genetic disorder; tumour; cancer.

OS Homo sapiens.  
 XX WO200224888-A2.  
 XX  
 PD 28-MAR-2002.  
 XX  
 PF 29-AUG-2001; 2001WO-US27099.  
 XX  
 PR 01-SEP-2000; 2000US-229896P.  
 PR 05-SEP-2000; 2000US-230621P.  
 PR 22-SEP-2000; 2000US-235147P.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 12-JAN-2001; 2001US-261878P.  
 PR 16-JAN-2001; 2001US-261910P.  
 PR 16-JAN-2001; 2001US-261939P.  
 PR 16-JAN-2001; 2001US-262150P.  
 PR 25-JAN-2001; 2001US-264395P.  
 PR 02-FEB-2001; 2001US-266421P.  
 PR 09-FEB-2001; 2001US-267623P.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 03-MAR-2001; 2001US-274399P.  
 PR 04-APR-2001; 2001US-280982P.  
 PR 04-APR-2001; 2001US-282129P.  
 PR 09-MAY-2001; 2001US-282199P.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 XX  
 PA (GENTH ) GENENTECH INC.  
 XX  
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;  
 PI Gurney AL, Smith V, Stephan U, Watanabe CK, Wood WI, Zhang Z;  
 PI Fong S;  
 DR WPI; 2002-362426/39.  
 DR N-PSDB; ABR69971.  
 XX  
 PT New PRO polypeptides and polynucleotides encoding the polypeptides,  
 PT useful in gene therapy, chromosome identification, tissue typing, or  
 PT for genetic analysis of individuals with genetic disorders -  
 XX  
 PS Claim 11; Figure 22; 218pp; English.  
 XX  
 CC This invention relates to the cDNA and protein sequences of novel  
 CC secreted and transmembrane polypeptides PRO polypeptides. The  
 CC invention also comprises a method for producing the proteins of the  
 CC of the invention. The antibody may be used for detecting the PRO  
 CC proteins of the invention and may be used to modify their activity.  
 CC polynucleotides may be used as hybridisation probes for a cDNA library  
 CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
 CC construct hybridisation probes for mapping the gene which encodes that  
 CC PRO and for genetic analysis of individuals with genetic disorders, in  
 CC assays to identify other proteins or molecules involved in binding  
 CC reaction, to generate transgenic animals or knock-out animals in  
 CC turn are useful in the development and screening of therapeutically  
 CC useful reagents, for chromosome identification, and tissue typing. The  
 CC PRO polypeptides are useful in gene therapy, and as molecular weight  
 CC markers for protein electrophoresis purposes. The sequences may  
 CC also be used to detect overexpression on PRO polypeptides in cancerous  
 CC tumours and for screening for differentially expressed genes using  
 CC microarray technology. The present sequence represents a human PRO  
 CC protein of the invention.  
 XX  
 SQ Sequence 99 AA;

Query Match 100.0%; Score 71; DB 23; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 1,6e-69;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EESTIENYASRPAFTPLNIDKRSAPFADEFLNMWHLFESIKKLPFLNWDAPPKL 60  
 DB 29 EESTIENYASRPAFTPLNIDKRSAPFADEFLNMWHLFESIKKLPFLNWDAPPKL 88  
 OY 61 KGLRSATPDAQ 71  
 DB 89 KGLRSATPDAQ 99  
 RESULT 10  
 ABB84882  
 ID ABB84882 standard; Protein; 99 AA.  
 XX  
 AC ABB84882;  
 XX  
 DT 16-MAY-2002 (first entry)  
 XX  
 DE Human PRO826 protein sequence SEQ ID NO:132.  
 XX  
 KW Human; angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;  
 KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; gene mapping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200200690-A2.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 20-JUN-2001; 2001WO-US19692.  
 XX  
 PR 23-JUN-2000; 2000US-213637P.  
 PR 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220664P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 02-AUG-2000; 2000US-222959P.  
 PR 17-AUG-2000; 2000US-0643657.  
 PR 23-AUG-2000; 2000WO-US33522.  
 PR 24-AUG-2000; 2000WO-US33328.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 18-SEP-2000; 2000US-0665350.  
 PR 24-OCT-2000; 2000US-242922P.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US32678.  
 PR 01-DEC-2000; 2000WO-US32573.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866038.  
 PR 25-MAY-2001; 2001US-0866038.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 XX  
 PA (GENTH ) GENENTECH INC.



Human, PRO; antiinflammatory; ophthalmological; vasotropic;  
 retinal cell injury; ocular disease; retinitis pigmentosa;  
 macular degeneration; retinal detachment; retinal tear; retinopathy;  
 retinal degenerative disease; macular hole; degenerative myopia;  
 acute retinal necrosis syndrome; traumatic choriorretinopathy;  
 Putscher's retinopathy; oedema; ischaemic condition;  
 retinal vision occlusion; collagen vascular disease;  
 thrombocytopaenic purpura; uveitis; retinal vasculitis; Bales disease;  
 systemic lupus erythematosus; environmental trauma.

OS Homo sapiens.  
 XX WO200109327-A2.  
 XX  
 PD 08-FEB-2001.  
 XX  
 PF 28-JUL-2000; 2000WO-US20710.  
 XX  
 PR 28-JUL-1999; 99US-146222P.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.

XX (GENTECH) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL,  
 PI Kijavich IU, Lafleur M, Mark MR, Marsters SA, Patti RM,  
 PI Watanabe CK, Wood WI;  
 XX  
 DR WPI; 2002-130120/17.  
 N-PSDB; ABK28660.

XX Promoting survival of retinal cells, or delaying or preventing retinal  
 PT cell injury or death, by contacting retinal cells with PRO175, 220,  
 PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132  
 PT polypeptide -  
 XX  
 PS Claim 44; Fig 25; 152pp; English.

XX The invention relates to promoting the survival of retinal cells, or  
 CC delaying or preventing retinal cell injury or death, by contacting the  
 CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
 CC PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO828, PRO826,  
 CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
 CC encoding the PRO proteins, a vector comprising the nucleic acid, a host  
 CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
 CC useful for promoting survival of retinal cells (retinal neurons such as  
 CC retinal ganglion cells, displaced retinal ganglion cells, amacrine  
 CC cells, displaced amacrine cells, horizontal neurons or bipolar neurons,  
 CC rod photoreceptors, or supportive cells such as Muller cells or pigment  
 CC epithelial cells), or delaying or preventing retinal cell injury or  
 CC death caused by ocular disease (which is or is associated with  
 CC retinitis pigmentosa, macular degeneration, retinal detachment, retinal  
 CC tear, retinopathy, retinal degenerative disease, macular hole,  
 CC degenerative myopia, acute retinal necrosis syndrome, traumatic  
 CC choriorretinopathy or contusion, Putscher's retinopathy, oedema, an  
 CC ischaemic condition, central or branch retinal vision occlusion,  
 CC collagen vascular disease, thrombocytopaenic purpura, uveitis, retinal  
 CC vasculitis, occlusion associated with Bales disease or systemic lupus  
 CC erythematosus), retinal injury or environmental trauma. The retinal  
 CC cell injury or death is delayed or prevented by substantially not

CC causing angiogenesis or mitogenesis. The present sequence represents  
 CC a PRO protein.  
 XX  
 XX Sequence 99 AA;  
 SQ  
 Query Match 100.0%; Score 71; DB 23; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-69;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPEAFNTPLNIDKRSAPRADEFLNHALFESTIKRLPLNMDAPKRL 60  
 DB 29 EESTIENYASRPEAFNTPLNIDKRSAPRADEFLNHALFESTIKRLPLNMDAPKRL 88  
 QY 61 KGLRSATPDQ 71  
 DB 89 KGLRSATPDQ 99

RESULT 13  
 ABUS9097  
 ID ABUS9097 standard; Protein; 99 AA.  
 XX  
 AC ABUS9097;  
 XX  
 DT 28-APR-2003 (first entry)  
 XX  
 DE Novel human secreted or transmembrane protein PRO826.  
 XX  
 KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibitor; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disorder;  
 KW mammalian kidney; mesangial cell proliferation; Berger disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis.

OS Homo sapiens.  
 XX  
 PN US2002132252-A1.  
 XX  
 PD 19-SEP-2002.  
 XX  
 PF 14-NOV-2001; 2001US-0990442.  
 XX  
 PR 05-NOV-1997; 97WO-US20069.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 06-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.

PR 30-MAR-2000; 2000MO-US08439.  
PR 15-MAY-2000; 2000MO-US13358.  
PR 17-MAY-2000; 2000MO-US13705.  
PR 22-MAY-2000; 2000MO-US14042.  
PR 30-MAY-2000; 2000MO-US14941.  
PR 02-JUN-2000; 2000MO-US15264.  
PR 28-JUL-2000; 2000MO-US20710.  
PR 11-AUG-2000; 2000MO-US22031.  
PR 23-AUG-2000; 2000MO-US23522.  
PR 24-AUG-2000; 2000MO-US23328.  
PR 08-NOV-2000; 2000MO-US30952.  
PR 01-DEC-2000; 2000MO-US32678.  
PR 28-FEB-2001; 2001MO-US06520.  
PR 01-JUN-2001; 2001MO-US17800.  
PR 20-JUN-2001; 2001MO-US19682.  
PR 29-JUN-2001; 2001MO-US21056.  
PR 09-JUL-2001; 2001MO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 13-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083323P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088861P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 28-AUG-2001; 2001US-0941992.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL,  
PI Ferrara N, Fong S, Gerber H, Gerlitsen ME, Goddard A, Godowski PJ,  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,

PI Roy MA, Stewart TR, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;  
XX  
DR WPI; 2003-247083/24.  
DR N-PSDB; ABX80254.  
XX  
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer  
PT treatments -  
XX  
PS Claim 12; Fig 129; 648bp; English.  
XX  
CC The invention describes an isolated human PRO polypeptide. The PRO  
CC polypeptides are useful in detecting human PRO polypeptides in a sample, in  
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
CC in modulating at least one biological activity of a cell expressing a PRO  
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
CC useful for treating cardiac insufficiency disorders. PRO1184 and PRO1186  
CC stimulate adrenal cortical capillary endothelial growth. PRO1346 and  
CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
CC useful for treating conditions or disorders where angiogenesis would be  
CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
CC useful for treating cancers/tumours. PRO812 inhibits vascular  
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing of  
CC immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of  
CC retinal neurons cells. (PRO132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813  
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and  
CC are thus useful for treating sports injuries, and arthritis. This  
CC is the amino acid sequence of a novel human PRO protein.  
XX  
SQ Sequence 99 AA;  
Query Match 100.0%; Score 71; DB 24; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1,6e-69;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EESTTENYASRPDAEPTPLNTIDKRSARFKADEPLNTHALFSGIKKLPFLWDAFPPK 60  
DB 29 EESTTENYASRPDAEPTPLNTIDKRSARFKADEPLNTHALFSGIKKLPFLWDAFPPK 88  
QY 61 KGLRSATPDAA 71  
DB 89 KGLRSATPDAA 99  
RESULT 14  
ABUS9244  
ID ABUS9244 standard; Protein; 99 AA.  
XX  
AC ABUS9244;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein, #78.  
XX  
XX Human, PRO; secreted; transmembrane; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
KW gene therapy; tumour-associated antigenic target; TAT; ADAPT;  
KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
XX

OS Homo sapiens.  
XX  
PN US2003027162-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 15-NOV-2001; 2001US-0997428.  
XX  
PR 05-NOV-1997; 97MO-US200069.  
PR 16-SEP-1998; 98MO-US199330.  
PR 17-SEP-1998; 98MO-US199437.  
PR 07-OCT-1998; 98MO-US21141.  
PR 01-DEC-1998; 98MO-US25108.  
PR 05-JAN-1999; 99MO-US00106.  
PR 08-MAR-1999; 99MO-US05028.  
PR 02-JUN-1999; 99MO-US12252.  
PR 15-SEP-1999; 99MO-US21090.  
PR 15-SEP-1999; 99MO-US21547.  
PR 30-NOV-1999; 99MO-US28313.  
PR 01-DEC-1999; 99MO-US28301.  
PR 01-DEC-1999; 99MO-US28634.  
PR 16-DEC-1999; 99MO-US30095.  
PR 20-DEC-1999; 99MO-US30911.  
PR 05-JAN-2000; 2000MO-US00219.  
PR 06-JAN-2000; 2000MO-US00376.  
PR 11-FEB-2000; 2000MO-US03565.  
PR 18-FEB-2000; 2000MO-US04341.  
PR 22-FEB-2000; 2000MO-US04414.  
PR 24-FEB-2000; 2000MO-US04914.  
PR 24-FEB-2000; 2000MO-US05004.  
PR 02-MAR-2000; 2000MO-US05841.  
PR 10-MAR-2000; 2000MO-US06319.  
PR 15-MAR-2000; 2000MO-US06884.  
PR 20-MAR-2000; 2000MO-US07377.  
PR 30-MAR-2000; 2000MO-US08439.  
PR 15-MAY-2000; 2000MO-US13358.  
PR 17-MAY-2000; 2000MO-US13705.  
PR 22-MAY-2000; 2000MO-US14042.  
PR 30-MAY-2000; 2000MO-US14941.  
PR 02-JUN-2000; 2000MO-US15264.  
PR 28-JUL-2000; 2000MO-US20710.  
PR 11-AUG-2000; 2000MO-US22031.  
PR 23-AUG-2000; 2000MO-US23522.  
PR 24-AUG-2000; 2000MO-US23328.  
PR 08-NOV-2000; 2000MO-US30952.  
PR 01-DEC-2000; 2000MO-US32678.  
PR 28-FEB-2001; 2001MO-US06520.  
PR 01-JUN-2001; 2001MO-US17800.  
PR 20-JUN-2001; 2001MO-US19692.  
PR 29-JUN-2001; 2001MO-US21066.  
PR 09-JUL-2001; 2001MO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083332P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
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Best Local Similarity 100.0%; Pred. No. 1,6e-69;

Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 KGLRSATPDAQ 71  
DB 89 KGLRSATPDAQ 99

RESULT 15

ABUS9393 standard; Protein; 99 AA.

AC ABUS9393;

DT 22-APR-2003 (first entry)

DE Novel human secreted or transmembrane protein PRO819.

XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KM cardiac insufficiency disorder; cancer; tumor; immune response;  
KM adrenal cortical capillary endothelial growth; c-fos induction;  
KM vascular endothelial growth factor inhibition; VEGF inhibition;  
KM endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KM retinal neurons cell survival; rod photoreceptor cell survival;  
KM retinal disorder; retinitis pigmentosa; kidney disorder;  
KM mammalian kidney mesangial cell proliferation; Berger disease;

KM dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KM chondrocyte redifferentiation; sports injury; arthritis.  
OS Homo sapiens.  
PN US2003027985-A1.  
XX 06-FEB-2003.  
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XX 05-NOV-1997; 97WO-US200069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 15-SEP-1999; 99WO-US21090.  
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PR 20-DEC-1999; 99WO-US30911.  
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PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
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100.0%; Score 71; DB 24; Length 99;

Best Local Similarity 100.0%; Pred. No. 1.6e-63; Mismatches 0; Indels 0; Gaps 0;

Matches 71; Conservative

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Search completed: November 28, 2003, 13:43:01  
Job time : 37 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:43:04 ; Search time 24 Seconds  
(Without alignments)  
545,645 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 3          | 71    | 100.0       | 99     | 9 US-09-989-729-201   | Sequence 201, App |
| 4          | 71    | 100.0       | 99     | 9 US-09-989-727-201   | Sequence 201, App |
| 5          | 71    | 100.0       | 99     | 10 US-09-989-731-201  | Sequence 201, App |
| 6          | 71    | 100.0       | 99     | 10 US-09-989-732-201  | Sequence 201, App |
| 7          | 71    | 100.0       | 99     | 10 US-09-991-073-201  | Sequence 201, App |
| 8          | 71    | 100.0       | 99     | 10 US-09-990-442-201  | Sequence 201, App |
| 9          | 71    | 100.0       | 99     | 10 US-09-991-163-201  | Sequence 201, App |
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| 13         | 71    | 100.0       | 99     | 10 US-09-992-598-201  | Sequence 142, App |
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| 45 | 71 | 100.0 | 99 | 11 US-09-989-729A-201 | Sequence 201, App |

## ALIGNMENTS

RESULT 1  
US-09-989-722-201  
Sequence 201, Application US/09989722  
Patent No. US200207067A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Garber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austen L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730pic63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17



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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
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Query Match 100.0%; Score 71; DB 9; Length 99;
Best Local Similarity 100.0%; Pred. No. 4.2e-66;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 89 KGLRSATPDQAQ 99
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RESULT 2

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US-09-989-723-201
; Sequence 201, Application US/09989723
; Patent No. US20020072092A1
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GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavich, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478

PRIOR FILING DATE: 1998-07-02  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 71; DB 9; Length 99;  
Best Local Similarity 100.0%; Pred. NO. 4.2e-66; Indels 0; Gaps 0;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 29 EESTIENYASRPEAFNTPFLINIDKLSAFRADEFNLNHALFESIKRKLPLINWDAPFPL 88

Qy 61 KGLRSATPDAQ 71  
Db 89 KGLRSATPDAQ 99

RESULT 3  
US-09-989-279-201  
Sequence 201, Application US/09989279  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC56  
CURRENT FILING DATE: US/09/989,279  
PRIOR APPLICATION NUMBER: 2001-11-19  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
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PRIOR FILING DATE: 1997-11-24

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;; PRIOR FILING DATE: 1998-07-02  
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Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 29 EEESTIENYASRPEAFNPFILNIDKLRSAFKADEFLNMHALFESIKRKLPIFNMDAPFL 88  
Qy 61 KGLRSATPDQAQ 71  
Db 89 KGLRSATPDQAQ 99  
  
RESULT 4  
US-09-989-727-201  
; Sequence 201 Application US/09989727  
; Patent No. US20020072497A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertlisen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC65  
; CURRENT APPLICATION NUMBER: US/09/989,727  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
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PRIOR APPLICATION NUMBER: 60/091978  
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PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09  
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DB 89 KGLRSATPDQ 99  
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Sequence 201, Application US/09989731  
Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerdler, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PLC70  
CURRENT APPLICATION NUMBER: US/09/989,731  
PRIOR FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1997-11-13  
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PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
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PRIOR FILING DATE: 1998-03-20  
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PRIOR FILING DATE: 1998-04-28

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| PRIOR FILING DATE:        | 1998-05-07 |
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| PRIOR FILING DATE:        | 1998-05-28 |
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[illegible]

PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 71; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4,2e-66;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEEESTENASRPEAFNTFPLNDKRSAPKADDEFINMTALBESITRKLPLNMDAPPL 60  
Db 29 EEEESTENASRPEAFNTFPLNDKRSAPKADDEFINMTALBESITRKLPLNMDAPPL 88

Qy 61 KGLRSATPDAQ 71  
Db 89 KGLRSATPDAQ 99

## RESULT 6

US-09-989-732-201  
Sequence 201 Application US/09989732  
Patent No. US20020123463A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
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APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
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APPLICANT: Paoni, Nicholas F.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C57

CURRENT APPLICATION NUMBER: US/09/989,732  
CURRENT FILING DATE: 2001-11-19

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;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982

;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09  
  
Query Match 100.0%; Score 71; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.2e-66;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 EESTIENYARPPAFNTPLNTDKLSAFKADSEFLNMWHLFEESIKRKLPELNDAPPKL 60  
Db 29 EESTIENYARPPAFNTPLNTDKLSAFKADSEFLNMWHLFEESIKRKLPELNDAPPKL 88  
Qy 61 KGLRSATPDQ 71  
Db 89 KGLRSATPDQ 99  
  
RESULT 7  
US-09-991-073-201  
; Sequence 201, Application US/09991073  
; Patent No. US20020127576A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Bolstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C15  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
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; PRIOR FILING DATE: 1998-05-07  
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; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02



Query Match 100.0%; Score 71; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4,28-66;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EESTIENYASRPFNFNFPLNIDKLSAFKADFLNHALFESIKRKLPLINMDAPFKL 60  
Db 29 EESTIENYASRPFNFNFPLNIDKLSAFKADFLNHALFESIKRKLPLINMDAPFKL 88

Qy 61 KGLRSATPDAQ 71  
Db 89 KGLRSATPDAQ 99

RESULT 8  
US-09-990-442-201  
Sequence 201: Application US/09990442  
Patent No. US620020132252A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerdler, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey E.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austlin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumaw, Daniel  
APPLICANT: Williams, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC8  
CURRENT APPLICATION NUMBER: US/09/990,442  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
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PRIOR APPLICATION NUMBER: 60/087609  
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PRIOR APPLICATION NUMBER: 60/087827  
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PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 71; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4,2e-66;

Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 29 EESTIENTYASPEAPNTEPFLNIDKRSAPKADFLNWHALPESIRKULPFLNWDAPPKL 88  
Qy 61 KGLRSATPDQAQ 71  
Db 89 KGLRSATPDQAQ 99

RESULT 9  
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Sequence 201, Application US/09991163  
Patent No. US20020132253A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Ausetin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C17  
CURRENT APPLICATION NUMBER: US/09/991,163  
CURRENT FILING DATE: 2001-11-14  
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Query Match 100.0%; Score 71; DB 10; Length 99;  
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RESULT 10  
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Sequence 201, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
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APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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FILE REFERENCE: P2730P1C25  
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 71; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.2e-66;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBSSTENTYASRPEANTPFLINDKRSAPKADDEFINMTALPBSIRKLPFLNMDAPFL 60  
DB 29 EBSSTENTYASRPEANTPFLINDKRSAPKADDEFINMTALPBSIRKLPFLNMDAPFL 88

QY 61 KGLRSATPDQA 71  
DB 89 KGLRSATPDQA 99

RESULT 11  
US-09-990-456-201  
Sequence 201, Application US/09990456  
Patent No. US20020137890A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Williams, P. Mickey  
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APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C22  
CURRENT FILING DATE: US/09/990.456  
CURRENT FILING DATE: 2001-11-14  
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PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 71; DB 10; Length 99;  
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Matches 71; Conservative 0; Mismatches 0

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Db 29 EBSSTIENYASRPEAFNTPTLINDKLSAFAKDEFLNWHALPESIKRKLPTLNDAPPL 88  
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Qy 61 KGLRSATPDQ 71  
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Db 89 KGLRSATPDQ 99

RESULT 12  
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Sequence 201, Application US/09989721  
Patent No. US20020142961A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Getder, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
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APPLICANT: Grimaldi, Paul J.  
APPLICANT: Gurney, Austin L.  
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APPLICANT: Pan, James  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC55  
CURRENT APPLICATION NUMBER: US/09/989,721  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
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APPLICANT: Eaton, Dan L.  
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APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC20  
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 71; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4, 2e-66;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 29 EESTIENYASRPFAFTPLNTDKLSAKADEFLMWHALFBSIKKKLPFLMWDAFPKL 88  
Oy 61 KGLSATPDQA 71  
Db 89 KGLSATPDQA 99

RESULT 14  
US-09-984-245-142  
; Sequence 142; Application US/099844245  
; Patent No. US20020165374A1

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GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004pl
CURRENT APPLICATION NUMBER: US/09/984,245
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
PRIOR FILING DATE: 1998-03-19
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PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/056,370
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: US 60/060,862
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 142
LENGTH: 99
TYPE: PRT
ORGANISM: Homo sapiens
US-09-984-245-142

Query Match      100.0%; Score 71; DB 10; Length 99;
Best Local Similarity 100.0%; Pred. No. 4,2e-66;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 15
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Sequence 201 Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Borstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Batcon, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
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Query Match 100.0%; Score 71; DB 10; Length 99;  
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Db 29 EESTTIVASRREAPRTPTINTDKRSARFADBEFLMWHALFSSIKKXLPFLMWDARPKL 88  
Qy 61 KGLRSATPDAQ 71  
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Db 89 KGLRSATPDAQ 99

Search completed: November 28, 2003, 13:45:14  
JOD time : 24 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 11:46:00 (Search time 2640 Seconds  
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Minimum DB seq length: 0

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Post-processing: listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
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#### SUMMARIES

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| 2          | 71    | 100.0                   | AR252517   | AR252517 Sequence |
| 3          | 71    | 100.0                   | AX077031   | AX077031 Sequence |
| 4          | 71    | 100.0                   | AX358892   | AX358892 Sequence |
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| 8          | 71    | 100.0                   | AX491024   | AX491024 Sequence |
| 9          | 71    | 100.0                   | AX574494   | AX574494 Sequence |
| 10         | 71    | 100.0                   | AX080815   | AX080815 Sequence |
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| 13         | 71    | 100.0                   | AX080817   | AX080817 Sequence |
| 14         | 59    | 83.1                    | AX080816   | AX080816 Sequence |
| 15         | 56    | 78.9                    | AX041085   | AX041085 Sequence |
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| 17         | 16    | 22.5                    | CH19721246 | CH19721246        |
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| 29         | 8     | 11.3                    | 12069      | 12069             |
| 30         | 8     | 11.3                    | 14530      | 14530             |
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| 37         | 8     | 11.3                    | 67870      | 67870             |
| 38         | 8     | 11.3                    | 69520      | 69520             |
| 39         | 8     | 11.3                    | 74149      | 74149             |
| 40         | 8     | 11.3                    | 88012      | 88012             |
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| 42         | 8     | 11.3                    | 100296     | 100296            |
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RESULT 1

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| DEFINITION   | Sequence 68 from Patent WO0073452.   |   |     |        |                 |
| ACCESSION  | AX055438   |   |     |        |                 |
| VERSION  | AX055438.1   | GI:12228711   |     |        |                 |
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| ORGANISM   | Homo sapiens (human)   |   |     |        |                 |
| REFERENCE  |  |   |     |        |                 |
| AUTHORS  | Homo sapiens<br>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. |   |     |        |                 |
| TITLE  |  |   |     |        |                 |
| JOURNAL  |  |   |     |        |                 |
| FEATURES   |  |   |     |        |                 |
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| Db   | 157  | CTGAACATCGACAAATTGCGATCTCGTTTAAAGCGTGATGAGTTCTGAACCTGGCACCGCC | 216 |        |                 |
| Qy   | 41   | LeuPhegluserlileAArgVleuAArgProPheLeuAanTPAspAlaPheProlyseu   | 60  |        |                 |
| Db   | 217  | CTCTTTGAGCTTATCAAAAGAACTTCTTCTTCAACTGGAGTCCCTTCTTAAGCTG       | 276 |        |                 |
| Qy   | 61   | LySGlyLeuAArgSerAlaThrProAspAlaGln                            | 71  |        |                 |
| Db   | 277  | AAAGACCTGAGAGGCGCAACTCTCATGCCCG 309                           |     |        |                 |
| RESULT 2   |  |   |     |        |                 |
| LOCUS  | AR252517   | 415 bp  | DNA | linear | PAT 20-DEC-2002 |
| DEFINITION   | Sequence 200 from patent US 6478825.   |   |     |        |                 |
| ACCESSION  | AR252517   |   |     |        |                 |
| VERSION  | AR252517.1   | GI:27300425   |     |        |                 |
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| SOURCE   |  |   |     |        |                 |
| ORGANISM   | Unknown.   |   |     |        |                 |
| REFERENCE  | Unclassified.  |   |     |        |                 |
| AUTHORS  | 1 (bases 1 to 415)<br>Wintersbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.   |   |     |        |                 |
| TITLE  | Implant, method of making same and use of the implant for the  |   |     |        |                 |
| JOURNAL  | treatment of bone defects  |   |     |        |                 |
| FEATURES   | Patent: US 6478825-A 200 12-NOV-2002;<br>Location/Qualifiers<br>1..415<br>/organism="unknown"  |   |     |        |                 |
| BASE COUNT   | 99 a 126 c 92 g 98 t   |   |     |        |                 |
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| DB:  | 6  | Gaps:  | 0               |
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| DB   | 157  | CTGAACATCGCAAAATTCGATCGCTTTAAGCTGATGATGCTTGAAGCTGACGCC   | 216             |
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| DB   | 217  | CTCTTTGAGTTATCAAAAGAACTTCCTTCTCTCACTGGAGTCCCTTCTTAAGCTG  | 276             |
| QY   | 61   | LYSGILEUARGSERALATHPROASPALGIN                           | 71              |
| DB   | 277  | AAAGACTGAGAGACGCACTCTCGATGCCAG                           | 309             |
| RESULT 3   |  |  |                 |
| LOCUS  | AK077031   | 415 bp   | DNA             |
| DEFINITION   | Sequence 19 from Patent WO0105972.                                     | linear   | PAT 22-FEB-2002 |
| ACCESSION  | AK077031   |  |                 |
| VERSION  | AK077031.1   | GI:13121661  |                 |
| KEYWORDS   |  |  |                 |
| SOURCE   | Homo sapiens (human)   |  |                 |
| ORGANISM   | Homo sapiens   |  |                 |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |  |                 |
| AUTHORS  | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.              |  |                 |
| TITLE  | 1 Ashkenazi, A.J., Baker, K.P., Fong, S., Goddard, A., Godowski, P.J., |  |                 |
|  | Gunney, A.L., Hillan, K.J., Mark, M.R., Marsters, S.A., Pitti, R.M.,   |  |                 |
|  | Tunias, D., Watanabe, C.K., and Wood, W.I.                             |  |                 |
|  | Compositions and methods for the treatment of immune related           |  |                 |
|  | diseases   |  |                 |
| JOURNAL  | Patent: WO 0105972-A 19 25-JUN-2001;                                   |  |                 |
| FEATURES   | Genentech, Inc. (US)   |  |                 |
| source   | location/Qualifiers  |  |                 |
|  | 1..415   |  |                 |
|  | /organism="Homo sapiens"   |  |                 |
|  | /mol_type="genomic DNA"  |  |                 |
|  | /db_xref="taxon:9606"  |  |                 |
| BASE COUNT   | 99 a 126 c 92 g 98 t   |  |                 |
| ORIGIN   |  |  |                 |
| Alignment Scores:                                      |  |  |                 |
| Pred. No.:   | 2,34e-69   | Length:  | 415             |
| Score:   | 71.00  | Matches:   | 71              |
| Percent Similarity:                                    | 100.00%  | Conservative:  | 0               |
| Best Local Similarity:                                 | 100.00%  | Mismatches:  | 0               |
| Query Match:   | 100.00%  | Indels:  | 0               |
| DB:  | 6  | Gaps:  | 0               |
| US-10-059-395-142_COPY_29_99 (1-71) x AK077031 (1-415) |  |  |                 |
| QY   | 1  | GIUGIUGUSERTHRIIEGIUASNTYRALASERARPROGIUALAPHEASNTHPRO   | 20              |
| DB   | 97   | GAGGAGAAACACCATTTAGATTATTCGTCACGACCCGAGGCGCTTAAACCCCGTTC | 156             |
| QY   | 21   | LEUASNTLEAPPLYLEUARGSERALAPHELYALAPROGIUPELEUASNTPHIALA  | 40              |
| DB   | 157  | CTGAACATCGCAAAATTCGATCGCTTTAAGCTGATGATGCTTGAAGCTGACGCC   | 216             |
| QY   | 41   | LEUPHEGIUSERTILEYASRGYLEUPROPHLEUASNTTPASPALAPHEPROLYSEU | 60              |

Db 217 CTCCTTGAGTCTATCAAAAGAACTTCTTCTCAACGTGGAGTCCCTTCTTAAGCTG 276  
Oy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAGGACTGAGAGCGCACTCTGATGCCAG 309

RESULT 4  
AX358892 415 bp DNA linear PAT 13-FEB-2002  
LOCUS Sequence 145 from Patent WO0193983.  
ACCESSION AX358892  
VERSION AX358892.1 GI:18675347  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
Watanabe, C.K. and Wood, W.I.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0193983-A 145 13-DEC-2001;  
Genentech Inc. (US)

FEATURES  
source 1..415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t

ORIGIN

Alignment Scores:  
Pred. No.: 2,34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX358892 (1-415)

Oy 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAGAAAGCACCACTTGAAATTATGCGTACACACCGAGCCCTTTAACACCCCGTTC 156  
Oy 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTriphHisAla 40  
Db 157 CTGAACATCGACAAATTGGCATCTCGTTTAAGGCTGATGAGTTCTCTGAACCTGGCACGCC 216  
Oy 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTriPAspAlaPheProLysLeu 60  
Db 217 CTCCTTGAGTCTATCAAAAGAACTTCTTCTCAACGTGGAGTCCCTTCTTAAGCTG 276  
Oy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAGGACTGAGAGCGCACTCTGATGCCAG 309

RESULT 5  
AX362385 415 bp DNA linear PAT 15-FEB-2002  
LOCUS Sequence 145 from Patent WO0208288.  
ACCESSION AX362385  
VERSION AX362385.1 GI:18694650  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,

TITLE Watanabe, C.K. and Wood, W.I.  
JOURNAL Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0208288-A 145 31-JAN-2002;  
Genentech, Inc. (US)

FEATURES  
source 1..415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t

ORIGIN

Alignment Scores:  
Pred. No.: 2,34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX362385 (1-415)

Oy 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAGAAAGCACCACTTGAAATTATGCGTACACACCGAGCCCTTTAACACCCCGTTC 156  
Oy 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTriphHisAla 40  
Db 157 CTGAACATCGACAAATTGGCATCTCGTTTAAGGCTGATGAGTTCTCTGAACCTGGCACGCC 216  
Oy 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTriPAspAlaPheProLysLeu 60  
Db 217 CTCCTTGAGTCTATCAAAAGAACTTCTTCTCAACGTGGAGTCCCTTCTTAAGCTG 276  
Oy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAGGACTGAGAGCGCACTCTGATGCCAG 309

RESULT 6  
AX403313 415 bp DNA linear PAT 14-JUN-2002  
LOCUS Sequence 200 from Patent WO0073454.  
ACCESSION AX403313  
VERSION AX403313.1 GI:21436871  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D.,  
Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,  
Grimaldi, C.J., Gurney, A.L., Kijavita, I., Napier, M.A., Pan, J.,  
Pao, N.F., Roy, M., Stewart, T.A., Tamas, D., Watanabe, C.K.,  
Williams, P., Wood, W.I. and Zhang, Z.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0073454-A 200 07-DEC-2000;  
Genentech Inc. (US)

FEATURES  
source 1..415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t

ORIGIN

Alignment Scores:  
Pred. No.: 2,34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AX403313 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAGAAAGACCAATTGAGATTATGCTGACGACCGAGGCTTTAACACCCCGCTTC 156

QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnThrPheIle 40  
DB 157 CTGAACATCGACCAATTGCGATGCGCTTAAGGCTGATGATGTTCTGAACCTGGACAGCC 216

QY 41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnThrPheAspAlaPheProIysLeu 60  
DB 217 CTCTTGAGCTCTATCAAAAAGAAACTCTCTTCTCTCAACTGGAGATGCTTTCCTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCACTCTCGATGCCAG 309

RESULT 7  
AX454546 415 bp DNA linear PAT 06-JUL-2002  
LOCUS AX454546  
DEFINITION Sequence 131 from Patent WO0208284.  
ACCESSION AX454546  
VERSION AX454546.1 GI:21713897  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.B., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.  
1 Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis  
Patent: WO 0208284-A 131 31-JAN-2002;  
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard, Hilary (US); Godowski, Paul J. (US); Gurney, Austin L. (US); Hillan, Kenneth J. (US); Marsters, Scott A. (US); Pan, James (US); Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US); Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William I. (US)

FEATURES  
Source Location/Qualifiers  
1..415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t

ORIGIN  
Alignment Scores: 2,34e-69 Length: 415  
Pred. No.: 71 Matches: 71  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 6

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX454546 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAGAAAGACCAATTGAGATTATGCTGACGACCGAGGCTTTAACACCCCGCTTC 156

QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnThrPheIle 40  
DB 157 CTGAACATCGACCAATTGCGATGCGCTTAAGGCTGATGATGTTCTGAACCTGGACAGCC 216

QY 41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnThrPheAspAlaPheProIysLeu 60  
DB 217 CTCTTGAGCTCTATCAAAAAGAAACTCTCTTCTCTCAACTGGAGATGCTTTCCTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCACTCTCGATGCCAG 309

RESULT 8  
AX491024 415 bp DNA linear PAT 16-AUG-2002  
LOCUS AX491024  
DEFINITION Sequence 131 from Patent WO0200690.  
ACCESSION AX491024  
VERSION AX491024.1 GI:22323849  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.B., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.  
1 Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis  
Patent: WO 0200690-A 131 03-JAN-2002;  
Genentech, Inc. (US)

FEATURES  
Source Location/Qualifiers  
1..415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t

ORIGIN  
Alignment Scores: 2,34e-69 Length: 415  
Pred. No.: 71 Matches: 71  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 6

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX491024 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAGAAAGACCAATTGAGATTATGCTGACGACCGAGGCTTTAACACCCCGCTTC 156

QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnThrPheIle 40  
DB 157 CTGAACATCGACCAATTGCGATGCGCTTAAGGCTGATGATGTTCTGAACCTGGACAGCC 216

QY 41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnThrPheAspAlaPheProIysLeu 60  
DB 217 CTCTTGAGCTCTATCAAAAAGAAACTCTCTTCTCTCAACTGGAGATGCTTTCCTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCACTCTCGATGCCAG 309

RESULT 9  
AX574494 415 bp DNA linear PAT 07-JAN-2003  
LOCUS AX574494  
DEFINITION Sequence 21 from Patent WO0224888.  
ACCESSION AX574494  
VERSION AX574494.1 GI:27551800  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Baker, K.P., Batton, D.L., Filvaroff, E., Goddard, A., Grimaldi, J.C.,  
Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., Wood, W.I.,  
Zhang, Z. and Fong, S.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0224888-A 21 28-MAR-2002;  
GENENTECH, INC. (US)  
FEATURES Location/Qualifiers  
source 1..415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 2,34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 6  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AX574494 (1-415)  
QY 1 GIUGUGUSeRTThllEGlUASnTYrAlASerAProGluAlaPheASnThProPhe 20  
DB 97 GAGGAGAAAGACACATTGAGATTATGCTCACACCCGAGCCCTTTAAACCCCGTTC 156  
QY 21 LeuAniLeaAPLyLeuAArgSerAlaPheLyAlaAPGluPheLeuAnThrPhIsAla 40  
DB 157 CTGAACATCGACAAATTGCGATCTGCTTTAAGCTGATGAGTCTCTGAACCTGGACGCC 216  
QY 41 LeuphegiuSeRiIeLyAArgLyLeuProPheLeuAnThrPASPAlaPheProLyLeu 60  
DB 217 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGATGCCCTTCTTAAGCTG 276  
QY 61 LysGlyLeuAArgSerAlaThrProASPAlaGln 71  
DB 277 AAAGACTGAGAGCGCAACTCTGATGCCG 309  
RESULT 10  
LOCUS AX080815 432 bp DNA linear PAT 27-FEB-2001  
DEFINITION Sequence 61 from Patent WO0109327.  
ACCESSION AX080815  
VERSION AX080815.1 GI:13169784  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Klajavin, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pittet, R.M.,  
Watanabe, C.K. and Wood, W.I.  
TITLE Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
JOURNAL Patent: WO 0109327-A 61 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..432  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Virtual DNA fragment used in the isolation of  
DNA57694." BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN  
Alignment Scores:  
Pred. No.: 2,43e-69 Length: 432  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080815 (1-432)

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080815 (1-432)  
QY 1 GIUGUGUSeRTThllEGlUASnTYrAlASerAProGluAlaPheASnThProPhe 20  
DB 96 GAGGAGAAAGACACATTGAGATTATGCTCACACCCGAGCCCTTTAAACCCCGTTC 155  
QY 21 LeuAniLeaAPLyLeuAArgSerAlaPheLyAlaAPGluPheLeuAnThrPhIsAla 40  
DB 156 CTGAACATCGACAAATTGCGATCTGCTTTAAGCTGATGAGTCTCTGAACCTGGACGCC 215  
QY 41 LeuphegiuSeRiIeLyAArgLyLeuProPheLeuAnThrPASPAlaPheProLyLeu 60  
DB 216 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGATGCCCTTCTTAAGCTG 275  
QY 61 LysGlyLeuAArgSerAlaThrProASPAlaGln 71  
DB 276 AAAGACTGAGAGCGCAACTCTGATGCCCA 308  
RESULT 11  
LOCUS AX080818 432 bp DNA linear PAT 27-FEB-2001  
DEFINITION Sequence 64 from Patent WO0109327.  
ACCESSION AX080818  
VERSION AX080818.1 GI:13169787  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Klajavin, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pittet, R.M.,  
Watanabe, C.K. and Wood, W.I.  
TITLE Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
JOURNAL Patent: WO 0109327-A 64 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..432  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN  
Alignment Scores:  
Pred. No.: 2,43e-69 Length: 432  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080818 (1-432)  
QY 1 GIUGUGUSeRTThllEGlUASnTYrAlASerAProGluAlaPheASnThProPhe 20  
DB 96 GAGGAGAAAGACACATTGAGATTATGCTCACACCCGAGCCCTTTAAACCCCGTTC 155  
QY 21 LeuAniLeaAPLyLeuAArgSerAlaPheLyAlaAPGluPheLeuAnThrPhIsAla 40  
DB 156 CTGAACATCGACAAATTGCGATCTGCTTTAAGCTGATGAGTCTCTGAACCTGGACGCC 215  
QY 41 LeuphegiuSeRiIeLyAArgLyLeuProPheLeuAnThrPASPAlaPheProLyLeu 60  
DB 216 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGATGCCCTTCTTAAGCTG 275  
QY 61 LysGlyLeuAArgSerAlaThrProASPAlaGln 71

Db 276 AAAGACTGAGAGCGCACTCTGATGCCCAA 308  
RESULT 12  
LOCUS BD082389 456 bp DNA linear PAT 27-AUG-2002  
DEFINITION 87 human secreted proteins.  
ACCESSION BD082389  
VERSION BD082389.1 GI:22627999  
KEYWORDS JP 2001522239-A/31.  
SOURCE Mastadenovirus  
ORGANISM Mastadenovirus  
REFERENCE 1 (bases 1 to 456)  
AUTHORS Young,P., Greene,J.M., Ferrite,A.M., Ruben,S.M., Rosen,C.A.,  
Duan,R.D., Hu,J.S., Florence,K.A., Olsen,H.S., Ebner,R.,  
Brewer,L.A., Moore,P.A., Shi,Y., Lafleur,D.W. and N.J.J.  
77 human secreted proteins  
Patent: JP 2001522239-A 31 13-NOV-2001;  
HUMAN GENOME SCIENCES INC SECRETARY OF THE DEPARTMENT OF HEALTH  
JOURNAL HUMAN SERVICES  
TITLE JP 2001522239-A/31  
COMMENT PD 13-NOV-2001  
PR 19-MAR-1998 JP 1998542119  
PR 21-MAR-1997 US 60/041281,21-MAR-1997 US 60/041276 PR  
21-MAR-1997 US 60/042344,21-MAR-1997 US 60/041277 PR  
30-MAY-1997 US 60/048355,30-MAY-1997 US 60/048096 PR  
30-MAY-1997 US 60/048351,30-MAY-1997 US 60/048154 PR  
30-MAY-1997 US 60/048150,30-MAY-1997 US 60/048069 PR  
30-MAY-1997 US 60/048151,30-MAY-1997 US 60/048186 PR  
30-MAY-1997 US 60/048099,30-MAY-1997 US 60/048187 PR  
30-MAY-1997 US 60/048099,30-MAY-1997 US 60/050937 PR  
30-MAY-1997 US 60/048352,30-MAY-1997 US 60/048135 PR  
30-MAY-1997 US 60/048188,30-MAY-1997 US 60/048094 PR  
30-MAY-1997 US 60/048350,05-AUG-1997 US 60/054804 PR  
19-AUG-1997 US 60/056370,02-OCT-1997 US 60/060862 PI PAUL  
YOUNG,JOHN W GREENE,ANN W FERRIE,STEVEN W RUBEN,CRAIG A PI  
ROSEN,  
PI ROXANNE D DUAN,JING SHAN HU,KIMBERLY A FLORENCE,HENRIK S  
OLSEN,  
PI REINHARD EBNER,LAURIE A BREWER,PAUL A MOORE,YANGGU SHI,DAVID W  
PI LAFLEUR,  
PI JIAN NI  
PC C07K14/00  
CC Strandedness: Double;  
CC Topology: Linear;  
FH Key Location/Qualifiers.  
FEATURES  
source 1.456  
Location/Qualifiers  
/organism="Mastadenovirus"  
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BASE COUNT 117 a 136 c 104 g 98 t 1 others  
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Alignment Scores:  
Pred. No.: 2.55e-69 Length: 456  
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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
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Db 105 GAGAGAAAGAACCACTTGAATATGCGTCAGACGCCGAGGCTTTAAACACCCGCTTC 164  
QY 21 LeuAnllAaSpLyLeuArSerAlaPhelYsAlaAaSpGUphLeuAenThrPhAla 40  
Db 165 CTGAACATCGACAAATTCGATTCGCTTTAAGGCTATGATGCTTCCTGAACCTGACAGCC 224

QY 41 LeuPhelGUSeThrlleYsArGUphLeuProPhLeuAenThrPhAlaPhaProLYsLeu 60  
Db 225 CTTTGAAGTCATCAAAAGAAACTCTCTTCTCTCACTGAGATCCCTTCTTAAGCTG 284  
QY 61 LyGGLyLeuArSerAlaThrProAaPhaLagln 71  
Db 285 AAAGACTGAGAGCGCACTCTGATGCCCAAG 317  
RESULT 13  
LOCUS AX080817 490 bp DNA linear PAT 27-FEB-2001  
DEFINITION Sequence 63 from Patent WO0109327.  
ACCESSION AX080817  
VERSION AX080817.1 GI:13169786  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L.,  
Kliverin,I.J., Lafleur,M., Mark,M.R., Masters,S.A., Pitti,R.M.,  
Watanabe,C.K. and Wood,W.I.  
Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
Patent: WO 0109327-A 63 08-FEB-2001;  
Genentech, Inc. (US)  
JOURNAL  
TITLE Location/Qualifiers  
source 1.490  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Virtual DNA fragment used in the isolation of  
DNA57694."  
BASE COUNT 118 a 149 c 116 g 107 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 2.72e-69 Length: 490  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
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QY 1 GUGUGUGUSeThrlleGUaenTYrAlaSeThrProGUAlaPhaenThrProPh 20  
Db 164 GAGAGAAAGAACCACTTGAATATGCGTCAGACGCCGAGGCTTTAAACACCCGCTTC 223  
QY 21 LeuAnllAaSpLyLeuArSerAlaPhelYsAlaAaSpGUphLeuAenThrPhAla 40  
Db 224 CTGAACATCGACAAATTCGATTCGCTTTAAGGCTATGATGCTTCCTGAACCTGACAGCC 283  
QY 41 LeuPhelGUSeThrlleYsArGUphLeuProPhLeuAenThrPhAlaPhaProLYsLeu 60  
Db 284 CTTTGAAGTCATCAAAAGAAACTCTCTTCTCTCACTGAGATCCCTTCTTAAGCTG 343  
QY 61 LyGGLyLeuArSerAlaThrProAaPhaLagln 71  
Db 344 AAAGACTGAGAGCGCACTCTGATGCCCAAG 376  
RESULT 14  
LOCUS AX080816 435 bp DNA linear PAT 27-FEB-2001  
DEFINITION Sequence 62 from Patent WO0109327.  
ACCESSION AX080816  
VERSION AX080816.1 GI:13169785  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L.,  
Kliverin,I.J., Lafleur,M., Mark,M.R., Masters,S.A., Pitti,R.M.,  
Watanabe,C.K. and Wood,W.I.  
Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
Patent: WO 0109327-A 62 08-FEB-2001;  
Genentech, Inc. (US)  
JOURNAL  
TITLE Location/Qualifiers  
source 1.435  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Virtual DNA fragment used in the isolation of  
DNA57694."  
BASE COUNT 118 a 149 c 116 g 107 t  
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Alignment Scores:  
Pred. No.: 2.72e-69 Length: 435  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080816 (1-435)

REFERENCE 1  
 AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L., Kijavits, I.J., Lafleur, M., Mark, M.R., Masters, S.A., Pitti, R.M., Matanabe, C.K., and Wood, W.I.  
 TITLE Method of preventing the injury or death of retinal cells and treating ocular diseases  
 JOURNAL Patent: WO 0109327-A 62 08-FEB-2001;  
 FEATURES Genentech, Inc. (US)  
 SOURCE Location/Qualifiers  
 1. 435  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="Virtual DNA fragment used in the isolation fo DNAB57694."

BASE COUNT 108 a 130 c 96 g 101 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 4.92e-56 Length: 435  
 Score: 59.00 Matches: 59  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 83.10% Indels: 0  
 DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX041085 (1-435)

QY 13 ProglutalpheAsnThrProPheLeuAniLeAspLyLeuArgSerAlaPheLySAla 32  
 Db 136 CCCGAGGCGCTTTAACACCCCGTCTCGAATCGACAAATTCGATCGCGTTTAAGGCT 195

QY 33 AsgGluPheLeuAsnThrPheAlaLeuPheGluSerIleLySArgLyLeuProPheLeu 52  
 Db 196 GATGAGTTCCTGACACTGCGACGCGCTCTTGAATCATCAAGGAACCTCTTCTCCTC 255

QY 53 AsnTPAspAlaPheProLyLeuLySArgSerAlaThrProAspAlaGln 71  
 Db 256 AACTGGAGTGCCTTCTTCAAGCTGAAGACTGAAGAGCGCACTCTGATGCCAG 312

RESULT 15  
 AX041085/c 278 bp DNA linear PAT 23-NOV-2000  
 LOCUS AX041085  
 DEFINITION Sequence 3 from Patent WO0065053.  
 ACCESSION AX041085  
 VERSION AX041085.1 GI:11340655  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
 AUTHORS Wang, T. and Dillon, D.C.  
 TITLE Compositions and methods for therapy and diagnosis of head/neck and lung squamous cell carcinoma  
 JOURNAL Patent: WO 0065053-A 3 02-NOV-2000;  
 FEATURES CORIXA CORPORATION (US)  
 SOURCE Location/Qualifiers  
 1. 278  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

BASE COUNT 70 a 57 c 80 g 71 t  
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 Score: 56.00 Matches: 56  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 78.87% Indels: 0  
 DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX041085 (1-278)

QY 16 PheAsnThrProPheLeuAniLeAspLyLeuArgSerAlaPheLySAlaAspGluPhe 35  
 Db 269 TTTAACACCCCGTCTCGAATCGACAAATTCGATCGCGTTTAAGGCTGATGAGTTC 210

QY 36 LeuAsnThrPheAlaLeuPheGluSerIleLySArgLyLeuProPheLeuAsnTPAsp 55  
 Db 209 CTGAAGTGGACGCGCTCTTGAATCATCAAGGAACCTCTTCTCTCACTGGGAT 150

QY 56 AlaPheProLyLeuLySArgSerAlaThrProAspAlaGln 71  
 Db 149 GCCTTCTTAAGCTGAAGACTGAAGAGCGCAACTCTGATGCCAG 102

Search completed: November 28, 2003, 13:05:56  
 Job time : 2642 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 11:01:55 / Search time 217 Seconds

(without alignments)  
883.226 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 71

Sequence: 1 EEBSTIENYASRPFAFTFP.....LMDAFPKLKGRLGATPDQA 71

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Ygapop 60.0, Ygapext 60.0  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Word size: 1

Total number of hits satisfying chosen parameters: 510367

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

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-LOOEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=ol1.go -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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-NO MMAP -LARGOUIRY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID        | Description         |
|------------|-------|-------------|--------|----|-----------|---------------------|
| 1          | 71    | 100.0       | 414    | 22 | AAC91475  | Human PRO826 cDNA.  |
| 2          | 71    | 100.0       | 414    | 24 | ABK28600  | Human DNA57694-134  |
| 3          | 71    | 100.0       | 415    | 21 | AAZ65018  | Membrane-bound pro  |
| 4          | 71    | 100.0       | 415    | 22 | AAFP3059  | Human cDNA encoding |
| 5          | 71    | 100.0       | 415    | 22 | AAFP44164 | Human PRO826 (UNO4  |
| 6          | 71    | 100.0       | 415    | 22 | AAC97491  | Human angiogenesis  |
| 7          | 71    | 100.0       | 415    | 24 | AB195626  | Human encoding      |
| 8          | 71    | 100.0       | 415    | 24 | ABK69971  | Human encoding huma |
| 9          | 71    | 100.0       | 415    | 24 | ABL88137  | Human PRO826 cDNA   |
| 10         | 71    | 100.0       | 415    | 24 | ABK33608  | Human encoding huma |
| 11         | 71    | 100.0       | 415    | 25 | ABK80255  | Novel human secret  |
| 12         | 71    | 100.0       | 415    | 25 | ABK80759  | Human secreted/cir  |
| 13         | 71    | 100.0       | 415    | 25 | ABK81142  | Novel human secret  |
| 14         | 71    | 100.0       | 415    | 25 | ABK90232  | Human secreted/cir  |
| 15         | 71    | 100.0       | 415    | 25 | ABK77843  | Human PRO polynuci  |
| 16         | 71    | 100.0       | 415    | 25 | ABK79439  | Human secreted/cir  |
| 17         | 71    | 100.0       | 415    | 25 | ABK64078  | Human encoding huma |
| 18         | 71    | 100.0       | 415    | 25 | ABK17042  | Human PRO polynuci  |
| 19         | 71    | 100.0       | 428    | 24 | ABK21803  | Human polynucleoti  |
| 20         | 71    | 100.0       | 456    | 20 | AAK00632  | Human secreted pro  |
| 21         | 71    | 100.0       | 518    | 22 | ABA09519  | Human secreted pro  |
| 22         | 56    | 78.9        | 278    | 21 | AAK68806  | Human head/neck tu  |
| 23         | 43    | 60.6        | 386    | 24 | ABZ11804  | Human polynucleoti  |
| 24         | 28    | 39.4        | 305    | 24 | ABZ11886  | Human polynucleoti  |
| 25         | 8     | 11.3        | 2001   | 24 | ABN67971  | Streptococcus poly  |
| 26         | 8     | 11.3        | 2298   | 21 | AAC95936  | Human secreted pro  |
| 27         | 8     | 11.3        | 12069  | 24 | ABK39931  | Human secreted pro  |
| 28         | 8     | 11.3        | 12212  | 24 | ABK12920  | Human SLC26A2 (sol  |
| 29         | 8     | 11.3        | 12212  | 24 | ABK12975  | Human SLC26A2 (sol  |
| 30         | 8     | 11.3        | 33795  | 24 | ABN56686  | Gene #2184 used to  |
| 31         | 8     | 11.3        | 215561 | 24 | ABN71527  | Streptococcus poly  |
| 32         | 7     | 9.9         | 65     | 24 | ABN1537   | Rat spliced transc  |
| 33         | 7     | 9.9         | 198    | 21 | AAC4586   | Human secreted pro  |
| 34         | 7     | 9.9         | 231    | 20 | AAH6401   | Human single nucle  |
| 35         | 7     | 9.9         | 231    | 20 | AAH6402   | Human single nucle  |
| 36         | 7     | 9.9         | 238    | 21 | AAH45447  | Human secreted exp  |
| 37         | 7     | 9.9         | 251    | 21 | AAC07741  | Human secreted pro  |
| 38         | 7     | 9.9         | 256    | 25 | ABK31899  | Human GDP-mannose   |
| 39         | 7     | 9.9         | 283    | 21 | AAC94607  | Cat flea hindgut a  |
| 40         | 7     | 9.9         | 294    | 20 | AAZ13185  | Human gene express  |
| 41         | 7     | 9.9         | 300    | 20 | AAK98312  | Human cancer cell   |
| 42         | 7     | 9.9         | 300    | 21 | AAK00085  | Human colon cancer  |
| 43         | 7     | 9.9         | 368    | 19 | AAV66404  | CDNA clone AA37708  |
| 44         | 7     | 9.9         | 419    | 21 | AAC31437  | Human secreted pro  |
| 45         | 7     | 9.9         | 438    | 24 | ABK29813  | Colon adenocarcino  |

## ALIGNMENTS

RESULT 1  
ID AAC91475 standard; cDNA; 414 BP.  
AAC91475;  
21-MAR-2001 (first entry)  
Human PRO826 cDNA.  
Human; PRO; antiinflammatory; dermatological; antifibrotic;  
antithrombotic; cardiac; antianemic; immunosuppressive; antihypoid;  
antidiabetic; noctropic; neuroprotective; hepatotropic; vitruclide;  
antiallergic; antistimatic; immune related disorder;  
hepatobiliary disease; autoimmune disease; allergy; ss.  
Homo sapiens.

XX PN WO200073452-A2.  
 XX 07-DEC-2000.  
 PD 02-JUN-2000; 2000WO-US15254.  
 PF 02-JUN-1999; 99WO-US12252.  
 XX 20-JUL-1999; 99US-0144732.  
 PR 20-JUL-1999; 99US-0144732.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 25-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 XX (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;  
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tunas D, Watanabe CK;  
 PI Wood WI;  
 XX WPI; 2001-025253/03.  
 DR P-PSDB; AAB50916.  
 PT Thirty three nucleic acids encoding PRO polypeptides which are useful  
 PT in the diagnosis and treatment of immune related disorders, e.g.  
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 PT thyroiditis and diabetes mellitus -  
 XX Claim 48; Fig 29; 218pp; English.  
 PS The present sequence is one of thirty three nucleic acids encoding PRO  
 XX polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and  
 CC antagonists are useful for treating and diagnosing immune related  
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
 CC (such as infectious, autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
 CC food hypersensitivity and urticaria), immunological diseases of the  
 CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
 CC and hypersensitivity pneumonitis), transplantation associated diseases  
 CC including graft rejection and graft-versus-host diseases.  
 XX Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:  
 Pred. No.: 3,23e-66 Length: 414  
 Score: 71.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
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 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0  
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 QY 1 GIUGLUGLuserThr1leGLuEntyTAlAsERaRgProGLuAlaPheAntHrProPhe 20  
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 QY 21 LeuAsn1leAspLysLeuArgSerAlaPheLysAlaAspGLuPheLeuAntTPI:sAla 40  
 DB 157 CTGAACATCGACCAATTCGATCGCTTTAAGCGTAGTAGTTCTTGAACCTGGACGCC 216  
 QY 41 LeuPheGLuser1leLysArgLysLeuProPheLeuAsnTTPAspAlaPheProLysLeu 60  
 DB 217 CTTTGAAGTCATCAAAAGAAACTTCCTTCCCTCAACTGGGATGCCCTTCTAAGCTG 276  
 QY 61 LysGLYLeuArgSerAlaThrProAspAlaGln 71  
 DB 277 AAAGACTGAGGAGCGCAACTCCTGATGCCGAG 309  
 RESULT 2  
 ABK28600 standard; cDNA, 414 BP.  
 ID ABK28600;  
 AC ABK28600;  
 XX 09-APR-2002 (first entry)  
 DT Human DNA57694-1341 encoding PRO826.  
 XX Human  
 XX Human DNA57694-1341 encoding PRO826.  
 XX Human; ss; gene; PRO; antiinflammatory; ophthalmological; vasotropic;  
 KW retinal cell injury; ocular disease; retinitis pigmentosa;  
 KW macular degeneration; retinal detachment; retinal tear; retinopathy;  
 KW retinal degenerative disease; macular hole; degenerative myopia;  
 KW acute retinal necrosis syndrome; traumatic choriorretinopathy;  
 KW Purtscher's retinopathy; oedema; ischaemic condition;  
 KW retinal vision occlusion; collagen vascular disease;  
 KW thrombocytopaenic purpura; uveitis; retinal vasculitis; Bales disease;  
 KW systemic lupus erythematosus; environmental trauma.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX WO200109327-A2.  
 PN 08-FEB-2001.  
 PD 28-JUL-2000; 2000WO-US20710.  
 PF 28-JUL-1999; 99US-146222P.  
 XX 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;  
PI Kljavin IJ, Lafleur M, Mark MR, Marsters SA, Pitti RM;  
PI Watanabe CK, Wood WI;  
XX WPI: 2002-130120/17.  
XX P-PSDB; AAU81964.  
XX  
XX Promoting survival of retinal cells, or delaying or preventing retinal  
XX cell injury or death, by contacting retinal cells with PRO175, 220,  
XX 215, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132  
XX polypeptide -  
XX  
XX Claim 33; Fig 24; 152pp; English.  
XX  
XX The invention relates to promoting the survival of retinal cells, or  
XX delaying or preventing retinal cell injury or death, by contacting the  
XX retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
XX PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO828, PRO826,  
XX PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
XX encoding the PRO proteins, a vector comprising the nucleic acid, a host  
XX cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
XX useful for promoting survival of retinal cells (retinal neurons such as  
XX cells, displaced amacrine cells, horizontal ganglion cells, amacrine  
XX rod photoreceptors, or supportive cells such as Muller cells or pigment  
XX epithelial cells), or delaying or preventing retinal cell injury or  
XX death caused by ocular disease (which is or is associated with  
XX retinitis pigmentosa, macular degeneration, retinal detachment, retinal  
XX tear, retinopathy, retinal degenerative disease, macular hole,  
XX degenerative myopia, acute retinal necrosis syndrome, traumatic  
XX chorioretinopathy or contusion, Purtscher's retinopathy, oedema, an  
XX ischaemic condition, central or branch retinal vein occlusion, an  
XX collagen vascular disease, thrombocytopenic purpura, uveitis, retinal  
XX vasculitis, occlusion associated with Siles disease or systemic lupus  
XX erythematosus), retinal injury or environmental trauma. The retinal  
XX cell injury or death is delayed or prevented by substantially not  
XX causing angiogenesis or mitogenesis. The present sequence is a cDNA  
XX encoding a PRO protein.  
XX  
XX Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 3,23e-66 Length: 414  
XX Score: 71.00 Matches: 71  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 100.00% Indels: 0  
XX DB: 24 Gaps: 0  
XX  
XX US-10-059-395-142\_COPY\_29\_99 (1-71) x ABK28660 (1-414)  
XX  
XX QY 1 GIUGIUGISERTHRIIEGLIAANTYRALASERARPROGJUALAPHEANTHPRophe 20  
XX DB 97 GAGGAGAAACACCATGGAATTATGCGTCACGACCCGAGCCTTAACCCCGTTC 156  
XX QY 21 LeuSantleaplyleuArSerAlaPheYsAlaApGluPheLeuAntTPHiaAla 40  
XX DB 157 CTGACACATGCAAAATTCGATCGCTTAAGGCTGATGAGTCTCGAAGCTGCACGCC 216  
XX QY 41 LeuSantleaplyleuArSerAlaPheYsAlaApGluPheLeuAntTPHiaAla 40  
XX DB 217 CTCCTTAGTCTATCAAAAGAACTTCCTTCCTCAACTGGATGCCCTTAAGCTG 276  
XX QY 61 LyeGlyLeuArSerAlaThrProAspAlaGln 71  
XX DB 277 AAAGAGCTGAGAGAGCGCAACTCTGATGCCAG 309  
XX  
XX RESULT 3  
XX AA265018  
XX ID AA265018 standard; cDNA; 415 BP.  
XX XX  
XX AA265018;

XX  
XX 05-APR-2000 (first entry)  
XX  
XX Membrane-bound protein PRO826 encoding cDNA.  
XX  
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
XX pharmaceutical; receptor immunoadhesin; gene mapping; ss.  
XX  
XX Homo sapiens.  
XX  
XX MO9963088-A2.  
XX  
XX 09-DEC-1999.  
XX  
XX 02-JUN-1999;  
XX  
XX 99MO-US12252.  
XX  
XX 02-JUN-1998; 98US-0087607.  
XX 02-JUN-1998; 98US-0087609.  
XX 02-JUN-1998; 98US-0087759.  
XX 03-JUN-1998; 98US-0087827.  
XX 04-JUN-1998; 98US-0088021.  
XX 04-JUN-1998; 98US-0088025.  
XX 04-JUN-1998; 98US-0088028.  
XX 04-JUN-1998; 98US-0088029.  
XX 04-JUN-1998; 98US-0088030.  
XX 04-JUN-1998; 98US-0088033.  
XX 04-JUN-1998; 98US-0088326.  
XX 05-JUN-1998; 98US-0088167.  
XX 05-JUN-1998; 98US-0088202.  
XX 05-JUN-1998; 98US-0088212.  
XX 05-JUN-1998; 98US-0088217.  
XX 09-JUN-1998; 98US-0088655.  
XX 10-JUN-1998; 98US-0088722.  
XX 10-JUN-1998; 98US-0088730.  
XX 10-JUN-1998; 98US-0088734.  
XX 10-JUN-1998; 98US-0088738.  
XX 10-JUN-1998; 98US-0088740.  
XX 10-JUN-1998; 98US-0088741.  
XX 10-JUN-1998; 98US-0088742.  
XX 10-JUN-1998; 98US-0088810.  
XX 10-JUN-1998; 98US-0088811.  
XX 10-JUN-1998; 98US-0088824.  
XX 10-JUN-1998; 98US-0088825.  
XX 10-JUN-1998; 98US-0088826.  
XX 11-JUN-1998; 98US-0088858.  
XX 11-JUN-1998; 98US-0088861.  
XX 11-JUN-1998; 98US-0088863.  
XX 11-JUN-1998; 98US-0088876.  
XX 12-JUN-1998; 98US-0089090.  
XX 12-JUN-1998; 98US-0089105.  
XX 16-JUN-1998; 98US-0089440.  
XX 16-JUN-1998; 98US-0089512.  
XX 16-JUN-1998; 98US-0089514.  
XX 17-JUN-1998; 98US-0089532.  
XX 17-JUN-1998; 98US-0089538.  
XX 17-JUN-1998; 98US-0089588.  
XX 17-JUN-1998; 98US-0089599.  
XX 17-JUN-1998; 98US-0089600.  
XX 17-JUN-1998; 98US-0089653.  
XX 18-JUN-1998; 98US-0089801.  
XX 18-JUN-1998; 98US-0089907.  
XX 18-JUN-1998; 98US-0089908.  
XX 18-JUN-1998; 98US-0089908.  
XX 19-JUN-1998; 98US-0089947.  
XX 19-JUN-1998; 98US-0089948.  
XX 19-JUN-1998; 98US-0089952.  
XX 22-JUN-1998; 98US-0090246.  
XX 22-JUN-1998; 98US-0090252.  
XX 22-JUN-1998; 98US-0090254.  
XX 23-JUN-1998; 98US-0090349.  
XX 23-JUN-1998; 98US-0090355.  
XX 24-JUN-1998; 98US-0090429.  
XX 24-JUN-1998; 98US-0090431.  
XX 24-JUN-1998; 98US-0090435.



KW antirheumatic; antiarthritic; antiinflammatory; antianaemic;  
 KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
 KW hepatotropic; virucide; dermatological; antipruritic;  
 KW antiaesthetic; antiallergic; immunostimulant; ss.  
 OS  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX CDS 13..312  
 XX FT /\*tag= a  
 XX FT sig\_peptide 13..78  
 XX FT /\*tag= b  
 XX FT mat\_peptide 79..309  
 XX FT /\*tag= c  
 XX  
 XX MO200105972-A1.  
 XX  
 XX 25-JAN-2001.  
 XX  
 XX 15-MAR-2000; 2000WO-US06884.  
 XX  
 XX 20-JUL-1999; 99US-0144758.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowaki PJ, Guirney AL;  
 XX Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;  
 XX Wood WJ;  
 XX WPI; 2001-103149/11.  
 XX P-PSDB; AAB20117.  
 XX  
 XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
 XX diagnosing and treating immune-related disorders, such as multiple  
 XX sclerosis, rheumatoid arthritis and diabetes -  
 XX  
 XX Claim 21; Fig 19; 127pp; English.  
 XX  
 XX The present sequence is that of cDNA clone DN57694-1341 (ATCC 203017)  
 XX encoding novel human immunomodulator protein PRO826 (UNQ467) (see  
 XX AAB20117). The clone was isolated following a database search by  
 XX applying a signal sequence algorithm. The predicted protein has a  
 XX mol.wt. of 11 kDa and a pI of 7.47. The invention provides  
 XX polynucleotides (see AAF30050-62) encoding novel human PRO proteins  
 XX (see AAB20108-20) including PRO826. Claimed compositions  
 XX comprising these proteins or their agonists are useful for increasing  
 XX infiltration of inflammatory cells into a tissue of a mammal,  
 XX stimulating or enhancing an immune response in a mammal, or  
 XX increasing the proliferation of T-lymphocytes in a mammal in response  
 XX to an antigen. Claimed compositions comprising the PRO polypeptide  
 XX or its antagonist have the opposite effect. A claimed method for  
 XX treating an immune related disorder, such as a T cell disorder,  
 XX involves administering the PRO polypeptide, an agonist antibody or  
 XX an antagonist antibody. The disorder is selected from systemic  
 XX lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 XX juvenile chronic arthritis, spondyloarthritis, systemic  
 XX sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome,  
 XX systemic vasculitis, sarcoidosis, autoimmune hemolytic anaemia,  
 XX autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 XX immune-mediated renal disease, demyelinated diseases (such as  
 XX multiple sclerosis), autoimmune chronic active hepatitis, primary  
 XX biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
 XX inflammatory bowel disease (ulcerative colitis and Crohn's disease),  
 XX gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated  
 XX skin diseases (such as bullous skin disease, erythema multiforme and  
 XX psoriasis), allergic diseases (such as asthma, allergic rhinitis,  
 XX atopic dermatitis, food hypersensitivity and urticaria), immunologic  
 XX diseases of the lung and transplantation associated diseases (such  
 XX as graft rejection and graft-versus-host disease) (all claimed).  
 XX Claimed methods of diagnosing these disorders comprise detecting  
 XX the level of expression of the PRO gene. Also claimed are a method  
 XX of identifying a compound capable of inhibiting the expression or  
 XX activity of the PRO polypeptide, vectors, host cells, antibodies

CC and a method of stimulating the proliferation of T-lymphocytes  
 CC using PRO826.  
 XX  
 XX Sequence 415 BP; 99 A, 126 C, 92 G, 98 T, 0 other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 3,24e-66 415  
 Score: 71.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0  
 US-10-059-395-142\_COPY\_29\_99 (1-71) x AAF30059 (1-415)  
 QY 1 GIUGIUGIUSERTHRIIEGLUASRTYRALASERAPROGLUALAPHEASRTN-PROPhE 20  
 DB 97 GAGGAGAGAAAGCCACCATTTGAGAAATTATGCGTCAGACCCAGGCGCTTTAACACCCCGCTTC 156  
 QY 21 LEUASNTLEASPLYSLEUARGSERALAPHELYALAPSPGIUPHEUASNTTROIHALA 40  
 DB 157 CTGAACATGACCAATATGCGATCTGCTTAAAGCTATGATGTTCTGAACCTGGACGCC 216  
 QY 41 LEUPHEGLUSERILEYSLARGYSLAUProPhELeUASNTTAPASAPALAPHEProLYSLAU 60  
 DB 217 CTCCTTAGGCTATACAAAGAACTTCCTTCTCACTGGAGTGCCTTTCCTTAAGCTG 276  
 QY 61 LYSGLYLEUARGSERALATNProASPALGln 71  
 DB 277 AAAGACTGAGAGCGCGCACTCCGTGATGCCAG 309  
 RESULT 5  
 AAF44164  
 ID AAF44164 standard; cDNA; 415 BP.  
 XX  
 XX AAF44164;  
 AC  
 XX  
 XX 02-APR-2001 (first entry)  
 DT  
 XX  
 XX Human PRO826 (UNQ467) nucleotide sequence SEQ ID NO:200.  
 DE  
 XX  
 XX Human; secreted and transmembrane protein; PRO; cytosolic;  
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX MO200073454-A1.  
 PN  
 XX  
 XX 07-DEC-2000.  
 PD  
 XX  
 XX 30-MAR-2000; 2000WO-US08439.  
 FP  
 XX  
 XX 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 17-AUG-1999; 99US-0149396.  
 PR 15-SEP-1999; 99WO-US21099.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 08-OCT-1999; 99US-0158663.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.

24-FEB-2000; 2000MO-US05004.  
PR 02-MAR-2000; 2000MO-US05841.  
PR 15-MAR-2000; 2000MO-US06884.  
PR 20-MAR-2000; 2000MO-US07377.  
XX  
XX (GENTH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
PI Ferrara N, Fong S, Gerber H, Gertsen ME, Goddard A, Godowski PJ,  
PI Grimaldi CJ, Gurney AL, Kijavira IJ, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;  
DR WPI; 2001-032160/04.  
DR P-PSDB; AAB65204.  
XX  
XX PRO polynucleotides used to produce polypeptides used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -  
XX  
XX Claim 2; Fig 128; 935pp; English.  
XX  
XX The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
CC can be used for targeted delivery of bioactive molecules, such as  
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
CC and DNA. They may also be used to produce transgenic animals which are  
CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
XX SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
XX  
XX Alignment Scores:  
Pred. No.: 3,24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) X AAF44164 (1-415)  
QY 1 GIUGIUGIUSERTHRIIEGLUASNTYRALASERARGPROGUAIAPEASNTHPROPE 20  
DB 97 GAGGAGAGAAACACATTGAGATTTATGCGTACAGACCCGAGGCTTTAAACACCCCGTTC 156  
QY 21 LEUASNTLEAPPLYLEUARGSERIALAPHELYSALAAPGULPHLEUASNTTHIALA 40  
DB 157 CTGAACATCGCAAAATTCGATCGCTTTAAGCTGATGATGATTCCTGAACCTGCACGCC 216  
QY 41 LEUPHEGUSERTILEYARGLYLEUPROPHLEUASNTTPASAPALAPHEPROLYSEU 60  
DB 217 CTTCTTAGAGTCTATCAAAAGAACTTCCTTCTCACTGAGATGCTTTCTTAAGCTG 276  
QY 61 LYSGLYLEUARGSERIALATHPROASPLAQLN 71  
DB 277 AAAGGACTGAGAGAGGCAACTCTGATGCCAG 309  
RESULT 6  
AAC97491 ID AAC97491 standard; cDNA, 415 BP.  
XX AAC97491;  
AC AAC97491;  
XX 28-FEB-2001 (first entry)  
DT XX

DE Human angiogenesis-associated protein PRO826 cDNA, SEQ ID NO:157.  
XX  
XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200053753-A2.  
PN  
XX 14-SEP-2000.  
PD  
XX  
XX 05-JAN-2000; 2000MO-US00219.  
PF  
XX  
XX 08-MAR-1999; 99MO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99MO-US12352.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99MO-US20111.  
PR 08-SEP-1999; 99MO-US20594.  
PR 15-SEP-1999; 99MO-US21090.  
PR 15-SEP-1999; 99MO-US21547.  
PR 05-OCT-1999; 99MO-US23089.  
PR 30-NOV-1999; 99MO-US28313.  
PR 30-NOV-1999; 99MO-US28409.  
PR 02-DEC-1999; 99MO-US28564.  
PR 02-DEC-1999; 99MO-US28565.  
XX  
XX (GENTH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A,  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA,  
PI Paoni NF, Pictl RM, Watanabe CK, Williams PM, Wood WI,  
PI  
DR WPI; 2001-090793/10.  
DR P-PSDB; AAB53094.  
XX  
XX New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
XX  
XX Claim 58; Fig 61; 293pp; English.  
PS  
XX  
XX The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's

CC disease, or stroke. PRO nucleic acids are additionally useful in the  
 CC recombinant production of PRO proteins, as hybridisation probes to  
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
 CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
 CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
 CC animals useful for the development and screening of potential  
 CC therapeutic agents. The present sequence represents a cDNA encoding a PRO  
 CC protein of the invention.

XX SO Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

# Alignment Scores:

Pred. No.: 3,24e-66 Length: 415  
 Score: 71.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AAC97491 (1-415)

Qy 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20

Db 97 GAGAAAGAAACACCATTTAGAAATTAATGCGACAGACCCGAGCCCTTTAACACCCCGCTTC 156

Qy 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPheAla 40

Db 157 CTGAACATCGACCAATTCGATCTGCGTTAAAGCTGATGAGTTCTCGAACTGGACGCC 216

Qy 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrPheAlaPheProLysLeu 60

Db 217 CTCCTTGAGCTATCAAAAGAAACCTTCCTTCTCAACTGGATGCTTCTTAAGGTG 276

Qy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71

Db 277 AAAGACTGAGAGACGCGCACTCGATGCCAG 309

## RESULT 7

ABL95626 ID ABL95626 standard; cDNA; 415 BP.

XX ABL95626;

XX 19-JUL-2002 (first entry)

XX DE Human angiogenesis related cDNA PRO826 SEQ ID NO: 131.

XX KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;

XX KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;

XX KW cardiatic; cyostatic; antiangiogenic; hypotensive; vulnerary;

XX KW antiarteriosclerotic; gene; ss.

XX OS Homo sapiens.

XX PN WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 28-JUL-2000; 2000US-220664P.

XX 02-AUG-2000; 2000WO-US20710.

XX 17-AUG-2000; 2000US-222895P.

XX 23-AUG-2000; 2000WO-US23522.

XX 07-SEP-2000; 2000US-230978P.

XX 15-SEP-2000; 2000US-000000P.

XX 18-SEP-2000; 2000US-0664610.

XX 18-SEP-2000; 2000US-0665350.

XX 24-OCT-2000; 2000US-242922P.

PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US30873.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 02-APR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001US-0819692.  
 PR 28-JUN-2001; 2001WO-US00000.

XX (GERTH ) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERE/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.

PA (PANO/) PAONI N F.

PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-171999/22.

XX P-PSDB; ABB95488.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial

PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 1; Fig 131; 567pp; English.

XX The present invention provides the protein and coding sequences of human

XX PRO proteins. These are useful for treating or diagnosing a

XX cardiovascular, endothelial or angiogenic disorder, including cardiac

XX hypertrophy, trauma, cancer, age-related macular degeneration,

XX atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound

XX healing. The present sequence is a coding sequence of the invention.

XX SO Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

## Alignment Scores:

Pred. No.: 3,24e-66 Length: 415  
 Score: 71.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x ABL95626 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAGAAAGACCATTCAGATTATGCGTCACGACCGAGGCCCTTTAAACCCCGCTTC 156  
QY 21 LeuAsnIleAspIleuArgSerAlaPheIleAlaAspGluPheLeuAsnTyrPheAla 40  
DB 157 CTGAAACATCGACAAATTGCGATCGCTTAAGGCTGATGAGTTCTGAACCTGGCAGCGCC 216  
QY 41 LeuPheIleuSerIleIleValArgIleuPhePheLeuAsnTyrAspAlaPheProIleu 60  
DB 217 CTCTTGAAGTCTATCAAAAGAACTCTTCTCTCAACTGGGATGCGCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCACTCCGATGCCGAG 309

RESULT 8  
ABK69971 ID ABK69971 standard; DNA; 415 BP.  
XX AC ABK69971;  
XX DT 15-JUL-2002 (first entry)  
XX DE cDNA encoding human Pro peptide #11.  
XX KM Human; ss: gene; PRO; secreted protein; transmembrane protein;  
XX KW genetic disorder; tumour; cancer.  
XX OS Homo sapiens.  
XX PN MO200224888-A2.  
XX PD 28-MAR-2002.  
XX PF 29-AUG-2001; 2001WO-US27099.  
XX PR 01-SEP-2000; 2000US-223896P.  
XX PR 05-SEP-2000; 2000US-230621P.  
XX PR 22-SEP-2000; 2000US-235147P.  
XX PR 10-NOV-2000; 2000WO-US30873.  
XX PR 12-JAN-2001; 2001US-261878P.  
XX PR 16-JAN-2001; 2001US-261910P.  
XX PR 15-JAN-2001; 2001US-261939P.  
XX PR 16-JAN-2001; 2001US-262150P.  
XX PR 25-JAN-2001; 2001US-264395P.  
XX PR 02-FEB-2001; 2001US-266421P.  
XX PR 09-FEB-2001; 2001US-267623P.  
XX PR 28-FEB-2001; 2001WO-US06520.  
XX PR 09-MAR-2001; 2001US-274399P.  
XX PR 03-APR-2001; 2001US-280982P.  
XX PR 04-APR-2001; 2001US-282128P.  
XX PR 04-APR-2001; 2001US-282199P.  
XX PR 09-MAY-2001; 2001US-290589P.  
XX PR 25-MAY-2001; 2001WO-US17092.  
XX PR 01-JUN-2001; 2001WO-US17800.  
XX PR 20-JUN-2001; 2001WO-US19692.  
XX PR 29-JUN-2001; 2001WO-US21066.  
XX PR 09-JUL-2001; 2001WO-US21735.  
XX PA (GERTH ) GENENTECH INC.  
XX PI Baker KP, Baton DU, Filvaroff E, Goddard A, Grimaldi JC,  
XX PI Guney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z,  
XX PI Fong S,  
XX WPI; 2002-362426/39.  
XX DR P-PSDB; ABG34040.  
XX PT New PRO polypeptides and polynucleotides encoding the polypeptides,

PT useful in gene therapy, chromosome identification, tissue typing, or  
XX for genetic analysis of individuals with genetic disorders  
XX PS Claim 2; Figure 21; 218pp; English.  
XX CC This invention relates to the cDNA and protein sequences of novel  
CC secreted and transmembrane polypeptides PRO polypeptides. The  
CC invention also comprises a method for producing the proteins of the  
CC invention by recombinant means and antibodies specific for the protein  
CC of the invention. The antibody may be used for detecting the PRO  
CC proteins of the invention and may be used to modify their activity.  
CC polynucleotides may be used as hybridisation probes for a cDNA library  
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
CC construct hybridisation probes for mapping the gene which encodes that  
CC PRO and for genetic analysis of individuals with genetic disorders, in  
CC assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knock-out animals which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides are useful in gene therapy, and as molecular weight  
CC markers for protein electrophoresis purposes. The sequences may  
CC also be used to detect overexpression on PRO polypeptides in cancerous  
CC tumours and for screening for differentially expressed genes using  
CC microarray technology. The present sequence represents a cDNA encoding  
CC a human PRO protein of the invention.  
XX SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
XX Alignment Scores:  
Pred. No.: 3,24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x ABK69971 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAGAAAGACCATTCAGATTATGCGTCACGACCGAGGCCCTTTAAACCCCGCTTC 156  
QY 21 LeuAsnIleAspIleuArgSerAlaPheIleAlaAspGluPheLeuAsnTyrPheAla 40  
DB 157 CTGAAACATCGACAAATTGCGATCGCTTAAGGCTGATGAGTTCTGAACCTGGCAGCGCC 216  
QY 41 LeuPheIleuSerIleIleValArgIleuPhePheLeuAsnTyrAspAlaPheProIleu 60  
DB 217 CTCTTGAAGTCTATCAAAAGAACTCTTCTCTCAACTGGGATGCGCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCACTCCGATGCCGAG 309

RESULT 9  
ABL88137 ID ABL88137 standard; cDNA; 415 BP.  
XX AC ABL88137;  
XX DT 16-MAY-2002 (first entry)  
XX DE Human PRO826 cDNA sequence SEQ ID NO:131.  
XX KM Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;  
XX KM vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
XX KM gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
XX KM angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
XX KM age-related macular degeneration; arterial restenosis; angina;  
XX KM rheumatoid arthritis; myocardial infarction; chromophlebitis;  
XX KM lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
XX KM wound healing; chromosome mapping; gene mapping; gene; ss.





|   |   |
|---|---|
| PA  | (GERTH ) GENENTECH INC.   |
| PX  |   |
| XX  | Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,              |
| XI  | Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI,        |
| DR  | WPI; 2002-172001/22.  |
| DR  | P-PSDB; AAU83664.   |
| XX  |   |
| PT  | One hundred and twenty two nucleic acids encoding PRO polypeptides,       |
| PT  | useful for treating a PRO related disorder and for diagnosing tumours     |
| XX  | such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal |
| XX  | tumour or liver tumour -  |
| PS  | Claim 2; Figure 145; 359pp; English.                                      |
| XX  |   |
| CC  | The invention relates to one hundred and twenty two nucleic acids         |
| CC  | encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides   |
| CC  | encode human secreted proteins. The PRO nucleic acids, polypeptides,      |
| CC  | agonists and antagonists are useful for treating a PRO related disorder.  |
| CC  | The PRO polypeptides are useful for diagnosing tumours, especially lung   |
| CC  | cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or    |
| CC  | liver tumour. The PRO polypeptides are useful for stimulating the         |
| CC  | proliferation of, or gene expression, in pericyte cells, for stimulating  |
| CC  | the proliferation or differentiation of chondrocyte cells, for            |
| CC  | stimulating the release of tumour necrosis factor-alpha from human blood, |
| CC  | for stimulating or inhibiting the proliferation of normal human dermal    |
| CC  | fibroblast cells. The PRO polypeptide may also be used as molecular       |
| CC  | weight markers and for tissue typing. The PRO nucleic acids have          |
| CC  | applications in molecular biology, including use as hybridisation probes, |
| CC  | and in chromosome and gene mapping. AAK3536-AAK3567 represent human       |
| CC  | PRO protein coding sequences of the invention.                            |
| SQ  | Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;                        |
| XX  |   |
| Alignment Scores:   |   |
| Pidg. No.:  | 3,24e-66 Length: 415  |
| Score:  | 71.00 Matches: 71   |
| Percent Similarity:   | 100.00% Conservative: 0   |
| Best Local Similarity:  | 100.00% Mismatches: 0   |
| Query Match:  | 100.00% Indels: 0   |
| DB:   | Gaps: 0   |
| US-10-059-395-142_COPY_29_99 (1-71) x AAK33608 (1-415)                  |   |
| OY  | 1 GluGluGluSerThrIleGluAsnTYrAlaSerArgProGluAlaPheAsnThrProPhe 20         |
| Db  | 97 GAGGAAGAAGAAACCAATTCATTGATTTGGTGCACACCAGAGCCTTTAACACCCCGCTTC 156       |
| OY  | 21 LeuAsnIleLeuArgLysLeuArgSerAlaPheLYrAlaAspGluPheLeuAsnTrpHisAla 40     |
| Db  | 157 CTGAACATGCACAATAATTCGATTCGTGCTTAAGGCTGGAAGTAATCTTAACCTGGCACGCC 216    |
| OY  | 41 LeuPheGluSerIleIleYSArGLySLeuProPheLeuAsnTrpAspAlaPheProLYsLeu 60      |
| Db  | 217 CTCCTTGAGCTCATCAAAGAAGAAACTCTCTTCTTCTCAACTGGGAGAGCGCTTCTTAGCTG 276    |
| OY  | 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71                                   |
| Db  | 277 AAAAGACTGAGAGCGCACTCTCGTAGTCCAGC 309                                  |
| RESULT 11   |   |
| ID  | ABX80255 standard; DNA, 415 BP.   |
| XX  |   |
| AC  | ABX80255;   |
| XX  |   |
| DT  | 28-APR-2003 (first entry)   |
| XX  |   |
| DE  | Novel human secreted or transmembrane protein PRO819 DNA.                 |
| XX  |   |
| Human, PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; |   |
| cardiac insufficiency disorder; cancer; tumour; immune response;        |   |
| KW  |   |

|    |  |
|----|--|
| KW | adrenal cortical capillary endothelial growth; c-fos induction;      |
| KW | vascular endothelial growth factor inhibition; VEGF inhibition;      |
| KM | endothelial cell growth inhibitor; T-lymphocyte stimulation;         |
| KW | retinal neurons cell survival; rod photoreceptor cell survival;      |
| KW | retinal disorder; retinitis pigmentosa; kidney disorder;             |
| KW | mammalian kidney mesangial cell proliferation; Berger disease;       |
| KW | dematitis; herpetiformis; Crohn's disease; chondrocyte proliferation |
| KX | chondrocyte redifferentiation; sports injury; arthritis; gene; ds.   |
| OS | Homo sapiens.  |
| XX |  |
| PN | US2002132252-A1.   |
| XX |  |
| PD | 19-SEP-2002.   |
| XX |  |
| PE | 14-NOV-2001; 2001US-0990442.   |
| XX |  |
| PR | 05-NOV-1997; 97WO-US20069.   |
| PR | 16-SEP-1998; 98WO-US19930.   |
| PR | 17-SEP-1998; 98WO-US19437.   |
| PR | 07-OCT-1998; 98WO-US21141.   |
| PR | 01-DEC-1998; 98WO-US25108.   |
| PR | 05-JAN-1999; 99MO-US00106.   |
| PR | 08-MAR-1999; 99MO-US05028.   |
| PR | 02-JUN-1999; 99MO-US12252.   |
| PR | 15-SEP-1999; 99MO-US21090.   |
| PR | 15-SEP-1999; 99MO-US21447.   |
| PR | 30-NOV-1999; 99MO-US28313.   |
| PR | 01-DEC-1999; 99MO-US28301.   |
| PR | 01-DEC-1999; 99MO-US28634.   |
| PR | 16-DEC-1999; 99MO-US30095.   |
| PR | 20-DEC-1999; 99MO-US03911.   |
| PR | 06-JAN-2000; 2000MO-US00219.   |
| PR | 06-JAN-2000; 2000MO-US00376.   |
| PR | 11-FEB-2000; 2000MO-US03665.   |
| PR | 18-FEB-2000; 2000MO-US04341.   |
| PR | 22-FEB-2000; 2000MO-US04414.   |
| PR | 24-FEB-2000; 2000MO-US04914.   |
| PR | 24-FEB-2000; 2000MO-US05004.   |
| PR | 02-MAR-2000; 2000MO-US05841.   |
| PR | 10-MAR-2000; 2000MO-US06319.   |
| PR | 15-MAR-2000; 2000MO-US06884.   |
| PR | 20-MAR-2000; 2000MO-US07377.   |
| PR | 30-MAR-2000; 2000MO-US09439.   |
| PR | 15-MAY-2000; 2000MO-US13358.   |
| PR | 17-MAY-2000; 2000MO-US13705.   |
| PR | 22-MAY-2000; 2000MO-US14042.   |
| PR | 30-MAY-2000; 2000MO-US14941.   |
| PR | 02-JUN-2000; 2000MO-US15644.   |
| PR | 28-JUN-2000; 2000MO-US20710.   |
| PR | 11-AUG-2000; 2000MO-US22031.   |
| PR | 23-AUG-2000; 2000MO-US23522.   |
| PR | 24-AUG-2000; 2000MO-US23328.   |
| PR | 08-NOV-2000; 2000MO-US30952.   |
| PR | 01-DEC-2000; 2000MO-US32678.   |
| PR | 28-FEB-2001; 2001MO-US06520.   |
| PR | 01-JUN-2001; 2001MO-US17800.   |
| PR | 20-JUN-2001; 2001MO-US19692.   |
| PR | 29-JUN-2001; 2001MO-US21066.   |
| PR | 09-JUL-2001; 2001MO-US21735.   |
| PR | 16-JUN-1997; 97US-049787P.   |
| PR | 17-OCT-1997; 97US-062250P.   |
| PR | 12-NOV-1997; 97US-065166P.   |
| PR | 13-NOV-1997; 97US-065311P.   |
| PR | 24-NOV-1997; 97US-066770P.   |
| PR | 25-FEB-1998; 98US-075945P.   |
| PR | 20-MAR-1998; 98US-078910P.   |
| PR | 28-APR-1998; 98US-083322P.   |
| PR | 07-MAY-1998; 98US-084600P.   |
| PR | 28-MAY-1998; 98US-087106P.   |
| PR | 02-JUN-1998; 98US-087609P.   |
| PR | 02-JUN-1998; 98US-087609P.   |
| PR | 02-JUN-1998; 98US-087759P.   |

PR 03-JUN-1998; 98US-087827P.  
 PR 04-JUN-1998; 98US-088021P.  
 PR 04-JUN-1998; 98US-088025P.  
 PR 04-JUN-1998; 98US-088026P.  
 PR 04-JUN-1998; 98US-088028P.  
 PR 04-JUN-1998; 98US-088029P.  
 PR 04-JUN-1998; 98US-088030P.  
 PR 04-JUN-1998; 98US-088033P.  
 PR 04-JUN-1998; 98US-088326P.  
 PR 05-JUN-1998; 98US-088167P.  
 PR 05-JUN-1998; 98US-088202P.  
 PR 05-JUN-1998; 98US-088212P.  
 PR 05-JUN-1998; 98US-088217P.  
 PR 09-JUN-1998; 98US-088655P.  
 PR 10-JUN-1998; 98US-088734P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088742P.  
 PR 10-JUN-1998; 98US-088810P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088826P.  
 PR 11-JUN-1998; 98US-088858P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088876P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089340P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 17-JUN-1998; 98US-089532P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089598P.  
 PR 17-JUN-1998; 98US-089599P.  
 PR 17-JUN-1998; 98US-089600P.  
 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089601P.  
 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.  
 XX  
 XX (GENTH ) GENENTECH INC.  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers J, Baton DU,  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;  
 XX  
 XX WPI; 2003-247083/24.  
 DR P-PSDB; ABUS9098.  
 XX  
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT are therapeutically useful for enhancing immune response and in cancer  
 PT treatments -  
 XX  
 XX Claim 2; Fig 130; 648bp; English.  
 XX  
 CC The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO132 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and angiogenesis of this polypeptide are  
 CC useful for treating cancerous tumours. PRO812 inhibits vascular  
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 CC cells and is thus useful for inhibiting endothelial cell growth in  
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing

CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disease associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or redifferentiation of chondrocytes in culture and  
 CC are thus useful for treating sports injuries, and arthritis. This  
 CC sequence represents a novel human PRO protein polynucleotide.  
 XX  
 SQ Sequence 415 BP, 99 A, 126 C, 92 G, 98 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3,24e-66 Length: 415  
 Score: 71.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Ds: 25 Gaps: 0  
 US-10-059-395-142\_COPY\_29\_99 (1-71) X ABX80255 (1-415)  
 QY 1 GUGUGUGUSeRTThlIeGUAsnTYRASeRrPProGUAlaPheAsnThrProPhe 20  
 Db 97 GAGGAGGAGAACACACCTTGAAGAAATTATCGTCAGACCCGAGGCTTTAAACCCCGTTC 156  
 QY 21 LeuAenITLeaPlyLeuAArgSerAlaPheLYsAlaAPGGLuPheLeuAsnTrpHisAla 40  
 Db 157 CTGAACATCGACCAANTTCGATCGATCGCTTTAAGGCTGATGAGTTCTTAACCTGACAGCCG 216  
 QY 41 LeuPheGUSeRITLeYsArgLYsLeuBProPheLeuAenTrpAspAlaPheProLYsLeu 60  
 Db 217 CTCTTGAGTCTATCAAAAGAAACTTCCTTCCTCAACTGGAGATGCTTCTCTAAGCTG 276  
 QY 61 LysGLYLeuAArgSerAlaThrProAspAlaGln 71  
 Db 277 AAAGGACTGAGAGAGGACCAACTCTGATGCCAG 309  
 RESULT 12  
 ABX80759  
 ID ABX80759 standard; cDNA, 415 BP.  
 XX  
 XX ABX80759;  
 AC  
 XX  
 XX 22-APR-2003 (first entry)  
 DT  
 XX  
 XX Human secreted/transmembrane protein cDNA, #78.  
 DS  
 XX Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
 KW diagnostic; biosensor; bioreactor; tumour; therapeutic;  
 KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;  
 KW antibody-dependent enzyme mediated prodnug therapy; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2003027162-A1.  
 PN  
 XX  
 PD 06-FEB-2003.  
 XX  
 PF 15-NOV-2001; 2001US-0997428.  
 XX  
 PR 05-NOV-1997; 97WO-US20069.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30995.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-04987P.  
PR 17-OCT-1997; 97US-06250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087753P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088326P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088213P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088825P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
  
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 DB 157 CTGAACATCGACAAATTCATCTGCGTTTAAAGCTGATAGTCTCGAAGCTGACGCC 216  
 QY 41 LeuPheGluSerIleIleYsArgLysLeuProPheLeuAsnThrPheAlaPheProLysLeu 60  
 DB 217 CTTCTTGAGCTCTTCACAAAGGAACTTCCTTCTCTCACTGGAGTGCCTTCTTAAGCTG 276  
 QY 61 IysGlyLeuArgSerAlaThrProAspAlaGln 71  
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RESULT 13  
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 ID ABX81142 standard; DNA; 415 BP.

AC ABX81142;  
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DT 22-APR-2003 (first entry)  
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DE Novel human secreted or transmembrane protein PRO819 DNA.  
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XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disorder;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis; herpesiformis; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis; gene; de.  
 XX Homo sapiens.  
 OS

XX US2003027985-A1.  
 XX 06-FEB-2003.  
 PD 14-NOV-2001; 2001US-0990562.  
 PF XX  
 PR 05-NOV-1997; 97WO-US20069.  
 PR 16-SEP-1998; 98WO-US19330.  
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 PR 05-JAN-1999; 99WO-US00106.  
 PR 08-MAR-1999; 99WO-US05028.  
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XX OS Homo sapiens.
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XX 31-OCT-2002.
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XX 05-NOV-1997; 97WO-US20066.
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XX 24-FEB-2000; 2000WO-US04914.
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XX 10-MAR-2000; 2000WO-US06319.
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XX 01-DEC-2000; 2000WO-US32678.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-JUN-2001; 2001WO-US17800.
XX 20-JUN-2001; 2001WO-US19692.
XX 29-JUN-2001; 2001WO-US21066.
XX 09-JUL-2001; 2001WO-US21735.
XX 16-JUL-1997; 97US-049787P.
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XX 12-NOV-1997; 97US-065186P.
XX 13-NOV-1997; 97US-065311P.
XX 24-NOV-1997; 97US-066770P.
XX 25-FEB-1998; 98US-075945P.
XX 20-MAR-1998; 98US-078910P.
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XX 18-JUN-1998; 98US-089807P.
XX 18-JUN-1998; 98US-089908P.
XX 28-AUG-2001; 2001US-0941592.
XX
XX (GENTECH ) GENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL,
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
XX Grimaldi JC, Gueney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
XX Zhang Z;
XX
XX WPI; 2003-288106/28.
XX P-PSDB; AB060528.
XX
XX New transmembrane polypeptides and nucleic acids encoding the
XX polypeptides, useful in gene therapy, in chromosome identification, as
XX chromosome markers, or in generating probes -
XX
XX Claim 2; Fig 128; 650bp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
XX comprising a sequence without signal peptide and the nucleic acid
XX encoding them. The polypeptides can be used to raise antibodies that
XX specifically bind to the PRO polypeptide, for linking a bioactive
XX molecule to a cell expressing a PRO protein and for modulating at least
XX one biological activity of a cell. The PRO polypeptides or
XX polynucleotides are also useful in gene therapy, in chromosome
XX identification, as chromosome markers, or in generating probes. The PRO
XX polypeptides are useful as molecular markers for protein
XX electrophoresis, and the isolated nucleic acids may be used for
XX recombinantly expressing these markers. The PRO polypeptides and nucleic
XX acids may also be used in tissue typing. Anti-PRO antibodies are useful
XX in diagnostic assays for PRO, and in affinity purification of PRO from
XX CC recombinant cell culture or natural sources. The sequences presented in
XX CC ABX90083-ABX90468 are the genes encoding, the primers amplifying, and the
XX CC probes detecting the PRO polynucleotides of the invention.
XX Note: The sequence data for this patent is also available in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
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XX Pred. No.: 3.24e-66 Length: 415
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XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0

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DB 157 CTGAACATGACCAAAATGCGATTCGCTTAAGCTGATGAGTTCCTGAACGCGACGCC 216  
QY 41 LeuPheGUSeRlIeYsaRgUyLeuProPheLeuAnTTrPaSaIaPhePProLYsIau 60  
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XX KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADAPT;  
XX KW antibody-dependent enzyme mediated prodng therapy.  
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XX US2003027163-A1.  
XX PD 06-FEB-2003.  
XX PF 15-NOV-2001; 2001US-0997666.  
XX 05-NOV-1997; 97WO-US20069.  
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XX 08-MAR-1999; 99WO-US12252.  
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XX 01-DEC-1999; 99WO-US28634.  
XX 16-DEC-1999; 99WO-US30095.  
XX 20-DEC-1999; 99WO-US30911.  
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XX 11-FEB-2000; 2000WO-US03565.  
XX 18-FEB-2000; 2000WO-US04341.  
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XX 15-MAR-2000; 2000WO-US06319.  
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XX 17-MAY-2000; 2000WO-US13705.  
XX 22-MAY-2000; 2000WO-US14042.

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PR 26-AUG-1998; 98US-097986P.  
PR 31-AUG-1998; 98US-098014P.  
PR 16-SEP-1998; 98US-098525P.  
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PR 17-SEP-1998; 98US-100858P.

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| DB | 157 | CTGAACATGACAAATTGGATCTGCGTTTAGGCTGATGATTCCTGAACGGACGCG      | 216 |
| QY | 41  | LeupheGIUSerIlelysaArgLysIeuProPheIuAnTrpAspAlaPheProLysIeu | 60  |
| DB | 217 | CTCTTGAGTCTATCAAAAGAACTTCCTTCCATCACTGGAGCCCTTCTTAAGCTG      | 276 |
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Search completed: November 28, 2003, 12:21.49  
Job time : 219 secs



APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
ACID ENCODING THE SAME  
FILE REFERENCE: P27301PC63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

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Score: 71.00 Matches: 71  
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## RESULT 2

US-09-989-723-200  
Sequence 200, Application US/09989723  
Patent No. US20020072092A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlt, Maury E.  
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Abustin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C62  
CURRENT APPLICATION NUMBER: US/09/989,723  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR FILING DATE: 1998-06-09

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US-09-989-279-200
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; Patent No. US20020072496A1
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RESULT 3
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; Sequence 200, Application US/09989279
; Patent No. US20020072496A1
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US-09-989-279-200
; Sequence 200, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:

RESULT 3
US-09-989-279-200
; Sequence 200, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:

Alignment Scores:
Pred. No.:      7,74e-66          Length:      415
Score:           71.00            Matches:     71
Percent Similarity: 100.00%       Conservative: 0
Best Local Similarity: 100.00%    Mismatches:  0
Query Match:      100.00%         Indels:      0
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APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
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APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
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APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC56  
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PRIOR FILING DATE: 1998-07-09

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Sequence 200, Application US/09989727  
Patent No. US20020072497A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Falcon, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paonli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1CS5  
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;; PRIOR FILING DATE: 1998-07-09

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Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
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RESULT 6  
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Sequence 200, Application US/09989732  
Patent No. US20020123463A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Borstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
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APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C57  
CURRENT APPLICATION NUMBER: US/09/989,732  
CURRENT FILING DATE: 2001-11-19  
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## Alignment Scores:

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US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-991-073-200 (1-415)

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Qy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
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## RESULT 8

US-09-990-442-200

Sequence 200, Application US/09990442

Patent No. US20020132252A1

GENERAL INFORMATION:

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APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyere, Luc  
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APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
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APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C8  
CURRENT FILING DATE: 2001-11-14  
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| 2  | APPLICANT:                  | Napier, Mary A.                                     |
| 3  | APPLICANT:                  | Pan, James  |
| 4  | APPLICANT:                  | Pooni, Nicholas F.                                  |
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| 13 | TITLE OF INVENTION:         | Acids Encoding the Same                             |
| 14 | FILE REFERENCE:             | P2730Pic17  |
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;; PRIOR FILING DATE: 1998-07-09

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QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrPheAlaPheProLysLeu 60  
DB 217 CTTTGTGATGATCAAAAGAACTTCCTTCTCAACTGGATGCTTCTTAAGCTG 276  
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; Sequence 200, Application US/09993604  
; Patent No. US20020137075A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David



APPLICANT: Deenoyers, Luc  
APPLICANT: Ealon, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlicsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
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APPLICANT: Pan, James  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C25  
CURRENT FILING DATE: 2001-11-14  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 7,74e-66 Length: 415  
Score: 71.00 Matches: 71  
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US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-993-604-200 (1-415)

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Db 217 CTTCTTGAATCTATCAAGAAAGAACTTCTTTCTTCACTGAGATGCGATCTTAAGCTG 276  
QY 61 LYGGLYeuArGSeRlAthrProApAlaGln 71

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Patent No. US20020137890A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC22  
CURRENT FILING DATE: 2001-11-14  
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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
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QY 61 LyegGlyLeuAtrSerAlaThrProAspAlaGln 71  
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Sequence 200, Application US/09989721  
Patent No. US20020142961A1  
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APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
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APPLICANT: Ferrara, Napoleone  
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APPLICANT: Gurney, Austin L.  
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APPLICANT: Tumes, Daniel  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids  
FILE REFERENCE: P27301C5  
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PRIOR FILING DATE: 1998-07-09

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APPLICANT: Ashkenazi, Avi J.  
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APPLICANT: Desnoyers, Luc  
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APPLICANT: Tumas, Daniel  
APPLICANT: Williams, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Acids Encoding and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C20  
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CURRENT FILING DATE: 2001-11-14  
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/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerltsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, U. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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/ PRIOR FILING DATE: 2001-11-20
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PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478

PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 7,74e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-989-293A-200 (1-415)

QY 1 GIUGIUGIUSERTHIIGLUSNTYRALASERARGPROGIIUALAPHEASNTHPROPHE 20  
DB 97 GAGGAAGAAAGACCATTCAGATTATGCTCAGACCGAGGCTTTAAACCCCGTTC 156  
QY 21 LEUANTILEAPLYLEUARGSERIALAPHELYSALIAAPGLUPHELEUANTTPHISALIA 40  
DB 157 CTGAACATCGACMAATTCGATCTGCTTAAGCTGATGATTCCTGAACGCAAGCC 216  
QY 41 LEUPHEGLUSERILEYARGLYSEUROPHELEUANTTPASPAAPHEPROLYSEU 60  
DB 217 CTCITTAGCTCTATATAAAGAACTTCCTTCCCACTGGAGATGCCCTTCTTAAGCTG 276  
QY 61 LYSGLYLEUARGSERIALTPHROBAPALAGIN 71  
DB 277 AAAGACTGAGGAGGCACTCTGATGCCG 309

RESULT 15  
US-09-989-735-200  
Sequence 200, Application US/09989735  
Publication No. US20020193299A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Geider, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same



[illegible]

/ PRIOR FILING DATE: 1998-06-25  
/ PRIOR APPLICATION NUMBER: 60/090696  
/ PRIOR FILING DATE: 1998-06-25  
/ PRIOR APPLICATION NUMBER: 60/090862  
/ PRIOR FILING DATE: 1998-06-26  
/ PRIOR APPLICATION NUMBER: 60/090863  
/ PRIOR FILING DATE: 1998-06-26  
/ PRIOR APPLICATION NUMBER: 60/091360  
/ PRIOR FILING DATE: 1998-07-01  
/ PRIOR APPLICATION NUMBER: 60/091478  
/ PRIOR FILING DATE: 1998-07-02  
/ PRIOR APPLICATION NUMBER: 60/091544  
/ PRIOR FILING DATE: 1998-07-01  
/ PRIOR APPLICATION NUMBER: 60/091519  
/ PRIOR FILING DATE: 1998-07-02  
/ PRIOR APPLICATION NUMBER: 60/091626  
/ PRIOR FILING DATE: 1998-07-02  
/ PRIOR APPLICATION NUMBER: 60/091633  
/ PRIOR FILING DATE: 1998-07-02  
/ PRIOR APPLICATION NUMBER: 60/091978  
/ PRIOR FILING DATE: 1998-07-07  
/ PRIOR APPLICATION NUMBER: 60/091982  
/ PRIOR FILING DATE: 1998-07-07  
/ PRIOR APPLICATION NUMBER: 60/092182  
/ PRIOR FILING DATE: 1998-07-09

Alignment Scores:

|                        |          |               |     |
|------------------------|----------|---------------|-----|
| Pred. No.:             | 7.74e-66 | Length:       | 415 |
| Score:                 | 71.00    | Matches:      | 71  |
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| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 10       | Gaps:         | 0   |

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-989-735-200 (1-415)

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| Db | 97  | GAAGAGAGAGAGCAACCAATTGAGATTATGCGTCACGACCCGAGCCCTTTAAACACCCCGTTC | 156 |
| Qy | 21  | LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla    | 40  |
| Db | 157 | CTGAACATCGACCAATTGCGATCTGGCTTTAAGGCTGATGAGTTCCTGAACGCGACGCGC    | 216 |
| Qy | 41  | LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu    | 60  |
| Db | 217 | CTCTTGAGTCTATCAAAAGAAACTTCCTTCCTCACTGGATGCTTCTTAAGCTG           | 276 |
| Qy | 61  | LysGlyLeuArgSerAlaThrProAspAlaGln                               | 71  |
| Db | 277 | AAAGACTGAGAGCGCAACTCTGATGCGCAG                                  | 309 |

Search completed: November 28, 2003, 13:38:07  
Job time : 251 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 10:23:55 ; Search time 2638 Seconds  
(without alignments)  
1101.055 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99  
Perfect score: 71  
Sequence: 1 EESTIENYASRPEAFNTPF.....LNMDFPKLKGSRATPDQAQ 71

Scoring table:  
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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5772890

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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-DB=genemb1 -QFMT=fastap -SUFFIX=ol1.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
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-NORM=ext -HAPSIZE=500 -MINLEN=2000000000  
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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : GenEmb1:\*

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| 2:  | gb_hcg:* |
| 3:  | gb_in:*  |
| 4:  | gb_om:*  |
| 5:  | gb_ov:*  |
| 6:  | gb_pat:* |
| 7:  | gb_ph:*  |
| 8:  | gb_pl:*  |
| 9:  | gb_pr:*  |
| 10: | gb_ro:*  |
| 11: | gb_scs:* |
| 12: | gb_sy:*  |
| 13: | gb_un:*  |
| 14: | gb_vl:*  |
| 15: | em_ba:*  |
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| 17: | em_hum:* |
| 18: | em_in:*  |
| 19: | em_mu:*  |
| 20: | em_om:*  |
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| 22: | em_ov:*  |
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| 26: | em_ro:*  |
| 27: | em_scs:* |
| 28: | em_un:*  |

29: em\_vl:\*

30: em\_hcg\_hum:\*

31: em\_hcg\_inv:\*

32: em\_hcg\_other:\*

33: em\_hcg\_mus:\*

34: em\_hcg\_pln:\*

35: em\_hcg\_rdi:\*

36: em\_hcg\_mam:\*

37: em\_hcg\_vrt:\*

38: em\_sy:\*

39: em\_hcgo\_hum:\*

40: em\_hcgo\_mus:\*

41: em\_hcgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1          | 71    | 100.0       | 414    | 6     | AX055438    |
| 2          | 71    | 100.0       | 415    | 6     | AR252517    |
| 3          | 71    | 100.0       | 415    | 6     | AX077031    |
| 4          | 71    | 100.0       | 415    | 6     | AX358892    |
| 5          | 71    | 100.0       | 415    | 6     | AX362385    |
| 6          | 71    | 100.0       | 415    | 6     | AX403313    |
| 7          | 71    | 100.0       | 415    | 6     | AX454546    |
| 8          | 71    | 100.0       | 415    | 6     | AX491024    |
| 9          | 71    | 100.0       | 415    | 6     | AX574494    |
| 10         | 71    | 100.0       | 432    | 6     | AX080815    |
| 11         | 71    | 100.0       | 432    | 6     | AX080818    |
| 12         | 71    | 100.0       | 456    | 6     | BD082389    |
| 13         | 71    | 100.0       | 490    | 6     | AX080817    |
| 14         | 59    | 83.1        | 435    | 6     | AX080816    |
| 15         | 56    | 78.9        | 278    | 6     | AX041085    |
| 16         | 46    | 64.8        | 529    | 9     | HSR233408   |
| 17         | 16    | 44.679      | 9      | 2     | CH19721246  |
| 18         | 9     | 12.7        | 205812 | 2     | AC141146    |
| 19         | 9     | 12.7        | 218382 | 2     | AC142461    |
| 20         | 9     | 12.7        | 236199 | 2     | AC110643    |
| 21         | 8     | 11.3        | 710    | 1     | YPU50902    |
| 22         | 8     | 11.3        | 943    | 3     | AF259957    |
| 23         | 8     | 11.3        | 2004   | 6     | AX606817    |
| 24         | 8     | 11.3        | 2590   | 9     | AX025078    |
| 25         | 8     | 11.3        | 7675   | 1     | AF157015    |
| 26         | 8     | 11.3        | 10193  | 1     | AF093787    |
| 27         | 8     | 11.3        | 10786  | 1     | AE013792    |
| 28         | 8     | 11.3        | 12035  | 14    | AF201902    |
| 29         | 8     | 11.3        | 12069  | 6     | AX348317    |
| 30         | 8     | 11.3        | 14530  | 1     | AE007605    |
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| 37         | 8     | 11.3        | 67870  | 2     | AC083787    |
| 38         | 8     | 11.3        | 69520  | 10    | AL669925    |
| 39         | 8     | 11.3        | 74149  | 2     | AC123879_3  |
| 40         | 8     | 11.3        | 88012  | 2     | AC011406    |
| 41         | 8     | 11.3        | 98530  | 2     | AC113088    |
| 42         | 8     | 11.3        | 100296 | 2     | AL590308    |
| 43         | 8     | 11.3        | 101579 | 2     | AC008227    |
| 44         | 8     | 11.3        | 101622 | 2     | AC123648_3  |
| 45         | 8     | 11.3        | 108449 | 9     | AC112650    |

RESULT 1

## ALIGNMENTS

| LOCUS  | AX055438   | 414 bp        | DNA | linear | PAT 13-JAN-2001 |
|--|--|---------------|-----|--------|-----------------|
| DEFINITION   | Sequence 68 from Patent WO0073452.   |               |     |        |                 |
| ACCESSION  | AX055438   |               |     |        |                 |
| VERSION  | AX055438.1   | GI:12228711   |     |        |                 |
| KEYWORDS   |  |               |     |        |                 |
| SOURCE   | Homo sapiens (human)   |               |     |        |                 |
| ORGANISM   | Homo sapiens   |               |     |        |                 |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.   |               |     |        |                 |
| AUTHORS  | 1 Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J., Gunney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L., Tamas, D., Watanabe, C.K. and Wood, W.I. |               |     |        |                 |
| TITLE  | Compositions and methods for the treatment of immune related diseases  |               |     |        |                 |
| JOURNAL  | Patent: WO 0073452-A 68 07-DEC-2000;   |               |     |        |                 |
| FEATURES   | Genentech, Inc. (US)   |               |     |        |                 |
| source   | Location/Qualifiers  |               |     |        |                 |
|  | 1..414   |               |     |        |                 |
|  | /organism="Homo sapiens"   |               |     |        |                 |
|  | /mol_type="genomic DNA"  |               |     |        |                 |
|  | /db_xref="taxon:9606"  |               |     |        |                 |
| BASE COUNT   | 98 a 126 c 92 g 98 t   |               |     |        |                 |
| ORIGIN   |  |               |     |        |                 |
| Alignment Scores:                                      |  |               |     |        |                 |
| Pred. No.:   | 2,33e-69   | Length:       | 414 |        |                 |
| Score:   | 71.00  | Matches:      | 71  |        |                 |
| Percent Similarity:                                    | 100.00%  | Conservative: | 0   |        |                 |
| Best Local Similarity:                                 | 100.00%  | Mismatches:   | 0   |        |                 |
| Query Match:   | 100.00%  | Indels:       | 0   |        |                 |
| DB:  | 6  | Gaps:         | 0   |        |                 |
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| QY   | 1 GUGUGUGUSeThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe   | 20            |     |        |                 |
| DB   | 97 GAGGAGAAAGACCATGAGATTATGCGTACACCGCGGCTTTAAACCCCCGTTT  | 156           |     |        |                 |
| QY   | 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTyrPhe   | 40            |     |        |                 |
| DB   | 157 CTGAACATCGCAAAATTCGATCTCGCTTAAAGCGCTGATGATCTGAACCTGCAAC  | 216           |     |        |                 |
| QY   | 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTyrAspAlaPheProLysLeu  | 60            |     |        |                 |
| DB   | 217 CTCTTGGCTCATATAAAAGAAATCTCTTCTCTCAACTGGGATGCCCTTCTTAAGCTG  | 276           |     |        |                 |
| QY   | 61 LysGlyLeuArgSerAlaThrProAspAlaGln   | 71            |     |        |                 |
| DB   | 277 AAAGACCTGAGGAGCGCAACTCTCATGCGCCAG  | 309           |     |        |                 |
| RESULT 2   |  |               |     |        |                 |
| LOCUS  | AR352517   | 415 bp        | DNA | linear | PAT 20-DEC-2002 |
| DEFINITION   | Sequence 200 from patent US 6478825.   |               |     |        |                 |
| ACCESSION  | AR352517   |               |     |        |                 |
| VERSION  | AR352517.1   | GI:27300425   |     |        |                 |
| KEYWORDS   |  |               |     |        |                 |
| SOURCE   | Unknown.   |               |     |        |                 |
| ORGANISM   | Unknown.   |               |     |        |                 |
| REFERENCE  | Unclassified.  |               |     |        |                 |
| AUTHORS  | 1 (bases 1 to 415)   |               |     |        |                 |
| TITLE  | Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, P.  |               |     |        |                 |
| JOURNAL  | Implant, method of making same and use of the Implant for the  |               |     |        |                 |
| FEATURES   | treatment of bone defects  |               |     |        |                 |
| source   | Patent: US 6478825-A 200 12-NOV-2002;  |               |     |        |                 |
|  | Location/Qualifiers  |               |     |        |                 |
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| BASE COUNT   | 99 a 126 c 92 g 98 t   |               |     |        |                 |
| ORIGIN   |  |               |     |        |                 |

| Alignment Scores:                                      | 2.34e-69   | Length: 415                       |
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| Pred. No.:   | 71.00  | Matches: 71                       |
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| Percent Similarity:                                    | 100.00%  | Mismatch: 0                       |
| Best Local Similarity:                                 | 100.00%  | Indels: 0                         |
| Query Match:   | 100.00%  | Gaps: 0                           |
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| QY   | 1  | 1                                 |
| DB   | 97   | 156                               |
| QY   | 21   | 40                                |
| DB   | 157  | 216                               |
| QY   | 41   | 60                                |
| DB   | 217  | 276                               |
| QY   | 61   | 71                                |
| DB   | 277  | 309                               |
| RESULT 3   |  |                                   |
| LOCUS  | AX077031   | 415 bp DNA linear PAT 22-FEB-2001 |
| DEFINITION   | Sequence 19 from Patent WO0105972.   |                                   |
| ACCESSION  | AX077031   |                                   |
| VERSION  | AX077031.1   | GI:13121661                       |
| KEYWORDS   |  |                                   |
| SOURCE   |  |                                   |
| ORGANISM   | Homo sapiens (human)   |                                   |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  |                                   |
| AUTHORS  | 1 Ashkenazi, A. J., Baker, K. P., Fong, S., Goddard, A., Godowski, P. J., Gunter, A. L., Hillan, K. J., Mark, M. R., Marsters, S. A., Pitti, R. M., Tumas, D., Watanabe, C. K. and Wood, W. I. |                                   |
| TITLE  | Compositions and methods for the treatment of immune related diseases  |                                   |
| JOURNAL  | Patent: WO 0105972-A 19 25-JAN-2001;   |                                   |
| FEATURES   | Genetech, Inc. (US)  |                                   |
| source   | Location/Qualifiers  |                                   |
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| BASE COUNT   | 99 a 126 c 92 g 98 t   |                                   |
| ORIGIN   |  |                                   |
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| Pred. No.:   | 71.00  | Matches: 71                       |
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| Best Local Similarity:                                 | 100.00%  | Indels: 0                         |
| Query Match:   | 100.00%  | Gaps: 0                           |
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| US-10-059-395-142_COPY_29_99 (1-71) x AX077031 (1-415) |  |                                   |
| QY   | 1  | 20                                |
| DB   | 97   | 156                               |
| QY   | 21   | 40                                |
| DB   | 157  | 216                               |
| QY   | 41   | 60                                |

Db 217 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCAACGTGGATGCTTTCTTAAGCTG 276  
Qy 61 LysGlyLeuArgSerAlaThrProhepAlaGln 71  
Db 277 AAAGACTGAGAGCGCACTCTGATGCCAG 309

RESULT 4  
AX358892 415 bp DNA linear PAT 13-FEB-2002  
LOCUS Sequence 145 from Patent WO0193983.  
ACCESSION AX358892  
VERSION AX358892.1 GI:18675347  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
Watanabe, C.K. and Wood, W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0193983-A 145 13-DEC-2001;  
Genentech Inc. (US)  
FEATURES  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2,34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX358892 (1-415)

Qy 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGAGAGAAAGACCATTTGAGATTAATGCGTACACAGCCGAGGCTTTAAACCCCGTTTC 156

Qy 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPheAla 40  
Db 157 CTGAACATCGACAAATTCGATCTCGTTTAAAGCTGATGATGCTTCTGAACGCGACGCC 216

Qy 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrPheAlaPheProLysLeu 60  
Db 217 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCAACGTGGATGCTTTCTTAAGCTG 276

Qy 61 LysGlyLeuArgSerAlaThrProhepAlaGln 71  
Db 277 AAAGACTGAGAGCGCACTCTGATGCCAG 309

RESULT 5  
AX362385 415 bp DNA linear PAT 15-FEB-2002  
LOCUS Sequence 145 from Patent WO0208288.  
ACCESSION AX362385  
VERSION AX362385.1 GI:18694650  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,

Watanabe, C.K. and Wood, W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0208288-A 145 31-JAN-2002;  
Genentech, Inc. (US)  
FEATURES  
source 1. 415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2,34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX362385 (1-415)

Qy 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGAGAGAAAGACCATTTGAGATTAATGCGTACACAGCCGAGGCTTTAAACCCCGTTTC 156

Qy 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPheAla 40  
Db 157 CTGAACATCGACAAATTCGATCTCGTTTAAAGCTGATGATGCTTCTGAACGCGACGCC 216

Qy 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrPheAlaPheProLysLeu 60  
Db 217 CTCTTGAGTCTATCAAAAGAACTTCCTTCTCAACGTGGATGCTTTCTTAAGCTG 276

Qy 61 LysGlyLeuArgSerAlaThrProhepAlaGln 71  
Db 277 AAAGACTGAGAGCGCACTCTGATGCCAG 309

RESULT 6  
AX403313 415 bp DNA linear PAT 14-JUN-2002  
LOCUS Sequence 200 from Patent WO0073454.  
ACCESSION AX403313  
VERSION AX403313.1 GI:21436871  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D.,  
Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,  
Grimaldi, C.J., Gurney, A.L., Kijavich, I., Napier, M.A., Pan, J.,  
Paoni, N.F., Roy, M., Stewart, T.A., Tamas, D., Watanabe, C.K.,  
Williams, P., Wood, W.I. and Zhang, Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0073454-A 200 07-DEC-2000;  
Genentech Inc. (US)  
FEATURES  
source 1. 415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2,34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX403313 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAGAAAGACCACTTGAGATTATGCTGACGACCCGAGGCTTTAAACCCCGTTC 156

QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnThrPheAla 40  
DB 157 CTGAGACATGACCAATTCGATCGCTTTAAGGCTGATGATGCTTCAACTGACGCGC 216

QY 41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnThrPheAlaPheProIysLeu 60  
DB 217 CTCTTGAGCTATCAAAAGAACTTCCTTCTCTCAAGTGAGATGCTTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCACTCCTGATGCCAG 309

RESULT 7  
AX454546 415 bp DNA linear PAT 06-JUL-2002  
LOCUS Sequence 131 from Patent WO0208284.  
ACCESSION AX454546  
VERSION AX454546.1 GI:21713897  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsers, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.  
Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis  
Patent: WO 0208284-A 131 31-JAN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsers, Scott A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)

FEATURES  
Source Location/Qualifiers  
1. 415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t

ORIGIN

Alignment Scores: 2,34e-69 Length: 415  
Pred. No.: 71.00 Matches: 71  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX454546 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAGAAAGACCACTTGAGATTATGCTGACGACCCGAGGCTTTAAACCCCGTTC 156

QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnThrPheAla 40  
DB 157 CTGAGACATGACCAATTCGATCGCTTTAAGGCTGATGATGCTTCTTAAGCTGACGCGC 216

QY 41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnThrPheAlaPheProIysLeu 60  
DB 217 CTCTTGAGCTATCAAAAGAACTTCCTTCTCTCAAGTGAGATGCTTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCAACTCCTGATGCCAG 309

RESULT 8  
AX491024 415 bp DNA linear PAT 16-AUG-2002  
LOCUS Sequence 131 from Patent WO0200690.  
ACCESSION AX491024  
VERSION AX491024.1 GI:22323849  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsers, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.  
Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis  
Patent: WO 0200690-A 131 03-JAN-2002;  
Genentech, Inc. (US)

FEATURES  
Source Location/Qualifiers  
1. 415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 99 a 126 c 92 g 98 t

ORIGIN

Alignment Scores: 2,34e-69 Length: 415  
Pred. No.: 71.00 Matches: 71  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX491024 (1-415)

QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAGAAAGACCACTTGAGATTATGCTGACGACCCGAGGCTTTAAACCCCGTTC 156

QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnThrPheAla 40  
DB 157 CTGAGACATGACCAATTCGATCGCTTTAAGGCTGATGATGCTTCTTAAGCTGACGCGC 216

QY 41 LeuPheGluSerIleIysArgIysLeuProPheLeuAsnThrPheAlaPheProIysLeu 60  
DB 217 CTCTTGAGCTATCAAAAGAACTTCCTTCTCTCAAGTGAGATGCTTTCTTAAGCTG 276

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGAGCGCAACTCCTGATGCCAG 309

RESULT 9  
AX574494 415 bp DNA linear PAT 07-JAN-2003  
LOCUS Sequence 21 from Patent WO0224888.  
ACCESSION AX574494  
VERSION AX574494.1 GI:27551800  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 Baker, K.P., Eaton, D.L., Pilyavoff, E., Goddard, A., Grimaldi, J.C.,  
Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K., Wood, W.I.,  
Zhang, Z., and Fong, S.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the name  
JOURNAL Patent: WO 0224888-A 21 28-MAR-2002;  
GENENTECH, INC. (US)  
FEATURES Location/Qualifiers  
source 1..415  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 99 a 126 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2,34e-69 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AK574494 (1-415)

QY 1 GIUGIUGIUSERTHRIIEGLUANTYRALASERARGPROGLUALAPHENANTHProphe 20  
DB 97 GAGGAAGAAAGACCATTTAGATTATGCGTCACGACCCGAGCCCTTTAAACCCCGTTT 156  
QY 21 LeuAnniLeaApLyLeuArSerAlaPheLySaLaAaSpGluPheLeuAnThrPhisAla 40  
DB 157 CTGAACATCGACAATTCGATCGCTTTAAAGCGTGAAGTCTCTGAACCTGGACCGCC 216  
QY 41 LeuphegiuSerIleLySaRgLyLeuProPheLeuAnThrPaSpAlaPheProLySleu 60  
DB 217 CTTTGTAGTCTATCAAAAGAACTCTCTTCTCAATGCGATGCGCTTCTTAAGCTG 276  
QY 61 LygGlyLeuArSerAlaThrProApAlaGln 71  
DB 277 AAAGACTGAGGAGCGCACTCTGATGCCAG 309

RESULT 10  
AX080815  
LOCUS AX080815 432 bp DNA linear PAT 27-FEB-2001  
DEFINITION Sequence 61 from Patent WO0109327.  
ACCESSION AX080815  
VERSION AX080815.1 GI:13169784  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 artificial sequences.  
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Kilavain, I.J., Lafleur, M., Mark, M.R., Martens, S.A., Pitti, R.M.,  
Watanabe, C.K., and Wood, W.I.  
TITLE Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
JOURNAL Patent: WO 0109327-A 61 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..432  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Virtual DNA fragment used in the isolation of  
DNA57694." BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN

Alignment Scores:  
Pred. No.: 2,43e-69 Length: 432  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080815 (1-432)

QY 1 GIUGIUGIUSERTHRIIEGLUANTYRALASERARGPROGLUALAPHENANTHProphe 20  
DB 96 GAGGAAGAAAGACCATTTAGATTATGCGTCACGACCCGAGCCCTTTAAACCCCGTTT 155  
QY 21 LeuAnniLeaApLyLeuArSerAlaPheLySaLaAaSpGluPheLeuAnThrPhisAla 40  
DB 156 CTGAACATCGACAATTCGATCGCTTTAAAGCGTGAAGTCTCTTAAGCTGAGCAAGCC 215  
QY 41 LeuphegiuSerIleLySaRgLyLeuProPheLeuAnThrPaSpAlaPheProLySleu 60  
DB 216 CTTTGTAGTCTATCAAAAGAACTCTCTTCTCAATGCGATGCGCTTCTTAAGCTG 275  
QY 61 LygGlyLeuArSerAlaThrProApAlaGln 71  
DB 276 AAAGACTGAGGAGCGCACTCTGATGCCCA 308

RESULT 11  
AX080818  
LOCUS AX080818 432 bp DNA linear PAT 27-FEB-2001  
DEFINITION Sequence 64 from Patent WO0109327.  
ACCESSION AX080818  
VERSION AX080818.1 GI:13169787  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Kilavain, I.J., Lafleur, M., Mark, M.R., Martens, S.A., Pitti, R.M.,  
Watanabe, C.K., and Wood, W.I.  
TITLE Method of preventing the injury or death of retinal cells and  
treating ocular diseases  
JOURNAL Patent: WO 0109327-A 64 08-FEB-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..432  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN

Alignment Scores:  
Pred. No.: 2,43e-69 Length: 432  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080818 (1-432)

QY 1 GIUGIUGIUSERTHRIIEGLUANTYRALASERARGPROGLUALAPHENANTHProphe 20  
DB 96 GAGGAAGAAAGACCATTTAGATTATGCGTCACGACCCGAGCCCTTTAAACCCCGTTT 155  
QY 21 LeuAnniLeaApLyLeuArSerAlaPheLySaLaAaSpGluPheLeuAnThrPhisAla 40  
DB 156 CTGAACATCGACAATTCGATCGCTTTAAAGCGTGAAGTCTCTTAAGCTGAGCAAGCC 215  
QY 41 LeuphegiuSerIleLySaRgLyLeuProPheLeuAnThrPaSpAlaPheProLySleu 60  
DB 216 CTTTGTAGTCTATCAAAAGAACTCTCTTCTCAATGCGATGCGCTTCTTAAGCTG 275  
QY 61 LygGlyLeuArSerAlaThrProApAlaGln 71

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080815 (1-432)

QY 1 GIUGIUGIUSERTHRIIEGLUANTYRALASERARGPROGLUALAPHENANTHProphe 20  
DB 96 GAGGAAGAAAGACCATTTAGATTATGCGTCACGACCCGAGCCCTTTAAACCCCGTTT 155  
QY 21 LeuAnniLeaApLyLeuArSerAlaPheLySaLaAaSpGluPheLeuAnThrPhisAla 40  
DB 156 CTGAACATCGACAATTCGATCGCTTTAAAGCGTGAAGTCTCTTAAGCTGAGCAAGCC 215  
QY 41 LeuphegiuSerIleLySaRgLyLeuProPheLeuAnThrPaSpAlaPheProLySleu 60  
DB 216 CTTTGTAGTCTATCAAAAGAACTCTCTTCTCAATGCGATGCGCTTCTTAAGCTG 275  
QY 61 LygGlyLeuArSerAlaThrProApAlaGln 71

Db 276 AAGGACTGAGAGCGGCACTCCGATGCCCA 308

RESULT 12

LOCUS BD082389 456 bp DNA linear PAT 27-AUG-2002

DEFINITION BD082389 87 human secreted proteins.

ACCESSION BD082389.1 GI:22627999

VERSION JP 2001522239-A/31.

KEYWORDS Mactadenovirus

SOURCE Mactadenovirus

ORGANISM Viruses; dsDNA viruses, no RNA stage; Adenoviridae.

REFERENCE 1 (bases 1 to 456)

AUTHORS Young, P., Greene, J.M., Ferrie, A.M., Ruben, S.M., Rosen, C.A., Duan, R.D., Hu, J.S., Florence, K.A., Olsen, H.S., Ebner, R., Brewer, L.A., Moore, P.A., Shi, Y., Lafleur, D.W. and Ni, J.

TITLE 87 human secreted proteins

JOURNAL Patent: JP 2001522239-A 31 13-NOV-2001;

HUMAN GENOME SCIENCES INC SECRETARY OF THE DEPARTMENT OF HEALTH

COMMENT PN JP 2001522239-A/31

PD 13-NOV-2001

PR 19-MAR-1998 JP 1998542119

PR 21-MAR-1997 US 60/041281, 21-MAR-1997 US 60/041276 PR

21-MAR-1997 US 60/042344, 21-MAR-1997 US 60/041277 PR

30-MAY-1997 US 60/048355, 30-MAY-1997 US 60/048066 PR

30-MAY-1997 US 60/048351, 30-MAY-1997 US 60/048154 PR

30-MAY-1997 US 60/048160, 30-MAY-1997 US 60/048069 PR

30-MAY-1997 US 60/048131, 30-MAY-1997 US 60/048186 PR

30-MAY-1997 US 60/048095, 30-MAY-1997 US 60/048187 PR

30-MAY-1997 US 60/048352, 30-MAY-1997 US 60/050937 PR

30-MAY-1997 US 60/048351, 30-MAY-1997 US 60/048135 PR

30-MAY-1997 US 60/048188, 30-MAY-1997 US 60/048094 PR

30-MAY-1997 US 60/048350, 05-AUG-1997 US 60/054804 PR

19-AUG-1997 US 60/056370, 02-OCT-1997 US 60/060862 PI PAUL

YOUNG, JOHN M GREENE, ANN M FERRIE, STEVEN M RUBEN, CRAIG A PI

ROSEN, ROXANNE D DUAN, JING SHAN HU, KIMBERLY A FLORENCE, HENRIK S

OLSEN, PI REINHARD EBNER, LAURIE A BREWER, PAUL A MOORE, YANGU SHI, DAVID W

PI LAFLUR,

PI JIAN NI

PC C07K14/00

CC Strandedness: Double;

CC Topology: Linear;

PH Key Location/Qualifiers.

FEATURES

source 1..456

Location/Qualifiers

1..456

/organism="Mactadenovirus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10503"

BASE COUNT 117 a 136 c 104 g 98 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 2,556-69 Length: 456

Score: 71.00 Matches: 71

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x BD082389 (1-456)

QY 1 GIUGUGUJuserThrllegluserTrrAlaserAsgProgluAlaPheasnthrProPhe 20

DB 105 GAGGAGAAAGCAACATTGAGATATGCGTCACGACCGGAGCCCTTTAAACCCCGCTTC 164

QY 21 LeuAenllaAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAenThrPheAla 40

DB 165 CTGAACATCGACAAATTGGCATCTGCTTTAAGCGCTGATGATTCCTGTAACCTGGACGCC 224

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAenThrPheAlaPheProLysLeu 60

DB 225 CTCTTGAGCTCTATCAAAAGAAATCTTCCTTCTCACTGGATGCGATTCCTTAAGCTG 284

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71

DB 285 AAGGACTGAGAGCGGCACTCCGATGCCAG 317

RESULT 13

LOCUS AX080817 490 bp DNA linear PAT 27-FEB-2001

DEFINITION AX080817 Sequence 63 from Patent WO0109327.

ACCESSION AX080817

VERSION AX080817.1 GI:13169786

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L., Kijavitt, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Picetti, R.M., Watanabe, C.K. and Wood, W.I.

TITLE Method of preventing the injury or death of retinal cells and treating ocular diseases

JOURNAL Patent: WO 0109327-A 63 08-FEB-2001;

Genentech, Inc. (US)

FEATURES

source 1..490

Location/Qualifiers

1..490

/organism="synthetic construct"

/mol\_type="genomic DNA"

/db\_xref="taxon:32630"

/note="Virtual DNA fragment used in the isolation of DN57664."

BASE COUNT 118 a 149 c 116 g 107 t

ORIGIN

Alignment Scores:

Pred. No.: 2,726-69 Length: 490

Score: 71.00 Matches: 71

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x AX080817 (1-490)

QY 1 GIUGUGUJuserThrllegluserTrrAlaserAsgProgluAlaPheasnthrProPhe 20

DB 164 GAGGAGAAAGCAACATTGAGATATGCGTCACGACCGGAGCCCTTTAAACCCCGCTTC 223

QY 21 LeuAenllaAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAenThrPheAla 40

DB 224 CTGAACATCGACAAATTGGCATCTGCTTTAAGCGCTGATGATTCCTGTAACCTGGACGCC 283

QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAenThrPheAlaPheProLysLeu 60

DB 284 CTCTTGAGCTCTATCAAAAGAAATCTTCCTTCTCACTGGATGCGATTCCTTAAGCTG 343

QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71

DB 344 AAGGACTGAGAGCGGCACTCCGATGCCAG 376

RESULT 14

LOCUS AX080816 435 bp DNA linear PAT 27-FEB-2001

DEFINITION AX080816 Sequence 62 from Patent WO0109327.

ACCESSION AX080816

VERSION AX080816.1 GI:13169785

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.



REFERENCE 1  
 AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.L.,  
 Kljavin, I.J., Lafleur, M., Mark, M.R., Masters, S.A., Pitti, R.M.,  
 Maranabe, C.K. and Wood, W.I.  
 TITLE Method of preventing the injury or death of retinal cells and  
 treating ocular diseases  
 JOURNAL Patent: WO 0109327-A 62 08-FEB-2001;  
 Genentech, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..435  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="Virtual DNA fragment used in the isolation fo  
 DNA57694."
   
 BASE COUNT 108 a 130 c 96 g 101 t  
 ORIGIN
   
 Alignment Scores:  
 Pred. No.: 4.92e-56 Length: 435  
 Score: 59.00 Matches: 59  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 83.10% Indels: 0  
 DB: Gaps: 0
   
 US-10-059-395-142\_COPY\_29\_99 (1-71) x AX041085 (1-435)
   
 QY 13 ProGluAlaPheAsnThrProPheLeuAenIleAspLysLeuArgSerAlaPheLysAla 32  
 DB 136 CCGGAGGCGCTTAAACACCCCGTTCCTGAACATCGACAATTCGATCTGCGTTAAGGCT 195  
 QY 33 AspGluPheLeuAsnThrPheIleAsnLeuPheGluSerIleLysArgLysLeuProPheLeu 52  
 DB 196 GATGAGTTCCTGAACCTGACGACGCCCTCTTGAAGTCTATCAAAAGAACTTCCTTCCCTC 255  
 QY 53 AsnTPAspAlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 71  
 DB 256 AACTGGATGCTTCTTCTTCTGAGTGAAGGACTGAGGAGCGCACTCTGATGCCCG 312
   
 RESULT 15  
 AX041085/c 278 bp DNA linear PAT 23-NOV-2000  
 LOCUS Sequence 3 from Patent WO0065053.  
 DEFINITION AX041085  
 ACCESSION AX041085  
 VERSION AX041085.1 GI:11340655  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
   
 REFERENCE 1  
 AUTHORS Wang, T. and Dillon, D.C.  
 TITLE Compositions and methods for therapy and diagnosis of head/neck and  
 lung squamous cell carcinoma  
 JOURNAL Patent: WO 0065053-A 3 02-NOV-2000;  
 CORIXA CORPORATION (US)  
 FEATURES Location/Qualifiers  
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 /mol\_type="genomic DNA"  
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 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
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US-10-059-395-142\_COPY\_29\_99 (1-71) x AX041085 (1-278)
   
 QY 16 PheAsnThrProPheLeuAenIleAspLysLeuArgSerAlaPheLysAlaAspGluPhe 35  
 DB 269 TTTAAACACCCCGTTCCTGAACATCGACAATTCGATCTGCGTTAAGGCTGATGATTTC 210  
 QY 36 LeuAsnTPHISAlaLeuPheGluSerIleLysArgLysLeuProPheLeuAsnThrPAsp 55  
 DB 209 CTGAACCTGGACGCGCCCTTTTGAAGTCTATCAAAAGAACTTCCTTCTCACTGGGAT 150  
 QY 56 AlaPheProLysLeuLysGlyLeuArgSerAlaThrProAspAlaGln 71  
 DB 149 GCCTTCTTAAGCTGAAGGACTGAGGAGCGCAACTCTGATGCCAG 102
   
 Search completed: November 28, 2003, 11:45:56  
 Job time : 2644 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 09:42:35 / Search time 217 Seconds

(without alignments)  
883.226 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 71

Sequence: 1 EESTIENYASRPSAFTNP.....LNMDFPKLGLRGAFTPDQ 71

Scoring table:

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Xgapop 60.0 , Xgapext 60.0

Ygapop 60.0 , Ygapext 60.0

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5103067

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-O=/cgn2.1/USPTO-epool/US10059395/runat\_25112003.140843.7657/app\_query.fasta\_1.263

-DB=N Geneseq 19Jun03 -QFWT=fastcap -SUFFIX=col1.rng -MINMATCH=0.1 -LOOPCL=0

-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=col1go -TRANS=human40.cdi

-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL

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25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2004.DAT:\*

and is derived by analysis of the total score distribution.

## SUMMARIES

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| 1          | 71    | 100.0       | 414    | 22 AAC91475 | Human PRO826 cDNA. |
| 2          | 71    | 100.0       | 414    | 24 ABK28600 | Human DNA57694-134 |
| 3          | 71    | 100.0       | 415    | 21 AAZ65018 | Membrane-bound pro |
| 4          | 71    | 100.0       | 415    | 22 AAF30059 | Human cDNA encodin |
| 5          | 71    | 100.0       | 415    | 22 AAF44164 | Human PRO826 (UNQ4 |
| 6          | 71    | 100.0       | 415    | 22 AAC97491 | Human angiogenesis |
| 7          | 71    | 100.0       | 415    | 24 ABL95626 | Human angiogenesis |
| 8          | 71    | 100.0       | 415    | 24 ABK65971 | cDNA encoding huma |
| 9          | 71    | 100.0       | 415    | 24 ABL88137 | Human PRO826 cDNA  |
| 10         | 71    | 100.0       | 415    | 24 ABK33608 | cDNA encoding huma |
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| 14         | 71    | 100.0       | 415    | 25 ABK90232 | Human secreted/tr  |
| 15         | 71    | 100.0       | 415    | 25 ABK79843 | Human PRO polynuci |
| 16         | 71    | 100.0       | 415    | 25 ABK79439 | Human secreted/tr  |
| 17         | 71    | 100.0       | 415    | 25 ABK64078 | cDNA encoding huma |
| 18         | 71    | 100.0       | 415    | 25 ABK17042 | Human PRO polynuci |
| 19         | 71    | 100.0       | 428    | 24 ABZ11803 | Human polynucleoti |
| 20         | 71    | 100.0       | 456    | 20 AAX00632 | Human secreted pro |
| 21         | 71    | 100.0       | 518    | 22 ABA09519 | Human secreted pro |
| 22         | 56    | 78.9        | 278    | 21 AAC68806 | Human head/neck tu |
| 23         | 43    | 60.6        | 386    | 24 ABZ11804 | Human polynucleoti |
| 24         | 28    | 39.4        | 305    | 24 ABZ11886 | Human polynucleoti |
| 25         | 8     | 11.3        | 2001   | 24 ABK67971 | Streptococcus poly |
| 26         | 8     | 11.3        | 2298   | 21 AAC59576 | Human secreted pro |
| 27         | 8     | 11.3        | 12069  | 24 ABK39931 | Human chemically p |
| 28         | 8     | 11.3        | 12212  | 24 ABK12920 | Human SLC25A2 (sol |
| 29         | 8     | 11.3        | 12212  | 24 ABK12975 | Human SLC25A2 (sol |
| 30         | 8     | 11.3        | 33795  | 24 ABK95666 | Gene #2184 used to |
| 31         | 8     | 11.3        | 215561 | 24 ABK71557 | Streptococcus poly |
| 32         | 7     | 9.9         | 65     | 24 ABK11537 | Rat spliced transc |
| 33         | 7     | 9.9         | 198    | 21 AAC24586 | Human secreted pro |
| 34         | 7     | 9.9         | 231    | 20 AAH64601 | Human single nucle |
| 35         | 7     | 9.9         | 231    | 20 AAH64602 | Human single nucle |
| 36         | 7     | 9.9         | 238    | 21 AAH45447 | Human secreted exp |
| 37         | 7     | 9.9         | 251    | 21 AAC07741 | Human secreted pro |
| 38         | 7     | 9.9         | 256    | 25 ABK31899 | Human GDP-mannose  |
| 39         | 7     | 9.9         | 283    | 21 AAC94607 | Cat flea hindgut a |
| 40         | 7     | 9.9         | 294    | 20 AAZ31185 | Human gene express |
| 41         | 7     | 9.9         | 300    | 20 AAZ31312 | Human cancer cell  |
| 42         | 7     | 9.9         | 300    | 21 AAJ00085 | Human colon cancer |
| 43         | 7     | 9.9         | 368    | 19 AAH64404 | cDNA clone AA37708 |
| 44         | 7     | 9.9         | 419    | 21 AAC31437 | Human secreted pro |
| 45         | 7     | 9.9         | 438    | 24 ABK29813 | Colon adenocarcino |

## ALIGNMENTS

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AAC91475 AAC91475 standard; cDNA; 414 BP.

AC AAC91475;

XX 21-MAR-2001 (first entry)

DE Human PRO826 cDNA.

XX Human; PRO: antiinflammatory; dermatological; antithyroid;

KW antirheumatic; cardiac; antianemic; immunosuppressive; antithyroid;

KW antidiabetic; neurotrophic; hepatocytic; virucide;

KW antiallergic; antiautomatic; immune related disorder;

KW hepatobiliary disease; autoimmune disease; allergy; ss.

XX Homo sapiens.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

XX MO200073452-A2.  
 PN 07-DEC-2000.  
 PD 02-JUN-2000; 2000WO-US15264.  
 XX 02-JUN-1999; 99WO-US12252.  
 PR 20-JUL-1999; 99US-0144732.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 XX (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AJ,  
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DU, Tumas D, Watanabe CK,  
 PI Wood WJ;  
 XX MPI: 2001-025253/03.  
 DR P-PEDB; AAB50916.  
 XX Thiry three nucleic acids encoding PRO polypeptides which are useful  
 PT in the diagnosis and treatment of immune related disorders, e.g.  
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 PT thyroiditis and diabetes mellitus -  
 XX Claim 48; Fig 29; 218pp; English.  
 PS The present sequence is one of thirty three nucleic acids encoding PRO  
 XX polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and  
 CC antagonists are useful for treating and diagnosing immune related  
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
 CC (such as infectious, autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
 CC food hypersensitivity and urticaria), immunological diseases of the  
 CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
 CC and hypersensitivity pneumonitis), transplantation associated diseases  
 CC including graft rejection and graft-versus-host diseases.  
 XX Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;  
 SQ

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 Pred. No.: 3,23e-66 Length: 414  
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 QY 21 LeuAsnIleAspIleuArgSerAlaPheIleAlaAspIleuAsnThrPheAla 40  
 Db 157 CTGAACATCGACCAATTCGATCTGCTTTAAGGCTATGATGCTTGAACAGGACGCC 216  
 QY 41 LeuPheGluSerIleuArgIleuProPheLeuAsnThrPheAlaPheProIleu 60  
 Db 217 CTCCTTAGCTATCAAAAGAAACTTCCTTCTCACTGGAGATGCTTTCTTAAGCTG 276  
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 Db 277 AAAGACTGAGAGAGCGCACTCTGATGCCAG 309  
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 XX AC  
 AC ABK28600;  
 XX DT 09-APR-2002 (first entry)  
 XX DE Human DNMS7694-1341 encoding PRO826.  
 XX DE Human; ss; gene; PRO; antiinflammatory; ophthalmological; vasotropic;  
 KW retinal cell injury; ocular disease; retinitis pigmentosa;  
 KW macular degeneration; retinal detachment; retinal tear; retinopathy;  
 KW retinal degenerative disease; macular hole; degenerative myopia;  
 KW acute retinal necrosis syndrome; traumatic choriorretinopathy;  
 KW Puttcher's retinopathy; oedema; ischaemic condition;  
 KW retinal vision occlusion; collagen vascular disease;  
 KW thrombocytopenic purpura; uveitis; retinal vasculitis; Pales disease;  
 KW systemic lupus erythematosus; environmental trauma.  
 XX OS Homo sapiens.  
 XX PN WO200109327-A2.  
 XX PD 08-FEB-2001.  
 XX 28-JUL-2000; 2000WO-US20710.  
 PF 28-JUL-1999; 99US-146222P.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US05064.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 XX PA (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;  
PI Kljavin ID, Lafleur M, Mark MR, Marsters SA, Pitti RM;  
PI Watanabe CK, Wood WI;  
XX WPI: 2002-130120/17.  
DR P-PSDB; AAU81964.  
XX  
XX Promoting survival of retinal cells, or delaying or preventing retinal  
PT cell injury or death, by contacting retinal cells with PRO175, 220,  
PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132  
XX polypeptide -  
XX  
XX Claim 33; Fig 24; 152pp; English.  
XX  
XX The invention relates to promoting the survival of retinal cells, or  
CC delaying or preventing retinal cell injury or death, by contacting the  
CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
CC PRO243, PRO306, PRO346, PRO322, PRO536, PRO840, PRO828, PRO826,  
CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
CC encoding the PRO proteins, a vector comprising the nucleic acid, a host  
CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
CC useful for promoting survival of retinal cells (retinal neurons such as  
CC retinal ganglion cells, displaced retinal ganglion cells, amacrine  
CC cells, displaced amacrine cells, horizontal neurons or bipolar neurons,  
CC rod photoreceptors, or supportive cells such as Muller cells or pigment  
CC epithelial cells), or delaying or preventing retinal cell injury or  
CC death caused by ocular disease (which is or is associated with  
CC retinitis pigmentosa, macular degeneration, retinal detachment, retinal  
CC tear, retinopathy, retinal degenerative disease, macular hole,  
CC degenerative myopia, acute retinal necrosis syndrome, traumatic  
CC chorioretinopathy or contusion), Purtscher's retinopathy, oedema, an  
CC ischaemic condition, central or branch retinal vision occlusion,  
CC collagen vascular disease, thrombocytopenic purpura, uveitis, retinal  
CC vasculitis, occlusion associated with Bales disease or systemic lupus  
CC erythematosus), retinal injury or environmental trauma. The retinal  
CC cell injury or death is delayed or prevented by substantially not  
CC causing angiogenesis or mitogenesis. The present sequence is a cDNA  
CC encoding a PRO protein.  
XX  
XX Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;  
SQ  
XX  
XX Alignment Scores:  
Pred. No.: 3,236-66 Length: 414  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x ABK28600 (1-414)  
QY 1 GUGUGUGUSERTHILGUGUANTYRALASERATGPROGLAALPheAsnThrProPhe 20  
Db 97 GAGGAAGAAAGACCATTCGAGATTATGCTCACACCCGAGGCTTTAAACCCCGTTTC 156  
QY 21 LeuAsnIleAspIleLeuArgSerAlaPheIysAlaAspGluPheLeuAsnThrPheAla 40  
Db 157 CTGAACATCGACAAATGCGATCTGCGTTAAGGCTGAGATTCCTTAAGACGACGCC 216  
QY 41 LeuphegiuserIleIysArgIysLeuProPheLeuAsnThrPheAlaPheProIysIleu 60  
Db 217 CTCTTGAGTCTATCAAAAAGAACTTCCTTCCCACTGGAGAGCCCTTCTTAAGCTG 276  
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Db 277 AAAGGACTGAGAGGCAACTCTGATGCCAG 309  
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ID AAZ65018 standard; cDNA; 415 BP.  
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AC AAZ65018;

XX 05-APR-2000 (first entry)  
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XX Membrane-bound protein PRO826 encoding cDNA.  
XX  
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
XX pharmacological; receptor immunoadhesin; gene mapping; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO963088-A2.  
XX  
XX 09-DEC-1999.  
XX  
XX 02-JUN-1999;  
XX  
XX 99WO-US12252.  
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XX 02-JUN-1998; 98US-0087607.  
XX 02-JUN-1998; 98US-0087609.  
XX 02-JUN-1998; 98US-0087759.  
XX 03-JUN-1998; 98US-0087827.  
XX 04-JUN-1998; 98US-0088021.  
XX 04-JUN-1998; 98US-0088025.  
XX 04-JUN-1998; 98US-0088028.  
XX 04-JUN-1998; 98US-0088029.  
XX 04-JUN-1998; 98US-0088030.  
XX 04-JUN-1998; 98US-0088033.  
XX 04-JUN-1998; 98US-0088326.  
XX 05-JUN-1998; 98US-0088167.  
XX 05-JUN-1998; 98US-0088202.  
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XX 09-JUN-1998; 98US-0088655.  
XX 10-JUN-1998; 98US-0088722.  
XX 10-JUN-1998; 98US-0088730.  
XX 10-JUN-1998; 98US-0088734.  
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XX 10-JUN-1998; 98US-0088825.  
XX 10-JUN-1998; 98US-0088826.  
XX 11-JUN-1998; 98US-0088856.  
XX 11-JUN-1998; 98US-0088861.  
XX 11-JUN-1998; 98US-0088863.  
XX 11-JUN-1998; 98US-0088876.  
XX 12-JUN-1998; 98US-0089090.  
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XX 16-JUN-1998; 98US-0089440.  
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XX 17-JUN-1998; 98US-0089532.  
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XX 17-JUN-1998; 98US-0089600.  
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XX 18-JUN-1998; 98US-0089801.  
XX 18-JUN-1998; 98US-0089907.  
XX 18-JUN-1998; 98US-0089908.  
XX 19-JUN-1998; 98US-0089947.  
XX 19-JUN-1998; 98US-0089948.  
XX 19-JUN-1998; 98US-0089952.  
XX 22-JUN-1998; 98US-0090246.  
XX 22-JUN-1998; 98US-0090252.  
XX 22-JUN-1998; 98US-0090254.  
XX 23-JUN-1998; 98US-0090349.  
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XX 24-JUN-1998; 98US-0090431.  
XX 24-JUN-1998; 98US-0090435.

PR 24-JUN-1998; 98US-0090444.  
 PR 24-JUN-1998; 98US-0090445.  
 PR 24-JUN-1998; 98US-0090461.  
 PR 24-JUN-1998; 98US-0090472.  
 PR 24-JUN-1998; 98US-0090535.  
 PR 24-JUN-1998; 98US-0090538.  
 PR 24-JUN-1998; 98US-0090540.  
 PR 24-JUN-1998; 98US-0090557.  
 PR 25-JUN-1998; 98US-0090676.  
 PR 25-JUN-1998; 98US-0090678.  
 PR 25-JUN-1998; 98US-0090688.  
 PR 25-JUN-1998; 98US-0090690.  
 PR 25-JUN-1998; 98US-0090691.  
 PR 25-JUN-1998; 98US-0090694.  
 PR 25-JUN-1998; 98US-0090695.  
 PR 25-JUN-1998; 98US-0090696.  
 PR 26-JUN-1998; 98US-0090862.  
 PR 26-JUN-1998; 98US-0090863.  
 PR 01-JUL-1998; 98US-0091358.  
 PR 01-JUL-1998; 98US-0091360.  
 PR 02-JUL-1998; 98US-0091544.  
 PR 02-JUL-1998; 98US-0091478.  
 PR 02-JUL-1998; 98US-0091486.  
 PR 02-JUL-1998; 98US-0091519.  
 PR 02-JUL-1998; 98US-0091626.  
 PR 02-JUL-1998; 98US-0091628.  
 PR 02-JUL-1998; 98US-0091633.  
 PR 02-JUL-1998; 98US-0091646.  
 PR 02-JUL-1998; 98US-0091673.  
 PR 07-JUL-1998; 98US-0091978.  
 PR 07-JUL-1998; 98US-0091982.  
 PR 09-JUL-1998; 98US-0092182.  
 PR 10-JUL-1998; 98US-0092472.  
 PR 20-JUL-1998; 98US-0093339.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 04-AUG-1998; 98US-0095282.  
 PR 04-AUG-1998; 98US-0095285.  
 PR 04-AUG-1998; 98US-0095301.  
 PR 04-AUG-1998; 98US-0095302.  
 PR 04-AUG-1998; 98US-0095318.  
 PR 04-AUG-1998; 98US-0095321.  
 PR 04-AUG-1998; 98US-0095325.  
 PR 10-AUG-1998; 98US-0095916.  
 PR 10-AUG-1998; 98US-0095929.  
 PR 10-AUG-1998; 98US-0096012.  
 PR 11-AUG-1998; 98US-0096143.  
 PR 11-AUG-1998; 98US-0096146.  
 PR 12-AUG-1998; 98US-0096328.  
 PR 17-AUG-1998; 98US-0096757.  
 PR 17-AUG-1998; 98US-0096766.  
 PR 17-AUG-1998; 98US-0096768.  
 PR 17-AUG-1998; 98US-0096773.  
 PR 17-AUG-1998; 98US-0096791.  
 PR 17-AUG-1998; 98US-0096867.  
 PR 17-AUG-1998; 98US-0096891.  
 PR 17-AUG-1998; 98US-0096894.  
 PR 17-AUG-1998; 98US-0096895.  
 PR 17-AUG-1998; 98US-0096897.  
 PR 18-AUG-1998; 98US-0096949.  
 PR 18-AUG-1998; 98US-0096950.  
 PR 18-AUG-1998; 98US-0096959.  
 PR 18-AUG-1998; 98US-0096960.  
 PR 18-AUG-1998; 98US-0097141.  
 PR 19-AUG-1998; 98US-0097141.  
 PR 20-AUG-1998; 98US-0097218.  
 PR 24-AUG-1998; 98US-0097661.  
 PR 26-AUG-1998; 98US-0097951.  
 PR 26-AUG-1998; 98US-0097952.  
 PR 26-AUG-1998; 98US-0097954.  
 PR 26-AUG-1998; 98US-0097955.  
 PR 26-AUG-1998; 98US-0097971.  
 PR 26-AUG-1998; 98US-0097974.  
 PR 26-AUG-1998; 98US-0097976.

PR 26-AUG-1998; 98US-0097979.  
 PR 26-AUG-1998; 98US-0097986.  
 PR 26-AUG-1998; 98US-0098014.  
 PR 31-AUG-1998; 98US-0098525.  
 PR 16-SEP-1998; 98US-0100634.  
 PR 12-JAN-1999; 98US-0115565.  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 PI Wood WI, Yuan J;  
 DR WPI, 2000-072883/06.  
 DR P-PSDB; AAY66681.  
 PT Membrane-bound proteins and related nucleotide sequences -  
 PS Claim 2, Fig 128; 822pp; English.  
 XX  
 CC The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, TIE  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences and in  
 CC will also be useful for the preparation of PRO polypeptides, especially  
 CC by recombinant techniques.  
 XX  
 SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3.24e-66 Length: 415  
 Score: 71.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0  
 US-10-059-395-142\_COPY\_29\_99 (1-71) x AAZ65018 (1-415)  
 QY 1 GIUGIUGIUSERTHRILLEGIAENTYRALASERARGPROGLUHLAPHEAENTRPROPH 20  
 DB 97 GAGGAGAGAGACCCATTGAGATTATGCTACGACCGAGGCCCTTAAACACCCGCTTC 156  
 QY 21 LEUASNILLEASPIYLSLEUARGSERALAPHELALASPGIUDPHELEUANTTPHIALA 40  
 DB 157 CTGAACATCGACAATGCGATCGCTTAAAGCTGATGATGTTCTGAACTGCGACGCC 216  
 QY 41 LEUPHEGLUSERLLEYSARGVLSLEUPROPHLEUASRTTPASPLAPHEPROLYLSLEU 60  
 DB 217 CTCCTTGAGTCATACAAAGAGAACTTCCTTCTCACTGAGGATGCTTTCCTTAAGCTG 276  
 QY 61 IYSGIYLSLEUARGSERALATNRPROASPLAAGLN 71  
 DB 277 AAAGGACTGAGAGCGCACTCTGATGCCAG 309  
 RESULT 4  
 AAF30059  
 ID AAF30059 standard; cDNA; 415 BP.  
 XX  
 AC AAF30059;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Human cDNA encoding PRO826.  
 XX  
 KW PRO826; UNQ467; human; immune disease; autoimmune disease;

KW anti-rheumatic; antiarthritic; anti-inflammatory; antianaemic;  
 KW immunosuppressive; antichyroid; antidiabetic; neuroprotective;  
 KW hepatocarcinoma; antitumor; dermatological; antiproliferative;  
 KW antiaesthetic; antiallergic; immunostimulant; ss.  
 OS Homo sapiens.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 13..312  
 FT sig\_peptide 13..78  
 FT mat\_peptide 79..309  
 FT /\*tag= a  
 FT /\*tag= b  
 FT /\*tag= c  
 PN MO200105972-A1.  
 PD 25-JAN-2001.  
 PF 15-MAR-2000; 2000WO-US06884.  
 PR 20-JUL-1999; 99US-0144758.  
 XX (GENET) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL,  
 PI Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK,  
 PI Wood WI;  
 DR WPI; 2001-103149/11.  
 XX P-PSDB; AAB20117.  
 PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
 PT diagnosing and treating immune-related disorders, such as multiple  
 PT sclerosis, rheumatoid arthritis and diabetes -  
 XX  
 XX Claim 21; Fig 19; 127P; English.  
 XX  
 XX The present sequence is that of cDNA clone DN57694-1341 (ATCC 203017)  
 XX encoding novel human immunomodulator protein PRO826 (UNQ467) (see  
 XX AAB20117). The clone was isolated following a database search by  
 XX applying a signal sequence algorithm. The predicted protein has a  
 XX mol. wt. of 11 kDa and a pI of 7.47. The invention provides  
 XX polynucleotides (see AAF30050-62) encoding novel human PRO proteins  
 XX (see AAB20108-20) including PRO826. Claimed compositions  
 XX comprising these proteins or their agonists are useful for increasing  
 XX infiltration of inflammatory cells into a tissue of a mammal,  
 XX stimulating or enhancing an immune response in a mammal, or  
 XX increasing the proliferation of T-lymphocytes in a mammal in response  
 XX to an antigen. Claimed compositions comprising the PRO polypeptide  
 XX or its antagonist have the opposite effect. A claimed method for  
 XX treating an immune related disorder, such as a T cell disorder,  
 XX involves administering the PRO polypeptide, an agonist antibody or  
 XX an antagonist antibody. The disorder is selected from systemic  
 XX lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 XX juvenile chronic arthritis, spondyloarthritis, systemic  
 XX sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome,  
 XX systemic vasculitis, sarcoidosis, autoimmune hemolytic anaemia,  
 XX autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 XX immune-mediated renal disease, demyelinated diseases (such as  
 XX multiple sclerosis), autoimmune chronic active hepatitis, primary  
 XX biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
 XX inflammatory bowel disease (ulcerative colitis and Crohn's disease),  
 XX gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated  
 XX skin diseases (such as bullous skin disease, erythema multiforme and  
 XX psoriasis), allergic diseases (such as asthma, allergic rhinitis,  
 XX atopic dermatitis, food hypersensitivity and urticaria), immunologic  
 XX diseases of the lung and transplantation associated diseases (such  
 XX as graft rejection and graft-versus-host disease) (all claimed).  
 XX Claimed methods of diagnosing these disorders comprise detecting  
 XX the level of expression of the PRO gene. Also claimed are a method  
 XX of identifying a compound capable of inhibiting the expression or  
 XX activity of the PRO polypeptide, vectors, host cells, antibodies

CC and a method of stimulating the proliferation of T-lymphocytes  
 CC using PRO826.  
 XX  
 XX Sequence 415 BP, 99 A, 126 C, 92 G, 98 T, 0 other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 3,24e-66 Length: 415  
 Score: 71.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0  
 US-10-059-395-142\_COPY\_29\_99 (1-71) x AAF30059 (1-415)  
 QY 1 GIUGUGUSERTHTTIEGLUANTYRLASERARGPROGUALAPHASNTHTROBHE 20  
 DB 97 GAGGAGAGAAACACCATGAGATTATGTCACGACCGAGGCTTTAAACCCCGTTC 156  
 QY 21 LEUANTLEAAPPYGLAARGSERLAPHELYSLAAPGILUPHELEAANTTHIALA 40  
 DB 157 CTGAACATCGACAATATGCGATCTGCGTTAAGCTGATGATCTTAACCTGCACGCC 216  
 QY 41 LEUPHEGUSERTLELYSARGLYLEUPROBHELEAANTTPASPALAPHEPROLYSLEU 60  
 DB 217 CTCCTTGAGTCTATCAAGAAACTTCTTCTCAACTGGATGCTTCTTCTTAAGCTG 276  
 QY 61 LYSGLYLEUARGSERLAPHTH-PROASPALAGLN 71  
 DB 277 AAAGGACTGAGAGCGCACTCGATGCCAG 309  
 RESULT 5  
 AAF4164  
 ID AAF4164 standard; cDNA; 415 BP.  
 XX  
 XX AAF4164;  
 AC  
 XX  
 XX 02-APR-2001 (first entry)  
 DT  
 XX  
 XX Human PRO826 (UNQ467) nucleotide sequence SEQ ID NO:200.  
 DE  
 XX  
 XX Human; secreted and transmembrane protein; PRO; cytosolic;  
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay; ss.  
 XX  
 OS Homo sapiens.  
 PN MO200073454-A1.  
 XX  
 XX 07-DEC-2000.  
 PD  
 XX  
 XX 30-MAR-2000; 2000WO-US08439.  
 PF  
 XX  
 XX 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 17-AUG-1999; 99US-0146222.  
 PR 17-AUG-1999; 99US-0149396.  
 PR 15-SEP-1999; 99WO-US31090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 08-OCT-1999; 99US-0158663.  
 PR 30-NOV-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00376.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
XX  
PA (GERTH ) GENENTECH INC.  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaldi CJ, Gurney AL, Hillan MJ, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;  
XX  
DR WPI; 2001-032160/04.  
DR P-PSDB; AAB65204.  
XX  
PT PRO polynucleotides used to produce polypeptides used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -  
XX  
PS Claim 2; Fig 128; 935pp; English.  
XX  
CC The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
CC can be used for targeted delivery of bioactive molecules, such as  
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
CC and DNA. They may also be used to produce transgenic animals which are  
CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
XX  
Alignment Scores:  
Pred. No.: 3,24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AAF44164 (1-415)  
QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAGAAACACACATTCGATATGCTGCACGACCCGAGGCTTTTACACCCCGTTC 156  
QY 21 LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGluPheLeuAsnThrIleAla 40  
Db 157 CTGAACATCGACCAATTCGATCTGCGTTAAGGCTGATGAGTCCCTGAACCTGGACGCC 216  
QY 41 LeuPheGluSerIleTyrArgIysLeuProPheLeuAsnTyrPAspAlaPheProIysLeu 60  
Db 217 CTTCTTGATGCTTATCAAAAGAACTTCCTTCCCAACTGGATGCTTTCCTTAAGTGTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGGACTGAGAGAGCGCAACTCTGATGCCAG 309  
RESULT 6  
ID AAC97491 standard; cDNA, 415 BP.  
XX AAC97491;  
XX AAC97491;  
XX 28-FEB-2001 (first entry)  
XX

DE Human angiogenesis-associated protein PRO826 cDNA, SEQ ID NO:157.  
XX  
XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
XX gene therapy; transgenic animal; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200053753-A2.  
XX  
PD 14-SEP-2000.  
XX  
PR 05-JAN-2000; 2000WO-US00219.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
XX  
XX (GERTH ) GENENTECH INC.  
XX  
PA Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A,  
PI Godowski PJ, Gurney AL, Hillan MJ, Kuo SS, Mark MR, Masters SA,  
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
XX  
DR WPI; 2001-090793/10.  
DR P-PSDB; AAB53094.  
XX  
XX New isolated nucleic acid for producing a PRO polypeptide, analyzing  
XX genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
XX  
XX Claim 58; Fig 61; 293pp; English.  
PS  
XX  
XX The invention relates to novel human angiogenesis-associated proteins  
XX designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
XX PRO proteins. The invention also relates to vectors and host cells  
XX comprising a PRO nucleic acid, the recombinant production of a PRO  
XX protein, PRO antibodies specific for a PRO protein, fusion proteins  
XX comprising a PRO protein, agonists or antagonists of a PRO protein, and  
XX compounds which inhibit the expression of a PRO gene. The invention  
XX additionally encompasses methods of identifying modulators of PRO  
XX expression or activity; diagnosing a cardiovascular, endothelial or  
XX angiogenic disorder, or a susceptibility to such a disorder by detecting  
XX mutations in a PRO gene, or the expression level of a PRO gene within a  
XX particular tissue; treating a cardiovascular, endothelial or angiogenic  
XX disorder via the administration of a PRO protein, PRO nucleic acid, or  
XX PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
XX PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
XX cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
XX administration of a PRO protein, or an agonist or antagonist thereof.  
XX PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
XX agonists and PRO antagonists may be used as therapeutic agents to treat  
XX cardiovascular, endothelial or angiogenic disorders, such as  
XX atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
XX diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
XX endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's





US-10-059-395-142\_COPY\_29\_99 (1-71) x ABL95626 (1-415)

Qy 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAGAAAGAACCCATTGAGAAATTATCGTCACGACCCGAGGCTTTAAACCCCGCTTC 156  
Qy 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAAATTCGATCGCTTAAAGCTGATAGTTCCTGAAGCTGCACGCGC 216  
Qy 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 217 CTCTTGAAGTCTATCAAAAGAACTTCCTTCTCAACTGGAATGCTTCTTAAGCTG 276  
Qy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGAGCGCACTCTGATGCCAG 309

RESULT 8  
ABK69971  
ID ABK69971 standard; DNA; 415 BP.  
XX  
AC ABK69971;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE cDNA encoding human Pro peptide #11.  
XX  
KW Human; ss; gene; PRO; secreted protein; transmembrane protein;  
KW genetic disorder; tumour; cancer.  
XX  
OS Homo sapiens.  
XX  
EN WO200224888-A2.  
XX  
PD 28-MAR-2002.  
XX  
PF 29-AUG-2001; 2001WO-US27099.  
XX  
PR 01-SEP-2000; 2000US-229896P.  
PR 05-SEP-2000; 2000US-230821P.  
PR 22-SEP-2000; 2000US-235147P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 12-JAN-2001; 2001US-261878P.  
PR 16-JAN-2001; 2001US-261910P.  
PR 16-JAN-2001; 2001US-261939P.  
PR 16-JAN-2001; 2001US-262150P.  
PR 25-JAN-2001; 2001US-264395P.  
PR 02-FEB-2001; 2001US-266421P.  
PR 09-FEB-2001; 2001US-267623P.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 09-MAR-2001; 2001US-274399P.  
PR 03-APR-2001; 2001US-280982P.  
PR 04-APR-2001; 2001US-282199P.  
PR 04-APR-2001; 2001US-282199P.  
PR 09-MAY-2001; 2001US-290589P.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
XX  
XX  
PA (GENTH ) GENENTECH INC.  
XX  
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,  
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WT, Zhang Z,  
PI Fong S;  
XX  
XX WPI; 2002-362426/39.  
DR P-PSDB; ABG34040.  
XX  
PT New PRO polypeptides and polynucleotides encoding the polypeptides,

PT useful in gene therapy, chromosome identification, tissue typing, or  
PT for genetic analysis of individuals with genetic disorders -  
XX  
PS Claim 2; Figure 21; 218pp; English.  
XX  
CC This invention relates to the cDNA and protein sequences of novel  
CC secreted and transmembrane polypeptides PRO polypeptides. The  
CC invention also comprises a method for producing the proteins of the  
CC invention by recombinant means and antibodies specific for the protein  
CC of the invention. The antibody may be used for detecting the PRO  
CC proteins of the invention and may be used to modify their activity.  
CC polynucleotides may be used as hybridisation probes for a cDNA library  
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
CC construct hybridisation probes for mapping the gene which encodes that  
CC PRO and for genetic analysis of individuals with genetic disorders, in  
CC assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knock-out animals which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides are useful in gene therapy, and as molecular weight  
CC markers for protein electrophoresis purposes. The sequences may  
CC also be used to detect overexpression on PRO polypeptides in cancerous  
CC tumours and for screening for differentially expressed genes using  
CC microarray technology. The present sequence represents a cDNA encoding  
CC a human PRO protein of the invention.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
XX  
Alignment Scores:  
Pred. No.: 3,246-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x ABK69971 (1-415)

Qy 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
Db 97 GAGGAGAAAGAACCCATTGAGAAATTATCGTCACGACCCGAGGCTTTAAACCCCGCTTC 156  
Qy 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAAATTCGATCGCTTAAAGCTGATAGTTCCTGAAGCTGCACGCGC 216  
Qy 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
Db 217 CTCTTGAAGTCTATCAAAAGAACTTCCTTCTCAACTGGAATGCTTCTTAAGCTG 276  
Qy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
Db 277 AAAGACTGAGAGCGCACTCTGATGCCAG 309

RESULT 9  
ABL88137  
ID ABL88137 standard; cDNA; 415 BP.  
XX  
AC ABL88137;  
XX  
DT 16-MAY-2002 (first entry)  
XX  
DE Human PRO826 cDNA sequence SEQ ID NO:131.  
XX  
KW Human; angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;  
KW vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
KW age-related macular degeneration; arterial restenosis; angina;  
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
KW wound healing; chromosome mapping; gene mapping; gene; ss.  
XX

OS Homo sapiens.  
 XX WO200200690-A2.  
 XX  
 XX  
 PD 03-JAN-2002.  
 XX  
 XX 20-JUN-2001; 2001WO-US19692.  
 XX  
 XX 23-JUN-2000; 2000US-213637P.  
 XX 20-JUL-2000; 2000US-219556P.  
 XX 25-JUL-2000; 2000US-220624P.  
 XX 25-JUL-2000; 2000US-220664P.  
 XX 28-JUL-2000; 2000WO-US20710.  
 XX 02-AUG-2000; 2000US-222695P.  
 XX 17-AUG-2000; 2000US-0643657.  
 XX 23-AUG-2000; 2000WO-US23522.  
 XX 24-AUG-2000; 2000WO-US23328.  
 XX 07-SEP-2000; 2000US-230978P.  
 XX 18-SEP-2000; 2000US-0664610.  
 XX 18-SEP-2000; 2000US-0665350.  
 XX 24-OCT-2000; 2000US-242922P.  
 XX 08-NOV-2000; 2000US-0709238.  
 XX 08-NOV-2000; 2000WO-US30952.  
 XX 10-NOV-2000; 2000WO-US30873.  
 XX 01-DEC-2000; 2000WO-US32678.  
 XX 20-DEC-2000; 2000US-0747259.  
 XX 20-DEC-2000; 2000WO-US34956.  
 XX 22-JAN-2001; 2001US-0767609.  
 XX 28-FEB-2001; 2001US-0796498.  
 XX 28-FEB-2001; 2001WO-US06520.  
 XX 01-MAR-2001; 2001WO-US06666.  
 XX 09-MAR-2001; 2001US-0802706.  
 XX 14-MAR-2001; 2001US-0806889.  
 XX 22-MAR-2001; 2001US-0816744.  
 XX 05-APR-2001; 2001US-0828366.  
 XX 10-MAY-2001; 2001US-0854280.  
 XX 10-MAY-2001; 2001US-0854280.  
 XX 25-MAY-2001; 2001US-0866028.  
 XX 25-MAY-2001; 2001WO-US17092.  
 XX 30-MAY-2001; 2001US-0870574.  
 XX 30-MAY-2001; 2001WO-US17443.  
 XX 01-JUN-2001; 2001WO-US17800.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CX, Williams PW, Wood WI, Ye W;  
 XX  
 DR WPI; 2002-090516/12.  
 DR P-PsDB; ABB84882.  
 XX  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX  
 PS Claim 2; Fig 131; 565bp; English.  
 XX  
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostratic,  
 CC antilangiogenic, hypotensive, vulnerary and antileiostoclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 CC carcinoma) and wound healing. The PRO polynucleotides have applications  
 CC in molecular biology, including use as hybridisation probes, and in  
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
 CC probes used in the exemplification of the present invention.

XX SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
 XX  
 XX Alignment Scores:  
 XX Pred. No.: 3,24e-66 Length: 415  
 XX Score: 71.00 Matches: 71  
 XX Percent Similarity: 100.00% Conservative: 0  
 XX Best Local Similarity: 100.00% Mismatches: 0  
 XX Query Match: 100.00% Indels: 0  
 XX DB: 24 Gaps: 0  
 XX  
 XX US-10-059-395-142\_COPY\_29\_99 (1-71) x ABL88137 (1-415)  
 QY 1 GIUGIUGIUSERTHILIGLUAANTYRLASERAGPGGIALAIPHASNTHPROBE 20  
 DB 97 GAGGAGAGAGACCATTCAGATTAATTCGTACGACCCGAGGCTTTAACACCCCGTTC 156  
 QY 21 LEUAENILASPIYLSLEUARGSERALAPHELYSALASPGIUPHELEUASNTTPIHSAIA 40  
 DB 157 CTGAACATCGACCAATTCGATCTGCTTAAGCTGATGAGTCTCTGAACCTGACGACGCC 216  
 QY 41 LEUPHEGIUSERIELYERAGYLSLEUDPROHELEUASNTTPASPALAPHEPROLYSLEU 60  
 DB 217 CTCTTGAGTCTATCAAAAGGAACTTCTTCTCAACTGAGATGCTTCTTAAGCTG 276  
 QY 61 LYSGLYLSLEUARGSERALATHPROASPALAQLN 71  
 DB 277 AAAGACTGAGAGGCGCACTCTGATGCCAG 309  
 XX  
 XX RESULT 10  
 XX ABLK33608  
 XX ID ABLK33608 standard; CDNA, 415 BP.  
 XX  
 XX ABLK33608;  
 XX  
 XX 08-MAY-2002 (first entry)  
 XX  
 XX CDNA encoding human PRO protein, Seq ID No 145.  
 XX  
 XX DE Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
 XX KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
 XX KW pericyte cell proliferation; chondrocyte cell proliferation;  
 XX KW tumour necrosis factor-alpha; gene; ss.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX PN WO200208288-A2.  
 XX  
 XX PD 31-JAN-2002.  
 XX  
 XX 29-JUN-2001; 2001WO-US21066.  
 XX  
 XX 20-JUL-2000; 2000US-219556P.  
 XX 25-JUL-2000; 2000US-220585P.  
 XX 25-JUL-2000; 2000US-220605P.  
 XX 25-JUL-2000; 2000US-220607P.  
 XX 25-JUL-2000; 2000US-220624P.  
 XX 25-JUL-2000; 2000US-220638P.  
 XX 25-JUL-2000; 2000US-220664P.  
 XX 25-JUL-2000; 2000US-220666P.  
 XX 26-JUL-2000; 2000US-220893P.  
 XX 28-JUL-2000; 2000WO-US20710.  
 XX 23-AUG-2000; 2000WO-US23522.  
 XX 24-AUG-2000; 2000WO-US23328.  
 XX 15-SEP-2000; 2000US-000000P.  
 XX 10-NOV-2000; 2000WO-US30873.  
 XX 28-NOV-2000; 2000US-253646P.  
 XX 01-DEC-2000; 2000WO-US32678.  
 XX 20-DEC-2000; 2000US-0747259.  
 XX 20-DEC-2000; 2000WO-US34956.  
 XX 28-FEB-2001; 2001WO-US06520.  
 XX 10-MAY-2001; 2001US-0854280.  
 XX 25-MAY-2001; 2001WO-US17092.

XX (GETH ) GENENTECH INC.  
PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;  
PI WPI; 2002-172001/22.  
XX P-PSDB; AAU83664.  
DR  
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for treating a PRO related disorder and for diagnosing tumours  
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
PT tumour or liver tumour -  
XX  
XX Claim 2; Figure 145; 359pp; English.  
XX  
XX The invention relates to one hundred and twenty two nucleic acids  
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
CC agonists and antagonists are useful for treating a PRO related disorder.  
CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
CC liver tumour. The PRO polypeptides are useful for stimulating the  
CC proliferation of, or gene expression, in pericyte cells, for stimulating  
CC the proliferation or differentiation of chondrocyte cells, for  
CC stimulating the release of tumour necrosis factor-alpha from human blood,  
CC for stimulating or inhibiting the proliferation of normal human dermal  
CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes,  
CC and in chromosome and gene mapping. ABK3536-ABK3657 represent human  
CC PRO protein coding sequences of the invention.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
Alignment Scores:  
Pred. No.: 3.24e-66 Length: 415  
Score: 71.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x ABK33608 (1-415)  
QY 1 GluIugIuSerThrlleGluAsnTYrAlaSerArProGluAlaPheAsnThrProPhe 20  
Db 97 GAGAAAGAAAGACACCTTGAATTAATCCGTCACGACCCGAGCCCTTTAAACCCCGCTTC 156  
QY 21 LeuAniIleApyLysLeuArgSerAlaPheLysAlaApyGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAATTCGATCGCTTAAGGTGATGAGTTCCTGAACCTGGCAGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAlaPheProLysLeu 60  
Db 217 CTTTGTAGTATCAAAAGAAACCTTCCTTCAACCTGGATGCCCTTTCCTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaIle 71  
Db 277 AAAGACTGAGAGCGCAACTCTGATGCCAG 309  
RESULT 11  
ABX80255  
ID ABX80255 standard; DNA; 415 BP.  
XX  
XX ABX80255;  
XX  
XX 28-APR-2003 (first entry)  
XX  
XX Novel human secreted or transmembrane protein PRO819 DNA.  
XX  
XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
XX cardiac insufficiency disorder; cancer; tumour; immune response;  
XX

KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
XX  
OS Homo sapiens.  
XX  
XX US2002132252-A1.  
XX  
XX 19-SEP-2002.  
XX  
XX  
PF 14-NOV-2001; 2001US-0990442.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US1252.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 06-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787F.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.

PR 03-JUN-1998; 98US-087827P.  
 PR 04-JUN-1998; 98US-088021P.  
 PR 04-JUN-1998; 98US-088025P.  
 PR 04-JUN-1998; 98US-088026P.  
 PR 04-JUN-1998; 98US-088028P.  
 PR 04-JUN-1998; 98US-088029P.  
 PR 04-JUN-1998; 98US-088030P.  
 PR 04-JUN-1998; 98US-088033P.  
 PR 04-JUN-1998; 98US-088036P.  
 PR 05-JUN-1998; 98US-088167P.  
 PR 05-JUN-1998; 98US-088202P.  
 PR 05-JUN-1998; 98US-088212P.  
 PR 05-JUN-1998; 98US-088217P.  
 PR 09-JUN-1998; 98US-088655P.  
 PR 10-JUN-1998; 98US-088734P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088742P.  
 PR 10-JUN-1998; 98US-088810P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088826P.  
 PR 11-JUN-1998; 98US-088858P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088876P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089440P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 17-JUN-1998; 98US-089532P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089598P.  
 PR 17-JUN-1998; 98US-089599P.  
 PR 17-JUN-1998; 98US-089600P.  
 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941992.

(GETH) GENENTECH INC.

PR Ashkenazi AJ, Baker KP, Botstein D, Desnoyers I, Eaton DL,  
 PI Ferrara N, Fong S, Gerber H, Gerltzen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT,  
 PI Zhang Z;

XX WPI; 2003-247083/24.  
 DR P-PSDB; ABUS9098.

PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT are therapeutically useful for enhancing immune response and in cancer  
 PT treatments

Claim 2; Fig 130; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 CC PRO1360 and PRO1387 induce C-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
 CC useful for treating cancerous tumors. PRO812 inhibits vascular  
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 CC cells and is thus useful for inhibiting endothelial cell growth in  
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing

CC immune response. PRO828, PRO826, PRO1068 or PRO1122 enhance survival of  
 CC retinal neurons cells (PRO1122 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with diabetes, herpeticiformis or Crohn's  
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or redifferentiation of chondrocytes in culture and  
 CC are thus useful for treating sports injuries, and arthritis. This  
 CC sequence represents a novel human PRO protein polynucleotide.

XX SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:

| Pred. No.:             | 3,24e-66 | Length:       | 415 |
|------------------------|----------|---------------|-----|
| Score:                 | 71.00    | Matches:      | 71  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 25       | Gaps:         | 0   |

US-10-059-395-142\_COPY\_29\_99 (1-71) x ABX80255 (1-415)

QY 1 GUGUGUGUSeRTThIleGUASeRTYAlaSeRTArpProGUAaPheASnThrProPhe 20  
 DB 97 GAGAGAGAAACACCATTTAGATTCGTCAGACCGCGAGCTTTAAACCCCGTTC 156  
 QY 21 LeuAnIleAPlyLeuArGSeRAlaPheYsAlaAPGluPheLeuASnThrPhe 40  
 DB 157 CTGAACATCGACAAATTCGATCGCTTTAAAGCTATGATGCTTCTGAACCTGACGCC 216  
 QY 41 LeuPheGluSeRTIleYsArGlyLeuProPheLeuAnThrPaAPAlaPheProIysLeu 60  
 DB 217 CTTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGGAGATGCTTCTTAAGCTG 276  
 QY 61 LysGlyLeuArGSeRAlaThrProASpAlaGln 71  
 DB 277 AAAGACTGAGAGACGCAACTCTGATGCCAG 309

RESULT 12

ABX80759 standard; cDNA; 415 BP.

AC ABX80759;

DT 22-APR-2003 (first entry)

DE Human secreted/transmembrane protein cDNA, #78.

KW Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;  
 KW diagnostic; biosensor; bioindicator; tumour; therapeutic;  
 KW gene therapy; tumour-associated antigenic target; TAT; ADEPT;  
 KW antibody-dependent enzyme mediated drug therapy; cytostatic.

OS Homo sapiens.

PN US2003027162-A1.

PD 06-FEB-2003.

PF 15-NOV-2001; 2001US-0997428.

XX 05-NOV-1997; 97WO-US20069.  
 XX 16-SEP-1998; 98WO-US19330.  
 XX 17-SEP-1998; 98WO-US19437.  
 XX 07-OCT-1998; 98WO-US21141.  
 XX 01-DEC-1998; 98WO-US25108.  
 XX 05-JAN-1999; 99WO-US00106.  
 XX 08-MAR-1999; 99WO-US05028.  
 XX 02-JUN-1999; 99WO-US12252.  
 XX 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99MO-US21547.  
PR 30-NOV-1999; 99MO-US28313.  
PR 01-DEC-1999; 99MO-US28301.  
PR 01-DEC-1999; 99MO-US28634.  
PR 16-DEC-1999; 99MO-US30095.  
PR 20-DEC-1999; 99MO-US30911.  
PR 05-JAN-2000; 2000MO-US00219.  
PR 06-JAN-2000; 2000MO-US00376.  
PR 11-FEB-2000; 2000MO-US03565.  
PR 18-FEB-2000; 2000MO-US04341.  
PR 22-FEB-2000; 2000MO-US04414.  
PR 24-FEB-2000; 2000MO-US04914.  
PR 02-MAR-2000; 2000MO-US05841.  
PR 10-MAR-2000; 2000MO-US06319.  
PR 15-MAR-2000; 2000MO-US06884.  
PR 20-MAR-2000; 2000MO-US07377.  
PR 30-MAR-2000; 2000MO-US08439.  
PR 15-MAY-2000; 2000MO-US13358.  
PR 17-MAY-2000; 2000MO-US13705.  
PR 22-MAY-2000; 2000MO-US14042.  
PR 30-MAY-2000; 2000MO-US14941.  
PR 02-JUN-2000; 2000MO-US15264.  
PR 28-JUL-2000; 2000MO-US20710.  
PR 11-AUG-2000; 2000MO-US22031.  
PR 23-AUG-2000; 2000MO-US23322.  
PR 24-AUG-2000; 2000MO-US23328.  
PR 08-NOV-2000; 2000MO-US30952.  
PR 01-DEC-2000; 2000MO-US32678.  
PR 28-FEB-2001; 2001MO-US06520.  
PR 01-JUN-2001; 2001MO-US17800.  
PR 20-JUN-2001; 2001MO-US19692.  
PR 29-JUN-2001; 2001MO-US21066.  
PR 09-JUL-2001; 2001MO-US21735.  
PR 16-JUN-1997; 97US-048787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 12-NOV-1997; 97US-065186P.  
PR 13-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083322P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088126P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
PR 05-JUN-1998; 98US-088212P.  
PR 05-JUN-1998; 98US-088217P.  
PR 09-JUN-1998; 98US-088655P.  
PR 10-JUN-1998; 98US-088734P.  
PR 10-JUN-1998; 98US-088738P.  
PR 10-JUN-1998; 98US-088742P.  
PR 10-JUN-1998; 98US-088810P.  
PR 10-JUN-1998; 98US-088824P.  
PR 10-JUN-1998; 98US-088826P.  
PR 11-JUN-1998; 98US-088858P.  
PR 11-JUN-1998; 98US-088861P.  
PR 11-JUN-1998; 98US-088876P.  
PR 12-JUN-1998; 98US-089105P.  
PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
  
PR 16-JUN-1998; 98US-089514P.  
PR 17-JUN-1998; 98US-089532P.  
PR 17-JUN-1998; 98US-089538P.  
PR 17-JUN-1998; 98US-089598P.  
PR 17-JUN-1998; 98US-089599P.  
PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089653P.  
PR 18-JUN-1998; 98US-089801P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
PR 19-JUN-1998; 98US-089947P.  
PR 19-JUN-1998; 98US-089948P.  
PR 19-JUN-1998; 98US-089952P.  
PR 22-JUN-1998; 98US-090246P.  
PR 22-JUN-1998; 98US-090252P.  
PR 22-JUN-1998; 98US-090254P.  
PR 23-JUN-1998; 98US-090349P.  
PR 23-JUN-1998; 98US-090355P.  
PR 24-JUN-1998; 98US-090429P.  
PR 24-JUN-1998; 98US-090431P.  
PR 24-JUN-1998; 98US-090435P.  
PR 24-JUN-1998; 98US-090444P.  
PR 24-JUN-1998; 98US-090445P.  
PR 24-JUN-1998; 98US-090472P.  
PR 24-JUN-1998; 98US-090535P.  
PR 24-JUN-1998; 98US-090540P.  
PR 24-JUN-1998; 98US-090542P.  
PR 24-JUN-1998; 98US-090557P.  
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| Db        | 97        | GAAGAAAGAAAGACCATTTAGAGATTATGCCGACAGACCCGAGGCTTTAAACACCCGGTTC   | 156 |
| Qy        | 21        | LeuAsnIleAspIlyLeuArGSerAlaPheYsAlaAspGIuPheLeuAsnTrpHisAla     | 40  |
| Db        | 157       | CTGAACATGACAAATTGGCATCTCCGTTTAAGGTGATGAGTTCCTGAACTGGCACGCC      | 216 |
| Qy        | 41        | LeuPheGLuSerIleYsArGlyLeuPProPheLeuAsnTrpAspAlaPheProLYsLeu     | 60  |
| Db        | 217       | CTCTTTGAGTCrATCAAAAGAAACTTCCTTCTCTCAACtGGATGcCTTTCCrTAAGCTG     | 276 |
| Qy        | 61        | LYsGIYLeuArGSerAlaThrProAspAlaGln                               | 71  |
| Db        | 277       | AAAGGACTGAGGAGCGCAACTCTCATGCCAG                                 | 309 |
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| XX        | DT        | 01-MAY-2003 (first entry)                                       |     |
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| XX        |           |   |     |
| KM        |           | Human, gene; ss; PRO, secreted; transmembrane; signal peptide;  |     |
| KW        |           | pharmaceutical; diagnostic; therapeutic; gene therapy.          |     |

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XX OS Homo sapiens.
XX US2002160384-A1.
XX
XX 31-OCT-2002.
XX
XX PF 14-NOV-2001; 2001US-0992598.
XX
XX 05-NOV-1997; 97WO-US20069.
XX 16-SEP-1998; 98WO-US19330.
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XX 01-DEC-1998; 98WO-US25108.
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XX 28-FEB-2001; 2001WO-US06520.
XX 01-JUN-2001; 2001WO-US17800.
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XX 29-JUN-2001; 2001WO-US21066.
XX 09-JUL-2001; 2001WO-US21735.
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PR 28-AUG-2001; 2001US-0941992.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL,
XX Ferrara N, Fong S, Gerber H, Gerltzen ME, Goddard A, Godowski PJ,
XX Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
XX Zhang Z;
XX
XX WPI; 2003-288106/28.
XX P-PSDB; ABU60528.
XX
XX New transmembrane polypeptides and nucleic acids encoding the
XX polypeptides, useful in gene therapy, in chromosome identification, as
XX chromosome markers, or in generating probes -
XX
XX Claim 2; Fig 128; 650bp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
XX comprising a sequence without signal peptide and the nucleic acid
XX encoding them. The polypeptides can be used to raise antibodies that
XX specifically bind to the PRO polypeptide, for linking a bioactive
XX molecule to a cell expressing a PRO protein and for modulating at least
XX one biological activity of a cell. The PRO polypeptides or
XX polynucleotides are also useful in gene therapy, in chromosome
XX identification, as chromosome markers, or in generating probes. The PRO
XX polypeptides are useful as molecular markers for protein
XX electrophoresis, and the isolated nucleic acids may be used for
XX recombinantly expressing those markers. The PRO polypeptides and nucleic
XX acids may also be used in tissue typing. Anti-PRO antibodies are useful
XX in diagnostic assays for PRO, and in affinity purification of PRO from
XX recombinant cell culture or natural sources. The sequences presented in
XX ABX90083-ABX90468 are the genes encoding, the primers amplifying and the
XX probes detecting the PRO polynucleotides of the invention.
XX Note: The sequence data for this patent is also available in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
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XX Score: 71.00 Matches: 71
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XX  
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XX  
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PR 26-AUG-1998; 98US-097952P.  
PR 26-AUG-1998; 98US-097954P.  
PR 26-AUG-1998; 98US-097955P.  
PR 26-AUG-1998; 98US-097971P.  
PR 26-AUG-1998; 98US-097974P.  
PR 26-AUG-1998; 98US-097978P.  
PR 26-AUG-1998; 98US-097979P.  
PR 26-AUG-1998; 98US-097986P.  
PR 26-AUG-1998; 98US-098014P.  
PR 31-AUG-1998; 98US-098525P.  
PR 16-SEP-1998; 98US-100634P.  
PR 17-SEP-1998; 98US-100856P.

PR 22-DEC-1998; 98US-113366P.  
PR 12-MAR-1999; 99US-123857P.  
PR 23-JUN-1999; 99US-141037P.  
PR 07-JUL-1999; 99US-143048P.

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| Query Match:           | 100.00%  | Mismatches:   | 0   |
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|                        |          | Gaps:         | 0   |

US-10-059-395-142\_COPY\_29\_99 (1-71) x ABX77843 (1-415)

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| Db | 97  | GAGGAAGAAAGCACCATTGAGATTATGCGTCACGACCCGAGGCTTTAACACCCCGTTC | 156 |
| Qy | 21  | LeuAenIIeApIyLeuArGSeRAlaPheIySaIaApGluPheLeuAnTRpHISaIa   | 40  |
| Db | 157 | CTGAACATCGACAAATGCGATCTCGTTAAGGCTGATGAGATTCTGAACTGGACGCC   | 216 |
| Qy | 41  | LeuPheGluSeRIeIySaRgIySeuPProPheLeuAnTRpAspAlaPheProIySeu  | 60  |
| Db | 217 | CTCTTGAGTCTATCAAAAGAACTTCTTCTTCACTGGAGATCCCTTCTAAGCTG      | 276 |
| Qy | 61  | IyGgIyLeuArGSeRAlaTRProAspAlaGin                           | 71  |
| Db | 277 | AAAGACTGAGGAGCGCACTCCTGATGCCAG                             | 309 |

Search completed: November 28, 2003, 11:01:48  
Job time : 221 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 10:58:05 ; Search time 250 Seconds  
(without alignments)  
935.692 Million cell updates/sec

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Title: US-10-059-395-142_COPY 29_99
Perfect score: 71
Sequence: 1 EEESTIENYASRPEAFNTPF.....LNWDAPFKLGLRSATPDAQ 71

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| Ygapop         | 60.0 , Ygapext 60.0 |
| Fgapop         | 6.0 , Fgapext 7.0   |
| Delop          | 6.0 , Delext 7.0    |

Searched: 2190069 seqs, 1647345023 residues

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Total number of hits satisfying chosen parameters: 4372088
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Post-processing: Listing first 45 summaries

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**Pred. No.** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

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| 12 | 71 | 100.0 | 415 | 10 | US-09-989-721-200  | Sequence 200, App |
| 13 | 71 | 100.0 | 415 | 10 | US-09-992-558-200  | Sequence 200, App |
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| 15 | 71 | 100.0 | 415 | 10 | US-09-989-735-200  | Sequence 200, App |
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## ALIGNMENTS

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RESULT 1
US-09-9689-722-200
: Sequence 200. Application US/099689722
: Patent No. US200200712067A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerlitsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gunney, Austin L.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Nadler, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel

```

APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OR INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
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## Alignment Scores:

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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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## RESULT 2

US-09-989-723-200  
; Sequence 200, Application US/09989723  
; Patent No. US20020072092A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gunney, Austin L.  
;; APPLICANT: Kijavini, Ivar J.  
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;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas P.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C62  
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P09678.1 1998-07-07    PRIOR APPLICATION NUMBER: 60/092182
P09678.1 1998-07-09    PRIOR FILING DATE: 1998-07-09

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Query Match:       100.00%      Indels:         0
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; Patent No. US20020072496A1
; GENERAL INFORMATION:

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APPLICANT: Aghkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desmoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Gottlieb, Mary E.  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P27301C56  
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APPLICANT: Baker, Kevin P.  
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APPLICANT: Desnoyers, Luc  
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PRIOR FILING DATE: 1998-07-09

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Pred. No.: 7.74e-66 Length: 415  
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Qy 41 LeuBhegluSerilelySarglyLeuProPheLeuansilTPaSPAlaPheProlySleu 60  
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Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
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APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zhenli  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C70  
CURRENT APPLICATION NUMBER: US/09/989,731  
CURRENT FILING DATE: 2001-11-20  
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DB 157 CTGAACATCGACCAATTGCGATCTGCTTTAAGGCTGATGATCTCTGAACCTGCACGCC 216
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US-09-989-732-200
Sequence 200, Application US/09989732
Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoves, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C57
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## RESULT 8

US-09-990-442-200

Sequence 200: Application US/09990442

Patent No. US20020132252A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
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 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.

APPLICANT: Zhang, Zhen  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

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| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
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## RESULT 10

US-09-993-604-200  
Sequence 200, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc  
APPLICANT: Ferrata, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zhenli  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C25  
CURRENT APPLICATION NUMBER: US/09/393,604  
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

Pred. No.: 7,74e-66 Length: 415  
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DB: 10 Gaps: 0

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; Sequence 200, Application US/09990456  
; Patent No. US20020137890A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Geider, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC22  
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; PRIOR FILING DATE: 2001-11-14  
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;; PRIOR FILING DATE: 1998-07-09

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Sequence 200, Application US/09989721  
Patent No. US20020142961A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bostein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Napier, Mary A.  
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APPLICANT: Paoni, Nicholas F.  
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APPLICANT: Tumas, Daniel  
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APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C55  
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PRIOR FILING DATE: 1998-07-09

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Patent No. US20020160384A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C20  
CURRENT APPLICATION NUMBER: US/09/992,598  
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Seceted and Transmembrane Polypeptides and Nucleic
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
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APPLICANT: Gerlitsen, Mary E.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tuma, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same

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| PRIOR APPLICATION NUMBER: 60/088810 |               |
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| PRIOR FILING DATE: 1998-06-11       |               |

[illegible]

;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090696  
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;; PRIOR APPLICATION NUMBER: 60/090862  
;; PRIOR FILING DATE: 1998-06-26  
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;; PRIOR APPLICATION NUMBER: 60/091360  
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;; PRIOR APPLICATION NUMBER: 60/091478  
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;; PRIOR APPLICATION NUMBER: 60/091519  
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;; PRIOR APPLICATION NUMBER: 60/091626  
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;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

|                        |          |               |     |
|------------------------|----------|---------------|-----|
| Pred. No.:             | 7.74e-66 | Length:       | 415 |
| Score:                 | 71.00    | Matches:      | 71  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 10       | Gaps:         | 0   |

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-989-735-200 (1-415)

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | GIUGIUGIUSERTHIIIGIUAANTYRAIASEATGP-ROGIUAIApheanTh-Prophe    | 20  |
| DB | 97  | GAGGAAGAAACACACATTGAGAAATTATGCTACAGACCGAGCCCTTAACACCCCGTTC    | 156 |
| QY | 21  | LeuAenTleAspLyLeuAArgSerAlaPheLySaIaAspGluPheLeuAenTropHisAla | 40  |
| DB | 157 | CTGAACATCGACAAATTGCGATTCGCTTAAGGCTGATGACTTCCTGAACGACGCC       | 216 |
| QY | 41  | LeuPheGluSerIleLyAArgLyLeuBProPheLeuAenTTPaspAlaPheProLyLeu   | 60  |
| DB | 217 | CTCTTGAGTCTATCAAAAGAAACTCTTCTCCCACTGGATGCTTCTTAAGCTG          | 276 |
| QY | 61  | LyseGlyLeuAArgSerAlaTh-PropAspAlaGln                          | 71  |
| DB | 277 | AAAGACTGAGAGGCGCAACTCTGATGCCAG                                | 309 |

Search completed: November 28, 2003, 12:18:04  
Job time : 252 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 12:21:56 ; Search time 47 Seconds

(without alignments)  
239.778 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 375  
Sequence: 1 EBESTINYSRPAFNTFP.....LNMDFPKKGRSATPDQAQ 71

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

A.GeneSeq\_19Jun03:\*

- 1: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1980.DAT:\*
- 2: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:\*
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- 6: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT:\*
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- 23: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:\*
- 24: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----|-------------|
| 1          | 375   | 100.0       | 99        | 20 | AAW67828    |
| 2          | 375   | 100.0       | 99        | 21 | AAW6681     |
| 3          | 375   | 100.0       | 99        | 22 | AAW620117   |
| 4          | 375   | 100.0       | 99        | 22 | AAW65204    |
| 5          | 375   | 100.0       | 99        | 22 | AAW60916    |
| 6          | 375   | 100.0       | 99        | 22 | AAW63094    |
| 7          | 375   | 100.0       | 99        | 23 | ABW6586     |
| 8          | 375   | 100.0       | 99        | 23 | ABW65488    |
| 9          | 375   | 100.0       | 99        | 23 | ABW634040   |

|    |      |       |      |    |          |                    |
|----|------|-------|------|----|----------|--------------------|
| 10 | 375  | 100.0 | 99   | 23 | ABW64882 | Human PRO826 prote |
| 11 | 375  | 100.0 | 99   | 23 | ABW63664 | Human PRO protein, |
| 12 | 375  | 100.0 | 99   | 23 | AAW61964 | Human PRO826. Hom  |
| 13 | 375  | 100.0 | 99   | 24 | ABW59097 | Novel human secret |
| 14 | 375  | 100.0 | 99   | 24 | ABW59244 | Human secreted/tr  |
| 15 | 375  | 100.0 | 99   | 24 | ABW59393 | Novel human secret |
| 16 | 375  | 100.0 | 99   | 24 | ABW60528 | Human secreted/tr  |
| 17 | 375  | 100.0 | 99   | 24 | ABW58019 | Human PRO polypept |
| 18 | 375  | 100.0 | 99   | 24 | ABW58950 | Human secreted/tr  |
| 19 | 375  | 100.0 | 99   | 24 | ABW13910 | Human PRO826 polyp |
| 20 | 375  | 100.0 | 99   | 24 | ABW10865 | Human PRO polypept |
| 21 | 286  | 76.3  | 85   | 23 | ABW69587 | Human polypeptide  |
| 22 | 166  | 44.3  | 88   | 23 | ABW72393 | Human polypeptide  |
| 23 | 143  | 38.1  | 96   | 23 | ABW69669 | Murine protein iso |
| 24 | 65.5 | 17.5  | 116  | 22 | AAW94219 | Human polypeptide  |
| 25 | 65.5 | 17.5  | 230  | 20 | AAW60066 | Human endometrium  |
| 26 | 65.5 | 17.5  | 479  | 21 | AAW50941 | Human adult skin c |
| 27 | 65   | 17.3  | 123  | 22 | AAW73503 | Human transferrase |
| 28 | 64   | 17.1  | 72   | 21 | AAW61482 | Human secreted pro |
| 29 | 64   | 17.1  | 72   | 21 | AAW61483 | Human secreted pro |
| 30 | 64   | 17.1  | 387  | 21 | ABW38324 | Amino acid sequenc |
| 31 | 64   | 17.1  | 808  | 23 | ABW69063 | Neisseria meningit |
| 32 | 62.5 | 16.7  | 526  | 21 | AAW75474 | Neisseria meningit |
| 33 | 62.5 | 16.7  | 526  | 21 | AAW75475 | Neisseria meningit |
| 34 | 62.5 | 16.7  | 526  | 21 | AAW75476 | Neisseria meningit |
| 35 | 60.5 | 16.1  | 1544 | 22 | ABW69002 | Drosophila melanog |
| 36 | 60   | 16.0  | 844  | 22 | ABW59956 | Human adult skin c |
| 37 | 58   | 15.5  | 369  | 21 | AAW50940 | Human PRO1411 (UNO |
| 38 | 58   | 15.5  | 440  | 21 | AAW93354 | Human PRO polypept |
| 39 | 58   | 15.5  | 440  | 22 | AAW92912 | Human PRO1411. Ho  |
| 40 | 58   | 15.5  | 440  | 22 | ABW7551  | Amino acid sequenc |
| 41 | 58   | 15.5  | 440  | 22 | ABW31205 | Protein of the inv |
| 42 | 58   | 15.5  | 440  | 23 | ABW6103  | Human secreted/tr  |
| 43 | 58   | 15.5  | 440  | 23 | ABW65876 | Human angiogenesis |
| 44 | 58   | 15.5  | 440  | 23 | ABW65497 | Human PRO1411 prot |
| 45 | 58   | 15.5  | 440  | 23 | ABW64891 |                    |

#### ALIGNMENTS

|          |  |
|----------|--|
| RESULT 1 |  |
| AAW67828 | AAW67828 standard; Protein; 99 AA.   |
| AC       | AAW67828;  |
| XX       |  |
| DT       | 25-MAR-1999 (first entry)  |
| XX       |  |
| DE       | Human secreted protein encoded by gene 22 clone HFEAF41.                   |
| XX       |  |
| KW       | Human; secreted protein; fusion protein; gene therapy; protein therapy;    |
| KW       | diagnosis; tissue; cancer; neurodegenerative disorder; leukemia;           |
| KW       | developmental abnormality; foetal deficiency; blood; allergy; renal;       |
| KW       | immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;      |
| KW       | inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;       |
| KW       | cognitive disorder; schizophrenia; prostate; obesity; osteoclasts; thymus; |
| KW       | osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;    |
| KW       | endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.     |
| XX       |  |
| OS       | Homo sapiens.  |
| XX       |  |
| XX       | WO9842738-A1.  |
| XX       |  |
| PD       | 01-OCT-1998.   |
| XX       |  |
| PF       | 19-MAR-1998; 98WO-US05311.   |
| XX       |  |
| PR       | 30-MAY-1997; 97US-0050937.   |
| PR       | 21-MAR-1997; 97US-0041276.   |
| PR       | 21-MAR-1997; 97US-0041277.   |
| PR       | 21-MAR-1997; 97US-0041281.   |
| PR       | 21-MAR-1997; 97US-0042344.   |

PR 30-MAY-1997; 97US-0048069.  
PR 30-MAY-1997; 97US-0048094.  
PR 30-MAY-1997; 97US-0048095.  
PR 30-MAY-1997; 97US-0048096.  
PR 30-MAY-1997; 97US-0048099.  
PR 30-MAY-1997; 97US-0048131.  
PR 30-MAY-1997; 97US-0048135.  
PR 30-MAY-1997; 97US-0048154.  
PR 30-MAY-1997; 97US-0048160.  
PR 30-MAY-1997; 97US-0048186.  
PR 30-MAY-1997; 97US-0048187.  
PR 30-MAY-1997; 97US-0048188.  
PR 30-MAY-1997; 97US-0048350.  
PR 30-MAY-1997; 97US-0048351.  
PR 30-MAY-1997; 97US-0048352.  
PR 30-MAY-1997; 97US-0048355.  
PR 05-AUG-1997; 97US-0054804.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PI Brewer LA, Duan R, Ebner R, Ferrie AM, Florence KA;  
PI Greene JM, Hu JS, Lafleur DW, Moore PA, Ni J, Olsen HS;  
PI Rosen CA, Ruden SM, Shi Y, Young P;  
XX WPI; 1999-070066/06.  
DR N-PSDB; AAX00632.  
XX  
XX New isolated human genes and the secreted polypeptides they encode -  
PT useful for diagnosis and treatment of e.g. cancer, neurological  
PT disorders, immune diseases, inflammation or blood disorders  
XX  
XX Claim 11; Page 285; 385pp; English.  
XX  
CC This sequence represents a secreted human protein encoded by the gene  
CC clone detailed in the descriptor line. The gene can be used to generate  
CC fusion proteins by linking to the gene to a human immunoglobulin Fc  
CC portion (e.g. AAX00602) for increasing the stability of the fused  
CC protein as compared to the human protein only.  
CC The invention relates to 87 novel genes and their fragments (nucleic  
CC acid sequences: AAX00611-X00724; amino acid sequences AAM67807-M68004)  
CC which are useful for preventing, treating or ameliorating medical  
CC conditions e.g. by protein or gene therapy. Also, pathological  
CC conditions can be diagnosed by determining the amount of the new  
CC polypeptides in a sample or by determining the presence of mutations in  
CC the new polynucleotides. Specific uses are described for each of the 87  
CC polynucleotides, based on which tissues they are most highly expressed in  
CC (see AAX00611 for described uses).  
XX  
XX Sequence 99 AA;  
SQ  
Query Match 100.0%; Score 375; DB 20; Length 99;  
Best Local Similarity 100.0%; Pred. No. 5,1e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EESSTIENYASRPEAFTPTPLNIDKRSAPFADEFLNHALFESIKRKLPLNWDAPFKL 60  
DB 29 EESSTIENYASRPEAFTPTPLNIDKRSAPFADEFLNHALFESIKRKLPLNWDAPFKL 88  
QY 61 KGLRSATPDQ 71  
DB 89 KGLRSATPDQ 99  
RESULT 2  
AAY66681  
ID AAY66681 standard; protein; 99 AA.  
XX  
XX AAY66681;  
XX AC  
XX DT 05-APR-2000 (first entry)  
XX DE Membrane-bound protein PRO826.  
XX

KM Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KM pharmacological; receptor immunoadhesin; gene mapping.  
XX Homo sapiens.  
XX OS  
XX NCBI:30963088-A2.  
XX PD  
XX 09-DEC-1999.  
XX  
XX 02-JUN-1999;  
XX  
XX 02-JUN-1998; 98US-0087607.  
XX 02-JUN-1998; 98US-0087609.  
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XX 03-JUN-1998; 98US-0087827.  
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XX 09-JUN-1998; 98US-0088655.  
XX 10-JUN-1998; 98US-0088722.  
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XX 12-JUN-1998; 98US-0089090.  
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XX 24-JUN-1998; 98US-0090535.

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PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
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PR 30-JUL-1998; 98US-0094651.
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PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
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PR 12-AUG-1998; 98US-0096329.
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PR 18-AUG-1998; 98US-0096950.
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PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 31-AUG-1998; 98US-0098014.
PR 16-SEP-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.

PR 12-JAN-1999; 99US-0115565.
PR (GETH ) GENENTECH INC.
PR Baker K, Chen Y, Goddard A, Gurney AL, Smith V, Watanabe CK,
PR Wood WJ, Yuan Y;
PR WPI; 2000-072883/06.
PR N-PSDB; AA265018.
PR Membrane-bound proteins and related nucleotide sequences -
PR claim 12; Fig 129; 822pp; English.
PR The invention provides membrane-bound PRO polypeptides and
PR polynucleotides encoding them. The PRO sequences of the invention were
PR identified based on extracellular domain homology screening. The PRO
PR sequences have homology with proteins including LDL receptors, TIR
PR ligands and various enzymes. The membrane-bound proteins and receptor
PR molecules are useful as pharmaceutical and diagnostic agents. Receptor
PR immunoadhesins, for instance, can be used as therapeutic agents to block
PR receptor-ligand interactions. The membrane-bound proteins can also be
PR employed for screening of potential peptide or small molecule inhibitors
PR of the relevant receptor/ligand interaction. The PRO encoding sequences
PR are useful as hybridization probes, in chromosome and gene mapping and in
PR the generation of antisense RNA and DNA. PRO nucleic acid sequences
PR will also be useful for the preparation of PRO polypeptides, especially
PR by recombinant techniques.
PR Sequence 99 AA:
PR
PR Query Match 100.0%; Score 375; DB 21; Length 99;
PR Best Local Similarity 100.0%; Pred. No. 5.1e-41;
PR Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR
PR QY 1 EESTIENYASRPAPFNPPINIDIKRSAPFADEFLMNAHAFESIKRCLPLINDAPKXL 60
PR |||||
PR Db 29 EESTIENYASRPAPFNPPINIDIKRSAPFADEFLMNAHAFESIKRCLPLINDAPKXL 88
PR |||||
PR QY 61 KGLRSATPDQAQ 71
PR |||||
PR Db 89 KGLRSATPDQAQ 99
PR |||||

RESULT 3
AAB20117
ID AAB20117 standard; Protein; 99 AA.
XX
AC AAB20117;
XX
DT 30-APR-2001 (first entry)
XX
DE Human immunostimulant PRO826.
XX
KW PRO826; UNQ467; human; immune disease; autoimmune disease;
KW antitumor; antitumor; antitumor; antitumor; antitumor;
KW immunosuppressive; antidiabetic; antidiabetic; antidiabetic;
KW hepatocellular; vitruce; dermatological; antiproliferative;
KW antiaesthetic; antiallergic; immunostimulant.
XX
OS Homo sapiens.
XX
FH Key
FH Peptide 1..22
FT /label= signal_peptide
FT Protein 23..99
FT /label= Mature_protein
FT Modified-site 22..28
FT /note= "N-myristoylation site"
FT Modified-site 90..96
FT /note= "N-myristoylation site"
FT Region 16..48
FT /note= "homology to peroxidase"

```

XX WO200105972-A1.  
 PN  
 XX  
 PD 25-JAN-2001.  
 XX  
 XX 15-MAR-2000; 2000WO-US06884.  
 PR 20-JUL-1999; 99US-0144758.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL,  
 PI Halian KU, Mark MR, Marceters SA, Pitli RM, Tumas D, Watanabe CK,  
 PI Wood WI;  
 XX  
 DR WPI; 2001-103149/11.  
 DR N-PSDB; AAF30059.  
 XX  
 PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
 PT diagnosing and treating immune-related disorders, such as multiple  
 PT sclerosis, rheumatoid arthritis and diabetes -  
 XX  
 PS Claim 20; Fig 20; 127pp; English.  
 XX  
 CC The present sequence is that of novel human immunomodulator PRO826  
 CC (UNQ467), as deduced from cDNA (see AAF30059) isolated from a  
 CC database screening. PRO826 has a mol.wt. of 11 kDa and a pI of  
 CC 7.47. The invention provides polynucleotides (see AAF30050-62)  
 CC encoding novel human PRO proteins (see AAB20108-20) including PRO826.  
 CC Claimed compositions comprising these proteins or their agonists  
 CC are useful for increasing infiltration of inflammatory cells into  
 CC a tissue of a mammal, stimulating or enhancing an immune  
 CC response, or increasing the proliferation of T-lymphocytes in a  
 CC mammal in response to an antigen. Claimed compositions comprising  
 CC a PRO polypeptide or its antagonist have the opposite effect. A  
 CC claimed method for treating an immune related disorder, such as a T  
 CC cell disorder, involves administering a PRO polypeptide, an agonist  
 CC antibody or an antagonist antibody. The disorder is selected from  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, spondyloarthritis, systemic sclerosis,  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated  
 CC renal disease, demyelinated diseases (such as multiple sclerosis),  
 CC autoimmune chronic active hepatitis, primary biliary cirrhosis,  
 CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel  
 CC disease (ulcerative colitis and Crohn's disease), gluten-sensitive  
 CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases  
 CC (such as bullous skin disease, erythema multiforme and psoriasis),  
 CC allergic diseases (such as asthma, allergic rhinitis, atopic  
 CC dermatitis, food hypersensitivity and urticaria), immunologic  
 CC diseases of the lung and transplantation associated diseases (such  
 CC as graft rejection and graft-versus-host disease) (all claimed).  
 CC Claimed methods of diagnosing these disorders comprise detecting  
 CC the level of expression of the PRO gene. Also claimed are a method  
 CC of identifying a compound capable of inhibiting the expression or  
 CC activity of the PRO polypeptide, vectors, host cells, antibodies,  
 CC and a method of stimulating the proliferation of T lymphocytes  
 CC using PRO826.  
 XX  
 SQ Sequence 99 AA;  
 Query Match 100.0%; Score 375; DB 22; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 5,1e-41;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
 AAB65204  
 ID AAB65204 standard; Protein; 99 AA.  
 XX  
 XX AC AAB65204;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Human PRO826 (UNQ467) protein sequence SEQ ID NO:201.  
 XX  
 XX Human; secreted and transmembrane protein; PRO; cytosolic;  
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
 KM diagnostic assay.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200073454-A1.  
 XX  
 PD 07-DEC-2000.  
 XX  
 PR 30-MAR-2000; 2000WO-US08439.  
 XX  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 07-JUL-1999; 99US-0143048.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 17-AUG-1999; 99US-0149396.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 08-OCT-1999; 99US-0158663.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03555.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04341.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Garber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi CU, Gurney AL, Kijavits ID, Napier MA, Pan U, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX  
 DR WPI; 2001-032160/04.  
 DR N-PSDB; AAF44164.  
 XX  
 PT PRO polynucleotides used to produce polypeptides used to target  
 PT bioactive molecules such as toxins, radiolabels or antibodies, to  
 PT specific cells, to cause targeted cell death -  
 XX  
 PS Claim 12; Fig 129; 935pp; English.  
 XX  
 CC The present invention describes human secreted and transmembrane PRO  
 CC proteins. The PRO proteins have cytotoxic activity. The PRO proteins  
 CC can be used for targeted delivery of bioactive molecules, such as  
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
 CC and DNA. They may also be used to produce transgenic animals which are

used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAF65154 to AAF65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

Sequence 99 AA:

Query Match 100.0%; Score 375; DB 22; Length 99;  
Best Local Similarity 100.0%; Pred. No. 5.1e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 60  
DB 29 EESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 88  
QY 61 KGLRSATPDQ 71  
DB 89 KGLRSATPDQ 99

RESULT 5  
AAB50916  
ID AAB50916 standard; Protein; 99 AA.

XX AAB50916;

DT 21-MAR-2001 (first entry)

XX Human PRO826 protein.

XX Human; PRO; antiinflammatory; dermatological; antiarthritic;  
XX antiinflammatory; cardiac; antianaemic; immunosuppressive; antithyroid;  
XX antidiabetic; neurotrophic; hepatotropic; virucide;  
XX antiallergic; antiasthmatic; immune related disorder;  
XX hepatobiliary disease; autoimmune disease; allergy.

XX Homo sapiens.

XX WO200073452-A2.

XX 07-DEC-2000.

PF 02-JUN-2000; 2000WO-US15264.

XX 02-JUN-1999; 99WO-US12252.

XX 20-JUL-1999; 99US-0144732.

XX 20-JUL-1999; 99US-0144758.

XX 28-JUL-1999; 99US-0146222.

XX 01-SEP-1999; 99WO-US20111.

XX 15-SEP-1999; 99WO-US21030.

XX 23-OCT-1999; 99WO-US21547.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1999; 99WO-US28634.

XX 09-DEC-1999; 99US-0170262.

XX 20-DEC-1999; 99WO-US30911.

XX 05-JAN-2000; 2000WO-US00219.

XX 06-JAN-2000; 2000WO-US00376.

XX 11-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 18-FEB-2000; 2000WO-US04342.

XX 24-FEB-2000; 2000WO-US04414.

XX 15-MAR-2000; 2000WO-US06884.

XX 20-MAR-2000; 2000WO-US07377.

XX 21-MAR-2000; 2000WO-US07532.

XX 17-MAR-2000; 2000WO-US08439.

XX 22-MAY-2000; 2000WO-US13705.

XX 22-MAY-2000; 2000WO-US14042.

PA (GENTH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;

PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tunas D, Watanabe CK;

PI Wood WI;

XX WPI, 2001-025253/03.

DR N-PSDB; AAC91475.

XX Thirty three nucleic acids encoding PRO polypeptides which are useful

PT in the diagnosis and treatment of immune related disorders, e.g.

PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

PT thyroiditis and diabetes mellitus -

XX Claim 58; Fig 30; 218pp; English.

The present sequence is one of thirty three novel PRO polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems (such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such as infectious, autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis), inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases (such as bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis), allergic diseases such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria), immunological diseases of the lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis), transplantation associated diseases including graft rejection and graft-versus-host diseases.

XX Sequence 99 AA;

Query Match 100.0%; Score 375; DB 22; Length 99;  
Best Local Similarity 100.0%; Pred. No. 5.1e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 60  
DB 29 EESTIENYASRPEAFNTPLNIDKLSAFKADFLNWHALFESIKRKLPLNWDAPPKL 88  
QY 61 KGLRSATPDQ 71  
DB 89 KGLRSATPDQ 99

RESULT 6

ID AAB53094 standard; Protein; 99 AA.

XX AAB53094;

DT 28-FEB-2001 (first entry)

XX Human angiogenesis-associated protein PRO826, SEQ ID NO:158.

XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;

XX cardiac hypertrophy; cardiovascular disorder; endothelial disorder;

XX angiogenic disorder; atherosclerosis; osteoporosis; hypertension;

XX myocardial infarction; diabetic retinopathy; rheumatoid arthritis;

XX Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;

XX Alzheimer's disease; Huntington's disease; stroke; drug screening;

XX gene therapy; transgenic animal.

XX Homo sapiens.



XX WO200053753-A2.  
 XX 14-SEP-2000.  
 XX 05-JAN-2000; 2000WO-US00219.  
 XX 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 XX (GERTH ) GENENTECH INC.  
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
 PI Gdowolski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
 PI Paoni NF, Pletti RM, Watanabe CK, Williams PM, Wood WI;  
 XX WPI; 2001-090793/10.  
 DR N-PSDB; AAC97491.  
 XX New isolated nucleic acid for producing a PRO polypeptide, analyzing  
 PT genetic disorders and treating cardiovascular, endothelial or  
 PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
 XX  
 XX Claim 69; Fig 62; 293pp; English.  
 CC The invention relates to novel human angiogenesis-associated proteins  
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
 CC PRO proteins. The invention also relates to vectors and host cells  
 CC comprising a PRO nucleic acid, the recombinant production of a PRO  
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
 CC compounds which inhibit the expression of a PRO gene. The invention  
 CC additionally encompasses methods of identifying modulators of PRO  
 CC expression or activity; diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
 CC mutations in a PRO gene, or the expression level of a PRO gene within a  
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
 CC administration of a PRO protein, or an agonist or antagonist thereof.  
 CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
 CC agonists and PRO antagonists may be used as therapeutic agents to treat  
 CC cardiovascular, endothelial or angiogenic disorders, such as  
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
 CC disease, or stroke. PRO nucleic acids are additionally useful in the  
 CC recombinant production of PRO proteins, as hybridisation probes to  
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
 CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
 CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
 CC animals useful for the development and screening of potential  
 CC therapeutic agents. The present sequence represents a PRO protein of the  
 CC invention.

Query Match 100.0%; Score 375; DB 22; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 5, 1e-41;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EEESTIENYASRPEAETPPLNIDKLSAFKADFLNWHALFESIRKLPFLNWDAPPKL 60  
 DB 29 EEESTIENYASRPEAETPPLNIDKLSAFKADFLNWHALFESIRKLPFLNWDAPPKL 88  
 QY 61 KGLRSATPDQ 71  
 DB 89 KGLRSATPDQ 99  
 RESULT 7  
 ID ABP69586 standard; Protein; 99 AA.  
 XX  
 AC ABP69586;  
 XX  
 DT 20-JAN-2003 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 1633.  
 XX  
 KW Human; genome mapping; gene therapy; food supplement; virus; fungus;  
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;  
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;  
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
 KW arthritis; cytostatic; immunomodulator; noctropic; neuroprotective;  
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
 KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
 KW antithrombotic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200270539-A2.  
 XX 12-SEP-2002.  
 PD  
 XX  
 PF 05-MAR-2002; 2002WO-US05095.  
 XX  
 PR 05-MAR-2001; 2001US-0799451.  
 XX  
 PA (HYSE-) HYSBQ INC.  
 XX  
 PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
 PI Wehrman T, Wang J, Wang D, Drmanac RT;  
 XX WPI; 2002-759812/82.  
 DR N-PSDB; AB211803.  
 XX  
 PT New polynucleotides comprising sequences assembled from expressed  
 PT sequence tags (ESTs), useful for treating cell-proliferative,  
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or  
 PT platelet or coagulation disorders -  
 XX  
 XX Claim 9; SEQ ID NO 1633; 1012pp + Sequence Listing; English.  
 CC The invention relates to an isolated polynucleotide (I) comprising a  
 CC nucleotide sequence selected from any of 948 sequences  
 CC (AB21113-AB212066) or their mature protein coding portion, active domain  
 CC coding protein or complementary sequences. The polynucleotides are useful  
 CC for identifying expressed genes or for physical mapping of human genome.  
 CC The encoded polypeptides (ABP68902-ABP69849) are useful as molecular  
 CC weight markers, as a food supplement, for generating antibodies, in  
 CC medical imaging, screening and diagnostic assays and for treating  
 CC cell-proliferative disorders (cancer), neurodegenerative diseases  
 CC (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple  
 CC sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid  
 CC disorders, platelet or coagulation disorders, wound, burns, incision,  
 CC ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,  
 CC parasitic), arthritis, etc.  
 CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPD  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 99 AA;

Query Match 100.0%; Score 375; DB 23; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-41;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPAFNTPLINIDKLSAFKADFLNMWALFESIKRKLPLNMDAPFKL 60  
 DB 29 EESTIENYASRPAFNTPLINIDKLSAFKADFLNMWALFESIKRKLPLNMDAPFKL 88  
 QY 61 KGLRSATPDAQ 71  
 DB 89 KGLRSATPDAQ 99

RESULT 8

AB95488 standard; Protein; 99 AA.

XX ABB95488;

DT 19-JUL-2002 (first entry)

DE Human angiogenesis related protein PRO826 SEQ ID NO: 132.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiac; cytoskeletal; antiangiogenic; hypotensive; vulnary;  
 KW antiarteriosclerotic.

XX Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.  
 XX 25-JUL-2000; 2000US-220624P.  
 XX 28-JUL-2000; 2000US-220664P.  
 XX 02-AUG-2000; 2000WO-US20710.

XX 17-AUG-2000; 2000US-0643657.

XX 23-AUG-2000; 2000WO-US23522.

XX 07-SEP-2000; 2000US-230978P.

XX 15-SEP-2000; 2000US-000000P.

XX 18-SEP-2000; 2000US-0664610.

XX 18-SEP-2000; 2000US-0665350.

XX 24-OCT-2000; 2000US-242922P.

XX 08-NOV-2000; 2000US-0709238.

XX 08-NOV-2000; 2000WO-US30952.

XX 10-NOV-2000; 2000WO-US30873.

XX 01-DEC-2000; 2000WO-US32678.

XX 20-DEC-2000; 2000WO-US34956.

XX 22-JAN-2001; 2001US-0767609.

XX 28-FEB-2001; 2001US-0796498.

XX 01-FEB-2001; 2001WO-US06520.

XX 09-MAR-2001; 2001US-0802706.

XX 14-MAR-2001; 2001US-0808689.

XX 22-MAR-2001; 2001US-0816744.

XX 05-APR-2001; 2001US-0828366.

XX 10-MAY-2001; 2001US-0854208.

XX 10-MAY-2001; 2001US-0854280.

XX 25-MAY-2001; 2001US-0866028.

XX 25-MAY-2001; 2001US-0866034.

XX 25-MAY-2001; 2001WO-US17092.

PR 30-MAY-2001; 2001US-0870574.  
 PR 30-MAY-2001; 2001WO-US17443.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 28-JUN-2001; 2001WO-US00000.

XX (GETH ) GENENTECH INC.

PA (BAKE) BAKER K P.

PA (FER) FERRARA N.

PA (GERB) GERBER H.

PA (GERR) GERITSEN M E.

PA (GODD) GODDARD A.

PA (GODO) GODOWSKI P J.

PA (GURN) GURNEY A L.

PA (HILL) HILLAN K J.

PA (MARS) MARSTERS S A.

PA (PANJ) PAN J.

PA (PAON) PAONI N F.

PA (STEP) STEPHAN J F.

PA (WATA) WATANABE C K.

PA (WILL) WILLIAMS P M.

PA (WOOD) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Geritsen ME, Goddard A,

PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,

PI Stephen JF, Watanabe CK, Williams PM, Wood WI, Ye W,

XX WPI; 2002-171999/22.

DR N-PSDB; ABL95626.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial

PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 11; Fig 132; 567pp; English.

XX The present invention provides the protein and coding sequences of human

CC PRO proteins. These are useful for treating or diagnosing a

CC cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

CC angina, myocardial infarction, thrombolytic, lymphangitis, tumour

CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound

CC healing. The present sequence is a PRO protein of the invention.

XX SQ Sequence 99 AA;

Query Match 100.0%; Score 375; DB 23; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-41;  
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPAFNTPLINIDKLSAFKADFLNMWALFESIKRKLPLNMDAPFKL 60  
 DB 29 EESTIENYASRPAFNTPLINIDKLSAFKADFLNMWALFESIKRKLPLNMDAPFKL 88  
 QY 61 KGLRSATPDAQ 71  
 DB 89 KGLRSATPDAQ 99

RESULT 9

ABG34040 standard; Protein; 99 AA.

XX ABG34040;

XX 15-JUL-2002 (first entry)

XX Human pro peptide #11.

XX Human; PRO; secreted protein; transmembrane protein;

XX genetic disorder; tumour; cancer.

OS Homo sapiens.  
XX  
XX WO20022488-A2.  
XX  
PD 28-MAR-2002.  
XX  
XX 29-AUG-2001; 2001WO-US27099.  
XX  
PR 01-SEP-2000; 2000US-229896P.  
PR 05-SEP-2000; 2000US-230621P.  
PR 22-SEP-2000; 2000US-235147P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 12-JAN-2001; 2001US-261878P.  
PR 16-JAN-2001; 2001US-261910P.  
PR 16-JAN-2001; 2001US-261939P.  
PR 16-JAN-2001; 2001US-262150P.  
PR 25-JAN-2001; 2001US-264395P.  
PR 02-FEB-2001; 2001US-266421P.  
PR 09-FEB-2001; 2001US-267623P.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 09-MAR-2001; 2001US-274399P.  
PR 03-APR-2001; 2001US-280982P.  
PR 04-APR-2001; 2001US-282129P.  
PR 09-MAY-2001; 2001US-290589P.  
PR 25-MAY-2001; 2001WO-US17800.  
PR 01-JUN-2001; 2001WO-US19692.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Baton DU, Filvaroff E, Goddard A, Grimaldi JC;  
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;  
PI Fong S;  
XX  
XX WPI; 2002-362426/39.  
XX  
XX N-PSDB; ABK69971.  
XX  
PT New PRO polypeptides and polynucleotides encoding the polypeptides,  
PT useful in gene therapy chromosome identification, tissue typing, or  
PT for genetic analysis of individuals with genetic disorders -  
XX  
XX Claim 11; Figure 22; 218pp; English.  
XX  
XX This invention relates to the cDNA and protein sequences of novel  
XX secreted and transmembrane polypeptides PRO polypeptides. The  
XX invention also comprises a method for producing the proteins of the  
XX invention by recombinant means and antibodies specific for the PRO  
XX of the invention. The antibody may be used for detecting the PRO  
XX proteins of the invention and may be used to modify their activity.  
XX polynucleotides may be used as hybridisation probes for a cDNA library  
XX to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
XX construct hybridisation probes for mapping the gene which encodes that  
XX PRO and for genetic analysis of individuals with genetic disorders. In  
XX assays to identify other proteins or molecules involved in binding  
XX reaction, to generate transgenic animals or knock-out animals which in  
XX turn are useful in the development and screening of therapeutically  
XX useful reagents, for chromosome identification, and as molecular weight  
XX PRO polypeptides are useful in gene therapy, and as molecular weight  
XX markers for protein electrophoresis purposes. The sequences may  
XX also be used to detect overexpression on PRO polypeptides in cancerous  
XX tumours and for screening for differentially expressed genes using  
XX microarray technology. The present sequence represents a human PRO  
XX protein of the invention.  
XX  
SQ Sequence 99 AA;  
XX  
Query Match 100.0%; Score 375; DB 23; Length 99;  
Best Local Similarity 100.0%; Pred. No. 5.1e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPEAFNTPEFLNIDKLSAFKADFLNWHALFESTIKRKLPFLNMDAPFYL 60  
DB 29 EESTIENYASRPEAFNTPEFLNIDKLSAFKADFLNWHALFESTIKRKLPFLNMDAPFYL 88  
QY 61 KGLRSATPDQAQ 71  
DB 89 KGLRSATPDQAQ 99  
RESULT 10  
ID ABB84882  
ID ABB84882 standard; Protein; 99 AA.  
XX  
XX ABB84882;  
AC XX  
DT 16-MAY-2002 (first entry)  
XX  
XX Human PRO826 protein sequence SEQ ID NO:132.  
XX  
XX Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;  
XX vlnuery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
XX age-related macular degeneration; arterial restenosis; angina;  
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
XX wound healing; chromosome mapping; gene mapping.  
XX  
XX Homo sapiens.  
XX  
XX WO200200690-A2.  
XX  
XX 03-JAN-2002.  
XX  
XX 20-JUN-2001; 2001WO-US19692.  
XX  
XX 23-JUN-2000; 2000US-213637P.  
XX 20-JUL-2000; 2000US-219566P.  
XX 25-JUL-2000; 2000US-220624P.  
XX 25-JUL-2000; 2000US-220664P.  
XX 28-JUL-2000; 2000WO-US20710.  
XX 02-AUG-2000; 2000US-222695P.  
XX 17-AUG-2000; 2000US-0643657.  
XX 23-AUG-2000; 2000WO-US23522.  
XX 24-AUG-2000; 2000WO-US23328.  
XX 07-SEP-2000; 2000US-230978P.  
XX 18-SEP-2000; 2000US-0664610.  
XX 24-OCT-2000; 2000US-242922P.  
XX 08-NOV-2000; 2000US-0709238.  
XX 10-NOV-2000; 2000WO-US30932.  
XX 01-DEC-2000; 2000WO-US32678.  
XX 20-DEC-2000; 2000US-0747259.  
XX 20-DEC-2000; 2000WO-US34956.  
XX 22-JAN-2001; 2001US-0767609.  
XX 28-FEB-2001; 2001US-0796498.  
XX 28-FEB-2001; 2001WO-US06520.  
XX 01-MAR-2001; 2001WO-US06666.  
XX 09-MAR-2001; 2001US-0802706.  
XX 14-MAR-2001; 2001US-0808689.  
XX 22-MAR-2001; 2001US-0816744.  
XX 05-APR-2001; 2001US-0828366.  
XX 10-MAY-2001; 2001US-0854208.  
XX 10-MAY-2001; 2001US-0854280.  
XX 25-MAY-2001; 2001US-0866028.  
XX 25-MAY-2001; 2001US-0866034.  
XX 25-MAY-2001; 2001WO-US17802.  
XX 30-MAY-2001; 2001US-0870574.  
XX 30-MAY-2001; 2001WO-US17443.  
XX 01-JUN-2001; 2001WO-US17800.  
XX  
XX (GETH ) GENENTECH INC.

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XX Baker KP, Ferrara N, Garber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Hillen KJ, Marsters SA, Pan U, Paoni NF,
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX WPI; 2002-090516/12.
DR N-PSDB; ABL88137.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 11; Fig 132; 565bp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABL884817 to
XX ABL885003. The PRO proteins and polynucleotides have cardiant, cyostatic,
XX antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX a cardiovascular, endothelial or angiogenic disorder in a mammal,
XX e.g. cardiac hypertrophy, trauma, cancer, age-related macular
XX degeneration, atherosclerosis, hypertension, arterial restenosis,
XX rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
XX lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
XX carcinoma) and wound healing. The PRO polynucleotides have applications
XX in molecular biology, including use as hybridisation probes, and in
XX chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
XX probes used in the exemplification of the present invention.
XX
XX Sequence 99 AA;
XX
XX Query Match 100.0%; Score 375; DB 23; Length 99;
XX Best Local Similarity 100.0%; Pred. No. 5.1e-41;
XX Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EESTIENYASRPEAFNTPFLNIDKLSAFKADDEFINWALFESIKRKLPLNWDAPFKL 60
XX DB 29 EESTIENYASRPEAFNTPFLNIDKLSAFKADDEFINWALFESIKRKLPLNWDAPFKL 88
XX QY 61 KGLRSATPDAQ 71
XX DB 89 KGLRSATPDAQ 99
XX
XX RESULT 11
XX AAU83664 standard; Protein; 99 AA.
XX
XX AC AAU83664;
XX
XX DT 08-MAY-2002 (first entry)
XX
XX DE Human PRO protein, Seq ID No 146.
XX
XX KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
XX breast cancer; prostate tumour; rectal tumour; liver tumour;
XX pericyte cell proliferation; chondrocyte cell proliferation;
XX tumour necrosis factor-alpha.
XX
XX OS Homo sapiens.
XX
XX PN WO200208288-A2.
XX
XX PD 31-JAN-2002.
XX
XX PF 29-JUN-2001; 2001WO-US21066.
XX
XX PR 20-JUL-2000; 2000US-219556P.
XX PR 25-JUL-2000; 2000US-220585P.
XX PR 25-JUL-2000; 2000US-220605P.
XX PR 25-JUL-2000; 2000US-220607P.
XX PR 25-JUL-2000; 2000US-220624P.
XX PR 25-JUL-2000; 2000US-220638P.

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PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.
PR 28-JUL-2000; 2000WO-US20710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US065520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-172001/22.
XX DR N-PSDB; ABL33608.
XX
XX PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for treating a PRO related disorder and for diagnosing tumours
XX such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
XX tumour or liver tumour -
XX
XX PS Claim 11; Figure 146; 359bp; English.
XX
XX CC The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumours, especially lung
XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
XX liver tumour. The PRO polypeptides are useful for stimulating the
XX proliferation of, or gene expression, in pericyte cells, for stimulating
XX the proliferation or differentiation of chondrocyte cells, for
XX stimulating the release of tumour necrosis factor-alpha from human blood,
XX for stimulating or inhibiting the proliferation of normal human dermal
XX fibroblast cells. The PRO polypeptide may also be used as molecular
XX weight markers and for tissue typing. The PRO nucleic acids have
XX applications in molecular biology, including use as hybridisation probes,
XX and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
XX protein sequences of the invention.
XX
XX SQ Sequence 99 AA;
XX
XX Query Match 100.0%; Score 375; DB 23; Length 99;
XX Best Local Similarity 100.0%; Pred. No. 5.1e-41;
XX Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EESTIENYASRPEAFNTPFLNIDKLSAFKADDEFINWALFESIKRKLPLNWDAPFKL 60
XX DB 29 EESTIENYASRPEAFNTPFLNIDKLSAFKADDEFINWALFESIKRKLPLNWDAPFKL 88
XX QY 61 KGLRSATPDAQ 71
XX DB 89 KGLRSATPDAQ 99
XX
XX RESULT 12
XX AAU81964 standard; Protein; 99 AA.
XX
XX AC AAU81964;
XX
XX DT 09-APR-2002 (first entry)
XX
XX DE Human PRO826.
XX

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|    |             |                 |
|----|-------------|-----------------|
| PR | 30-MAR-2000 | 2000MO-US04439. |
| PR | 15-MAY-2000 | 2000MO-US13358. |
| PR | 17-MAY-2000 | 2000MO-US13705. |
| PR | 22-MAY-2000 | 2000MO-US14042. |
| PR | 30-MAY-2000 | 2000MO-US14941. |
| PR | 02-JUN-2000 | 2000MO-US15264. |
| PR | 28-JUL-2000 | 2000MO-US20710. |
| PR | 11-AUG-2000 | 2000MO-US22031. |
| PR | 23-AUG-2000 | 2000MO-US23522. |
| PR | 24-AUG-2000 | 2000MO-US23328. |
| PR | 08-NOV-2000 | 2000MO-US30952. |
| PR | 01-DEC-2000 | 2000MO-US32678. |
| PR | 28-FEB-2001 | 2001MO-US06520. |
| PR | 01-JUN-2001 | 2001MO-US17800. |
| PR | 20-JUN-2001 | 2001MO-US19692. |
| PR | 29-JUN-2001 | 2001MO-US21066. |
| PR | 09-JUL-2001 | 2001MO-US21735. |
| PR | 16-JUN-1997 | 97US-049787P.   |
| PR | 17-OCT-1997 | 97US-062250P.   |
| PR | 12-NOV-1997 | 97US-065186P.   |
| PR | 13-NOV-1997 | 97US-065311P.   |
| PR | 24-NOV-1997 | 97US-066770P.   |
| PR | 25-FEB-1998 | 98US-075945P.   |
| PR | 20-MAR-1998 | 98US-078910P.   |
| PR | 28-APR-1998 | 98US-083322P.   |
| PR | 07-MAY-1998 | 98US-084600P.   |
| PR | 28-MAY-1998 | 98US-087106P.   |
| PR | 02-JUN-1998 | 98US-087607P.   |
| PR | 02-JUN-1998 | 98US-087609P.   |
| PR | 02-JUN-1998 | 98US-087759P.   |
| PR | 03-JUN-1998 | 98US-087827P.   |
| PR | 04-JUN-1998 | 98US-088021P.   |
| PR | 04-JUN-1998 | 98US-088025P.   |
| PR | 04-JUN-1998 | 98US-088026P.   |
| PR | 04-JUN-1998 | 98US-088028P.   |
| PR | 04-JUN-1998 | 98US-088029P.   |
| PR | 04-JUN-1998 | 98US-088030P.   |
| PR | 04-JUN-1998 | 98US-088033P.   |
| PR | 04-JUN-1998 | 98US-088326P.   |
| PR | 05-JUN-1998 | 98US-088167P.   |
| PR | 05-JUN-1998 | 98US-088202P.   |
| PR | 05-JUN-1998 | 98US-088212P.   |
| PR | 05-JUN-1998 | 98US-088217P.   |
| PR | 09-JUN-1998 | 98US-088655P.   |
| PR | 09-JUN-1998 | 98US-088734P.   |
| PR | 10-JUN-1998 | 98US-088738P.   |
| PR | 10-JUN-1998 | 98US-088742P.   |
| PR | 10-JUN-1998 | 98US-088810P.   |
| PR | 10-JUN-1998 | 98US-088824P.   |
| PR | 10-JUN-1998 | 98US-088826P.   |
| PR | 11-JUN-1998 | 98US-088858P.   |
| PR | 11-JUN-1998 | 98US-088861P.   |
| PR | 11-JUN-1998 | 98US-088876P.   |
| PR | 12-JUN-1998 | 98US-089105P.   |
| PR | 16-JUN-1998 | 98US-089440P.   |
| PR | 16-JUN-1998 | 98US-089512P.   |
| PR | 16-JUN-1998 | 98US-089514P.   |
| PR | 17-JUN-1998 | 98US-089532P.   |
| PR | 17-JUN-1998 | 98US-089538P.   |
| PR | 17-JUN-1998 | 98US-089548P.   |
| PR | 17-JUN-1998 | 98US-089599P.   |
| PR | 17-JUN-1998 | 98US-089600P.   |
| PR | 17-JUN-1998 | 98US-089653P.   |
| PR | 18-JUN-1998 | 98US-089801P.   |
| PR | 18-JUN-1998 | 98US-089907P.   |
| PR | 18-JUN-1998 | 98US-089908P.   |
| PR | 28-AUG-2001 | 2001US-094199Z. |

PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Garber H, Gerritsen ME, Goddard A, Godowski P;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;

PI ROY MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WJ;  
PI Zhang Z;  
XX  
XX  
DR N-PSDB; ABR80254.  
XX WPI; 2003-247083/24.  
DR N-PSDB; ABR80254.  
XX  
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1164, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer  
PT treatments -  
XX  
XX  
PS Claim 12; Fig 129; 648pp; English.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO828, PRO926, PRO1068 or PRO535, PRO826, PRO819, PRO126, PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antegenist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO829, PRO826, PRO1068 or PRO1132 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpeticiforms or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein.

**SQ Sequence 99 AA;**

|             |         |            |        |            |
|-------------|---------|------------|--------|------------|
| Query Match | 100.0%; | Score 375; | DB 24; | Length 99; |
|-------------|---------|------------|--------|------------|

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Matches      71; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
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QY 1 EEESTIENASRPEAFNTPTFLNIDKRSAFKADFLNHWALFESIIRKRPFLNWDAPFKL 60  
DB 29 EEESTIENASRPEAFNTPTFLNIDKRSAFKADFLNHWALFESIIRKRPFLNWDAPFKL 88

|    |    |             |    |
|----|----|-------------|----|
| QY | 61 | KGLRSATPDAQ | 71 |
|    |    |             |    |
| Db | 89 | KGLRSATPDAQ | 99 |

## RESULT 14

ID ABU59244 standard; Protein; 99 AA

AC ABU59244;

DT 22-APR-2003 (first entry)  
VV

**DE Human secreted/transmembrane protein, #78.**

KM Human;PRO; secreted; transmembrane; pharmaceutical;  
 KM diagnostic; biosensor; bioreactor; tumour; therapeutic;  
 KM gene therapy; tumour-associated antigenic target; TAT; ADPRT;  
 KM antibody-dependent enzyme mediated prodrug therapy; cytostatic.  
 XX

OS Homo sapiens.  
XX US2003027162-A1.  
XX  
PD 06-FEB-2003.  
XX  
PF 15-NOV-2001; 2001US-0997428.  
XX  
PR 05-NOV-1997; 97WO-US20069.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
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PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUN-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
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PR 16-JUN-1998; 98US-089440P.  
PR 16-JUN-1998; 98US-089512P.  
PR 16-JUN-1998; 98US-089514P.  
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PR 17-JUN-1998; 98US-089600P.  
PR 17-JUN-1998; 98US-089601P.  
PR 18-JUN-1998; 98US-089907P.  
PR 18-JUN-1998; 98US-089908P.  
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PR 19-JUN-1998; 98US-089952P.  
PR 22-JUN-1998; 98US-090246P.  
PR 22-JUN-1998; 98US-090252P.  
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PR 23-JUN-1998; 98US-090349P.  
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RESULT 15

ABUS9393 standard; Protein; 99 AA.

AC ABUS9393;  
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DT 22-APR-2003 (first entry)

DE Novel human secreted or transmembrane protein PRO819.

XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;

KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.  
XX Homo sapiens.  
XX US2003027985-A1.  
PD 06-FEB-2003.  
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PF 14-NOV-2001; 2001US-0990562.  
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GenCore version 5.1.6  
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Listing first 45 summaries

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#### ALIGNMENTS

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Sequence 201, Application US/09989722  
Patent No. US20020072067A1  
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APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Boctstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
RTE REFERENCE: P2730PIC3  
CURRENT APPLICATION NUMBER: US/09/989,722  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17



PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 9; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7,9e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EESSTENYASRPEAFNTPLNIDKLSAFKADDEFNLNHALFESTKRLPLNMDAPKRL 60  
Db 29 EESSTENYASRPEAFNTPLNIDKLSAFKADDEFNLNHALFESTKRLPLNMDAPKRL 88

Qy 61 KGLRSATPDQ 71  
Db 89 KGLRSATPDQ 99

RESULT 2  
US-09-989-723-201  
Sequence 201, Application US/09989723  
Patent No. US20020072092A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gutney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C62  
CURRENT APPLICATION NUMBER: US/09/989,723  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
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PRIOR APPLICATION NUMBER: 60/065311

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PRIOR FILING DATE: 1998-02-25  
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PRIOR FILING DATE: 1998-04-28  
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PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478

PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 9; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7.9e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTTENYASRPEANTPEINIDKLSAFKADPEINWHALESTIKRKLPIINWDAFPKL 60  
DB 29 EESTTENYASRPEANTPEINIDKLSAFKADPEINWHALESTIKRKLPIINWDAFPKL 88  
QY 61 KGLRSATPDQAQ 71  
DB 89 KGLRSATPDQAQ 99

RESULT 3  
US-09-989-279-201  
; Sequence 201, Application US/09989279  
; Patent No. US20020072496A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Guiney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C56  
; CURRENT APPLICATION NUMBER: US/09/989,279  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24

[illegible]

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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 9; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7, 9e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 KGLRSATPDAQ 71  
DB 89 KGLRSATPDAQ 99

RESULT 4  
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Sequence 201, Application US/09989727  
Patent No. US20020072497A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Iyar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zhenli  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P27301C65  
CURRENT APPLICATION NUMBER: US/09/989,727  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/045787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
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PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20  
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PRIOR APPLICATION NUMBER: 60/084600  
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PRIOR FILING DATE: 1998-07-02  
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PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626

PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 9; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7, 9e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBSSTIENVASRPAAFTPLNIDKLSAFKADEFNLWHLFESIKRKLFLWWDAPPKL 60  
Db 29 EESTIENVASRPAAFTPLNIDKLSAFKADEFNLWHLFESIKRKLFLWWDAPPKL 88

Qy 61 KGLSATPDQA 71  
Db 89 KGLSATPDQA 99

RESULT 5  
US-09-989-731-201  
Sequence 201, Application US/09989731  
Patent No. US20020103125A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Batou, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Goddard, Audrey E.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C70  
CURRENT APPLICATION NUMBER: US/09/989,731  
PRIOR FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
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PRIOR FILING DATE: 1998-02-25  
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PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28





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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 375; DB 10; Length 99;
Best Local Similarity 100.0%; Pred. No. 7,96-41;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EESSTIENVASPEAFNTPLNIDLRSAFKADEFNLNHALFESIKRKLPLNMDAPFKL 60
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RESULT 6
US-09-989-732-201
; Sequence 201, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gutney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C57
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US/09/989,732
; PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-02  
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PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09  
Query Match 100.0%; Score 375; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7,9e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 29 EESTTENYASRPEANPEFLNIDKLSAFKDEFLNWHALPESTKRKLPFLNMDAEPKL 88  
Qy 61 KGLRSATPDAQ 71  
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US-09-991-073-201  
Sequence 201, Application US/09991073  
Patent No. US20020127576A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
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APPLICANT: Goddard, Audrey  
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APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin U.  
APPLICANT: Kijavlin, Ivar J.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zenlin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730P1C15  
CURRENT APPLICATION NUMBER: US/09/991,073  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
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[illegible]

Query Match 100.0%; Score 375; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7,9e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEEETIENVSRPFAFTPTPLINIKLSAPFADDFLNMWALFESIKRKLPLFNDAPPKL 60  
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QY 61 KGLRSATPDAQ 71  
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RESULT 8  
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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C8  
CURRENT APPLICATION NUMBER: US/09/990,442  
PRIOR FILING DATE: 2001-11-14  
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Query Match 100.0%; Score 375; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7.9e-41;

Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 29 EESTIENVASRPEAFNTPLINIDKRSAPRADEFLLMWHALFESIKRKLPLINDAPFKL 88  
Qy 61 KGLRSATPDAQ 71  
Db 89 KGLRSATPDAQ 99

RESULT 9  
US-09-991-163-201  
Sequence 201, Application US/09991163  
Patent No. US20020132253A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Baton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C17  
CURRENT APPLICATION NUMBER: US/09/991.163  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7, 9e-41;  
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Qy 61 KGLRSATPDQA 71  
Db 89 KGLRSATPDQA 99

RESULT 10  
US-09-993-604-201  
Sequence 201, Application US/09993604  
Patent No. US20020137075A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Denoyers, Luc  
APPLICANT: Baton, Dan L.  
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APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, Nicholas P.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730PIC25  
CURRENT APPLICATION NUMBER: US/09/993,604  
PRIOR FILING DATE: 2001-11-14  
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PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 10; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7, 9e-41;  
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EESTIENYASRPEAFNTPTNIXKRSAPKADBEFLMWAUFESI KRLDPLFNDWAPFKL 60  
DB 29 EESTIENYASRPEAFNTPTNIXKRSAPKADBEFLMWAUFESI KRLDPLFNDWAPFKL 88

QY 61 KGLRSATPDQAQ 71  
DB 89 KGLRSATPDQAQ 99

RESULT 11  
US-09-990-456-201  
Sequence 201, Application US/09990456  
Patent No. US20020137890A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Kljavin, Ivar J.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PLC22  
CURRENT APPLICATION NUMBER: US/09/990,456  
CURRENT FILING DATE: 2001-11-14  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 10; Length 99;  
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Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 61 KGLRSATPDQAO 71  
DB 89 KGLRSATPDQAO 99

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Patent No. US20020142961A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Fong, Sherman  
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APPLICANT: Gurney, Austin L.  
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APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Tumas, Daniel  
APPLICANT: Williams, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730P1C55  
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CURRENT FILING DATE: 2001-11-19  
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Query Match 100.0%; Score 375; DB 10; Length 99;  
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;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Denoyers, Luc  
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;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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## Query Match

100.0% Score 375; DB 10; Length 99;

Best Local Similarity 100.0%; Pred. No. 7, 9e-41; Indels 0; Gaps 0;

Matches 71; Conservative 0; Mismatches 0;

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## RESULT 14

US-09-984-245-142

Sequence 142, Application US/09984245

Patent No. US20020165374A1

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GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: P2004P1
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PRIOR FILING DATE: 1997-10-02
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Db 89 KGLRSATPDQ 99

RESULT 15
US-09-989-293A-201
Sequence 201, Application us/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Getzler, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijaviri, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 375; DB 10; Length 99;

Best Local Similarity 100.0%; Pred. No. 7, 9e-41; Indels 0; Gaps 0;

Matches 71; Conservative 0; Mismatches 0;

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Db 29 EBSSTIENVASRPAFTPTPLNTDKLSARKADEFILWHALFBSIKRKLPLNWDAPKYL 88  
Qy 61 KGLRSATPDQ 71  
|||||

Sat Nov 29 17:52:41 2003

us-10-059-395-142\_copy\_29\_99.rapb

Page 23

Db 89 KGLRSATPDAQ 99

Search completed: November 28, 2003, 13:42:18  
Job time : 43 secs

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GenCore version 5.1.6  
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# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 13:43:49; Search time 217 Seconds  
(without alignments)

883.226 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 375  
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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pco -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-DEV MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
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Database : N Geneseq\_19Jun03.\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length  | DB ID        | Description         |
|------------|-------|-------------|---------|--------------|---------------------|
| 1          | 375   | 100.0       | 414     | 22 AAC91475  | Human PRO826 cDNA.  |
| 2          | 375   | 100.0       | 414     | 24 ABK28600  | Human DNAS7694-134  |
| 3          | 375   | 100.0       | 415     | 21 AAZ65018  | Membrane-bound pro  |
| 4          | 375   | 100.0       | 415     | 22 AAF30059  | Human cDNA encodin  |
| 5          | 375   | 100.0       | 415     | 22 AAF4154   | Human PRO826 (UNQ4  |
| 6          | 375   | 100.0       | 415     | 22 AAC97491  | Human angiotensin   |
| 7          | 375   | 100.0       | 415     | 24 ABK5626   | Human angiotensin   |
| 8          | 375   | 100.0       | 415     | 24 ABK69971  | cDNA encoding huma  |
| 9          | 375   | 100.0       | 415     | 24 ABK81817  | Human PRO826 cDNA   |
| 10         | 375   | 100.0       | 415     | 24 ABK33608  | cDNA encoding huma  |
| 11         | 375   | 100.0       | 415     | 25 ABK80255  | Novel human secret  |
| 12         | 375   | 100.0       | 415     | 25 ABK80759  | Novel human secret  |
| 13         | 375   | 100.0       | 415     | 25 ABK81142  | Novel human secret  |
| 14         | 375   | 100.0       | 415     | 25 ABK90232  | Human secreted/tira |
| 15         | 375   | 100.0       | 415     | 25 ABK77843  | Human PRO polynuci  |
| 16         | 375   | 100.0       | 415     | 25 ABK79439  | Human secreted/tr   |
| 17         | 375   | 100.0       | 415     | 25 ABK64078  | cDNA encoding huma  |
| 18         | 375   | 100.0       | 415     | 25 ABK17042  | Human PRO polynuci  |
| 19         | 375   | 100.0       | 428     | 24 ABZ11803  | Human polynucleoti  |
| 20         | 375   | 100.0       | 456     | 20 AAX00632  | Human secreted pro  |
| 21         | 375   | 100.0       | 518     | 22 ABA09519  | Human secreted pro  |
| 22         | 308   | 82.1        | 278     | 21 AAC68806  | Human head/neck tu  |
| 23         | 286   | 76.3        | 386     | 24 ABZ11804  | Human polynucleoti  |
| 24         | 210.5 | 56.1        | 288     | 25 ABK85674  | Corn ear-derived p  |
| 25         | 166   | 44.3        | 413     | 24 ABK5083   | Murine cDNA isolat  |
| 26         | 143   | 38.1        | 305     | 24 ABZ11886  | Human polynucleoti  |
| 27         | 82.5  | 22.0        | 530     | 21 AAC01489  | Human secreted pro  |
| 28         | 78.5  | 20.9        | 437     | 24 ABV96116  | Human pancreatic c  |
| 29         | 78.5  | 20.9        | 686     | 21 AAZ80280  | Human colon cancer  |
| 30         | 78.5  | 20.9        | 700     | 22 AAH23810  | Human transferrase  |
| 31         | 78    | 20.8        | 3525    | 23 ABZ3024   | Drosophila melanog  |
| 32         | 78    | 20.8        | 5397    | 23 ABK08196  | Drosophila melanog  |
| 33         | 69    | 18.4        | 641     | 24 ABQ39286  | Oligonucleotide fo  |
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| 35         | 69    | 18.4        | 1152    | 24 ABK67526  | Streptococcus poly  |
| 36         | 69    | 18.4        | 2155551 | 24 ABK71527  | Streptococcus poly  |
| 37         | 67.5  | 18.0        | 1830121 | 17 AAT742063 | Haemophilus influe  |
| 38         | 65.5  | 17.5        | 349     | 22 AAL00189  | Human reproductive  |
| 39         | 65.5  | 17.5        | 914     | 20 AAZ42019  | Human endometrium   |
| 40         | 65.5  | 17.5        | 1897    | 21 AAZ43803  | Human adult skin c  |
| 41         | 65    | 17.3        | 398     | 25 ABK19934  | Human GTP-nanose    |
| 42         | 65    | 17.3        | 349980  | 22 AAH41225  | Pyrococcus abyssi   |
| 43         | 64.5  | 17.2        | 352     | 21 AAC01488  | Human secreted pro  |
| 44         | 64.5  | 17.2        | 349980  | 24 ABQ81845  | Bifidobacterium lo  |
| 45         | 64    | 17.1        | 447     | 23 ABV17783  | Human prostate exp  |

## ALIGNMENTS

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ID AAC91475 standard; cDNA; 414 BP.  
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DT 21-MAR-2001 (first entry)  
XX  
DE Human PRO826 cDNA.  
KW Human, PRO; antiinflammatory; dermatological; antiarthritic;  
KW antidiabetic; cardiant; antianemic; immunosuppressive; antihypertoid;  
KW antidiabetic; nootropic; neuroprotective; hepatotropic; vituric;  
KW antiallergic; antiautomatic; immune related disorder;  
KW hepatobiliary disease; autoimmune disease; allergy; ss.  
OS Homo sapiens.

XX PN WO200073452-A2.  
 XX PD 07-DEC-2000.  
 XX PF 02-JUN-2000; 2000WO-US15284.  
 XX PR 02-JUN-1999; 99WO-US12252.  
 PR 20-JUL-1999; 99US-0144732.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 23-OCT-1999; 99WO-US21547.  
 PR 30-NOV-1999; 99US-0162506.  
 PR 01-DEC-1999; 99WO-US28313.  
 PR 09-DEC-1999; 99WO-US28634.  
 PR 20-DEC-1999; 99US-0170262.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 XX (GETH ) GENENTECH INC.  
 PA Aahkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL,  
 PI Herbert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;  
 PI Wood WI;  
 XX WPI; 2001-025253/03.  
 DR P-PSDB; AAB50916.  
 PT Thirty three nucleic acids encoding PRO polypeptides which are useful  
 in the diagnosis and treatment of immune related disorders, e.g.  
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 PT thyroiditis and diabetes mellitus -  
 XX Claim 48; Fig 29; 21bp; English.  
 PS The present sequence is one of thirty three nucleic acids encoding PRO  
 CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and  
 CC antagonists are useful for treating and diagnosing immune related  
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic chronic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic  
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic  
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases  
 CC (such as infectious, autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
 CC food hypersensitivity and urticaria), immunological diseases of the  
 CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis  
 CC and hypersensitivity pneumonitis), transplantation associated diseases  
 CC including graft rejection and graft-versus-host diseases.  
 XX Sequence 414 BP; 98 A; 126 C; 92 G; 98 T; 0 other;

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 Score: 375.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
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 QY 21 LEUANILASPLYSLEUARGSERIALAPHEYSALASPGLUPLHEUANTRPHISALA 40  
 DB 157 CTGAACATGACCAAAATGCGATCTGGTTAAAGGCTGATGAGTCTCTGAACCTGGACGCC 216  
 QY 41 LEUPHEGLUSERILEYSARGLYSLEUPROPELEUANTRPAAPALAPHEPROLYSLEU 60  
 DB 217 CTTTGGAGCTTATCAAAAGAAACTCTTCTTCTCACTGGGATGCCCTTCTTAAGCTG 276  
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 XX AC ABK28600;  
 XX DT 09-APR-2002 (first entry)  
 XX DE Human DNA57694-1341 encoding PRO826.  
 XX KW Human; ss; gene; PRO; antiinflammatory; ophthalmological; vasotropic;  
 KW retinal cell injury; ocular disease; retinitis pigmentosa;  
 KW macular degeneration; retinal detachment; retinal tear; retinopathy;  
 KW retinal degenerative disease; macular hole; degenerative myopia;  
 KW acute retinal necrosis syndrome; traumatic choriorretinopathy;  
 KW Putticher's retinopathy; Oedema; ischaemic condition;  
 KW retinal vision occlusion; collagen vascular disease;  
 KW thrombocytopaenic purpura; uveitis; retinal vasculitis; Bales disease;  
 KW systemic lupus erythematosus; environmental trauma.  
 XX OS Homo sapiens.  
 XX PN WO200109327-A2.  
 XX PD 08-FEB-2001.  
 XX PF 28-JUL-2000; 2000WO-US20710.  
 XX PR 28-JUL-1999; 99US-146222P.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 XX (GETH ) GENENTECH INC.



|    |             |              |
|----|-------------|--------------|
| PR | 24-JUN-1998 | 98US-0090444 |
| PR | 24-JUN-1998 | 98US-0090445 |
| PR | 24-JUN-1998 | 98US-0090461 |
| PR | 24-JUN-1998 | 98US-0090472 |
| PR | 24-JUN-1998 | 98US-0090533 |
| PR | 24-JUN-1998 | 98US-0090538 |
| PR | 24-JUN-1998 | 98US-0090540 |
| PR | 24-JUN-1998 | 98US-0090557 |
| PR | 25-JUN-1998 | 98US-0090675 |
| PR | 25-JUN-1998 | 98US-0090676 |
| PR | 25-JUN-1998 | 98US-0090689 |
| PR | 25-JUN-1998 | 98US-0090690 |
| PR | 25-JUN-1998 | 98US-0090691 |
| PR | 25-JUN-1998 | 98US-0090694 |
| PR | 25-JUN-1998 | 98US-0091544 |
| PR | 02-JUL-1998 | 98US-0091476 |
| PR | 02-JUL-1998 | 98US-0091487 |
| PR | 02-JUL-1998 | 98US-0091513 |
| PR | 02-JUL-1998 | 98US-0091626 |
| PR | 02-JUL-1998 | 98US-0091628 |
| PR | 02-JUL-1998 | 98US-0091633 |
| PR | 02-JUL-1998 | 98US-0091646 |
| PR | 02-JUL-1998 | 98US-0091671 |
| PR | 07-JUL-1998 | 98US-0091978 |
| PR | 07-JUL-1998 | 98US-0091982 |
| PR | 09-JUL-1998 | 98US-0092182 |
| PR | 10-JUL-1998 | 98US-0092472 |
| PR | 20-JUL-1998 | 98US-0093339 |
| PR | 30-JUL-1998 | 98US-0094651 |
| PR | 04-AUG-1998 | 98US-0095282 |
| PR | 04-AUG-1998 | 98US-0095285 |
| PR | 04-AUG-1998 | 98US-0095301 |
| PR | 04-AUG-1998 | 98US-0095302 |
| PR | 04-AUG-1998 | 98US-0095318 |
| PR | 04-AUG-1998 | 98US-0095321 |
| PR | 04-AUG-1998 | 98US-0095325 |
| PR | 10-AUG-1998 | 98US-0095916 |
| PR | 10-AUG-1998 | 98US-0095929 |
| PR | 10-AUG-1998 | 98US-0096012 |
| PR | 11-AUG-1998 | 98US-0096146 |
| PR | 11-AUG-1998 | 98US-0096147 |
| PR | 12-AUG-1998 | 98US-0096329 |
| PR | 17-AUG-1998 | 98US-0096757 |
| PR | 17-AUG-1998 | 98US-0096766 |
| PR | 17-AUG-1998 | 98US-0096768 |
| PR | 17-AUG-1998 | 98US-0096773 |
| PR | 17-AUG-1998 | 98US-0096791 |
| PR | 17-AUG-1998 | 98US-0096861 |
| PR | 17-AUG-1998 | 98US-0096891 |
| PR | 17-AUG-1998 | 98US-0096894 |
| PR | 17-AUG-1998 | 98US-0096895 |
| PR | 17-AUG-1998 | 98US-0096897 |
| PR | 18-AUG-1998 | 98US-0096949 |
| PR | 18-AUG-1998 | 98US-0096950 |
| PR | 18-AUG-1998 | 98US-0096959 |
| PR | 18-AUG-1998 | 98US-0096960 |
| PR | 18-AUG-1998 | 98US-0097022 |
| PR | 18-AUG-1998 | 98US-0097141 |
| PR | 19-AUG-1998 | 98US-0097142 |
| PR | 20-AUG-1998 | 98US-0097218 |
| PR | 20-AUG-1998 | 98US-0097661 |
| PR | 26-AUG-1998 | 98US-0097951 |
| PR | 26-AUG-1998 | 98US-0097952 |
| PR | 26-AUG-1998 | 98US-0097954 |
| PR | 26-AUG-1998 | 98US-0097955 |
| PR | 26-AUG-1998 | 98US-0097971 |
| PR | 26-AUG-1998 | 98US-0097974 |
| PR | 26-AUG-1998 | 98US-0097978 |

|  |   |   |                 |
|--|---|---|-----------------|
| PR   | 26-AUG-1998;  | 98US-0097979.   |                 |
| PR   | 26-AUG-1998;  | 98US-0097986.   |                 |
| PR   | 26-AUG-1998;  | 98US-0098014.   |                 |
| PR   | 31-AUG-1998;  | 98US-0098525.   |                 |
| PR   | 16-SEP-1998;  | 98US-0100634.   |                 |
| PR   | 12-JAN-1999;  | 99US-0115565.   |                 |
| XX   |   |   |                 |
| XX   | (GERTH ) GENENTECH INC.   |   |                 |
| PI   | Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;              |   |                 |
| PI   | Wood WJ, Yuan J;  |   |                 |
| XX   |   |   |                 |
| DR   | WPI; 2000-072883/06.  |   |                 |
| DR   | P-PSDB; AAY66681.   |   |                 |
| PT   |   |   |                 |
| XX   | Membrane-bound proteins and related nucleotide sequences                  |   |                 |
| XX   |   |   |                 |
| XX   | Claim 2; Fig 128; 822pp; English.   |   |                 |
| CC   |   |   |                 |
| CC   | The invention provides membrane-bound PRO polypeptides and                |   |                 |
| CC   | polynucleotides encoding them. The PRO sequences of the invention were    |   |                 |
| CC   | identified based on extracellular domain homology screening. The PRO      |   |                 |
| CC   | sequences have homology with proteins including LDL receptors, TIR        |   |                 |
| CC   | ligands and various enzymes. The membrane-bound proteins and receptor     |   |                 |
| CC   | molecules are useful as pharmaceutical and diagnostic agents. Receptor    |   |                 |
| CC   | immunoadhesins, for instance, can be used as therapeutic agents to block  |   |                 |
| CC   | receptor-ligand interactions. The membrane-bound proteins can also be     |   |                 |
| CC   | employed for screening of potential peptide or small molecule inhibitors  |   |                 |
| CC   | of the relevant receptor/ligand interaction. The PRO encoding sequences   |   |                 |
| CC   | are useful as hybridization probes, in chromosome and gene mapping and in |   |                 |
| CC   | the generation of antisense RNA and DNA. PRO nucleic acid sequences       |   |                 |
| CC   | will also be useful for the preparation of PRO polypeptides, especially   |   |                 |
| CC   | by recombinant techniques.  |   |                 |
| XX   |   |   |                 |
| XX   |   |   |                 |
| XX   | Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;                        |   |                 |
| SO   |   |   |                 |
|  | Alignment Scores:   |   |                 |
|  | Pred. No.:  | 7.89e-47  | Length: 415     |
|  | Score:  | 375.00  | Matches: 71     |
|  | Percent Similarity:   | 100.00%   | Conservative: 0 |
|  | Best local Similarity:  | 100.00%   | Mismatches: 0   |
|  | Query Match:  | 100.00%   | Indels: 0       |
|  | DB:   | 21  | Gaps: 0         |
| US-10-059-395-142_COPY_29_99 (1-71) x AA265018 (1-415) |   |   |                 |
| OY   | 1   | GIUGIUGUSERTHRIIEGLUASNTYRLASERARPGIUAIALPHEASNTHPRO          | 20              |
| DB   | 97  | GAGAAAGAAACACCATTTGAGAAATTATGCGTCAAGACCCGAGCCTTTAAACACCCCGTTT | 156             |
| OY   | 21  | LEUASNTLEAPPLYLEUARGSERIALPHELYSALAAPGILUPELEUASNTTPHISALA    | 40              |
| DB   | 157   | CTGAACATCCGCAATATGCGATCTGCGTTTAAAGCTGATGATTCCTGAACGACGCC      | 216             |
| OY   | 41  | LEUHEGUGUSERTILEYARGLYLEUENPROHELEUASNTTPASAPLAPHEPROLYSEU    | 60              |
| DB   | 217   | CTCTTTGATGTATCAAAAAGAACTCTTCTCTCAACTGGAGTCCCTTCTTAAGCTG       | 276             |
| OY   | 61  | LYSGLYLEUARGSERIALATHPROASPALAGIN                             | 71              |
| DB   | 277   | AAAGGACTGAGGAGCGCAACTCTCGATGCCGAG                             | 309             |
| RESULT 4   |   |   |                 |
| AAAF30059  |   |   |                 |
| ID   | AAAF30059 standard; CDNA; 415 BP.   |   |                 |
| XX   | AAAF30059;  |   |                 |
| XX   | AC  |   |                 |
| XX   | 30-APR-2001 (first entry)   |   |                 |
| XX   | Human CDNA encoding PRO826.   |   |                 |
| XX   |   |   |                 |
| XX   | PRO826; UNQ467; human; immune disease; autoimmune disease;                |   |                 |

[illegible]

|  |   |  |     |  |  |  |
|--|---|--|-----|--|--|--|
| CC   | and a method of stimulating the proliferation of T-lymphocytes        |  |     |  |  |  |
| CC   | using PRO826.   |  |     |  |  |  |
| XX   |   |  |     |  |  |  |
| SQ   | Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;                    |  |     |  |  |  |
| <hr/>  |   |  |     |  |  |  |
| Alignment Scores:                                      |   |  |     |  |  |  |
| Pred. No.:   | 7,89e-47  | Length:  | 415 |  |  |  |
| Score:   | 375.00  | Matches:   | 71  |  |  |  |
| Percent Similarity:                                    | 100.00%   | Conservative:  | 0   |  |  |  |
| Best Local Similarity:                                 | 100.00%   | Mismatches:  | 0   |  |  |  |
| Query Match:   | 100.00%   | Indels:  | 0   |  |  |  |
| DB:  | 22  | Gaps:  | 0   |  |  |  |
| <hr/>  |   |  |     |  |  |  |
| US-10-059-395-142_COPY_29_99 (1-71) x AAF30059 (1-415) |   |  |     |  |  |  |
| OY   | 1   | GLUGLUGInserThrIleGluAsnTrpAlaSerArgProGluValaphneAsnThrProPhe | 20  |  |  |  |
| Db   | 97  | GAGAAAGAAAAGCACCAATTAGAATTAATGCACGCCAAGCGGGCCTTTAACACCCCGTTC   | 156 |  |  |  |
| OY   | 21  | LeuAsnIleAspIysLeuArgSerAlaPheLYsaIAepGIupheLeuAsnTriPhIAla    | 40  |  |  |  |
| Db   | 157   | CTGAACACTGCACAATAATGGCATCTCGCTTTAAGGTGATGAGTTCCTGAACCTGGACGCC  | 216 |  |  |  |
| OY   | 41  | LeupheGInserIleLYsaRglYsLeuProphelueAsnTriPAapAlaPheProLYsLeu  | 60  |  |  |  |
| Db   | 217   | CTCTTGAGCTCATCAAAGAAACCTTCCTTCTCAACTGGATGCGCTTCTTAAGCTG        | 276 |  |  |  |
| OY   | 61  | LYeGIYleuArgSerIalathrProApblagln                              | 71  |  |  |  |
| Db   | 277   | AAGAGACTGAGNGAGCGCAACTCTGATGCCAG                               | 309 |  |  |  |
| <hr/>  |   |  |     |  |  |  |
| RESULT 5   |   |  |     |  |  |  |
| AAF44164   |   |  |     |  |  |  |
| ID   | AAF44164 standard; cDNA; 415 BP.                                      |  |     |  |  |  |
| XX   |   |  |     |  |  |  |
| AC   | AAF44164;   |  |     |  |  |  |
| XX   |   |  |     |  |  |  |
| DT   | 02-APR-2001 (first entry)   |  |     |  |  |  |
| XX   |   |  |     |  |  |  |
| DE   | Human PRO826 (UNO467) nucleotide sequence SEQ ID NO:200.              |  |     |  |  |  |
| KW   | Human; secreted and transmembrane protein; PRO; cytosolic;            |  |     |  |  |  |
| KW   | cell death; cancer; chromosomal mapping; gene mapping; tissue typing; |  |     |  |  |  |
| KM   | diagnostic assay; ss.   |  |     |  |  |  |
| XX   |   |  |     |  |  |  |
| OS   | Homo sapiens.   |  |     |  |  |  |
| PM   | MO200073454-A1.   |  |     |  |  |  |
| XX   |   |  |     |  |  |  |
| PD   | 07-DEC-2000.  |  |     |  |  |  |
| XX   |   |  |     |  |  |  |
| PF   | 30-MAR-2000; 200OMC-US08439.  |  |     |  |  |  |
| XX   |   |  |     |  |  |  |
| PR   | 02-JUN-1999;  | 99WO-US12252-  |     |  |  |  |
| PR   | 23-JUN-1999;  | 99US-0141037.  |     |  |  |  |
| PR   | 07-JUL-1999;  | 99US-0143048.  |     |  |  |  |
| PR   | 20-JUL-1999;  | 99US-0144758.  |     |  |  |  |
| PR   | 26-JUL-1999;  | 99US-0145698.  |     |  |  |  |
| PR   | 28-JUL-1999;  | 99US-0146222.  |     |  |  |  |
| PR   | 17-AUG-1999;  | 99US-0149396.  |     |  |  |  |
| PR   | 15-SEP-1999;  | 99WO-US21090.  |     |  |  |  |
| PR   | 15-SEP-1999;  | 99WO-US21547.  |     |  |  |  |
| PR   | 08-OCT-1999;  | 99US-0158663.  |     |  |  |  |
| PR   | 30-NOV-1999;  | 99WO-US28513.  |     |  |  |  |
| PR   | 01-DEC-1999;  | 99WO-US28301.  |     |  |  |  |
| PR   | 16-DEC-1999;  | 99WO-US30095.  |     |  |  |  |
| PR   | 20-DEC-1999;  | 99WO-US30911.  |     |  |  |  |
| PR   | 05-JAN-2000;  | 200OMC-US00219.  |     |  |  |  |
| PR   | 06-JAN-2000;  | 200OMC-US00376.  |     |  |  |  |
| PR   | 11-FEB-2000;  | 200OMC-US03565.  |     |  |  |  |
| PR   | 18-FEB-2000;  | 200OMC-US04341.  |     |  |  |  |
| PR   | 22-FEB-2000;  | 200OMC-US04414.  |     |  |  |  |
| PR   | 24-FEB-2000;  | 200OMC-US04914.  |     |  |  |  |

24-FEB-2000; 2000MO-US05004.  
PR 02-MAR-2000; 2000MO-US050841.  
PR 15-MAR-2000; 2000MO-US06884.  
PR 20-MAR-2000; 2000MO-US07377.  
XX  
XX (GENTH ) GENENTECH INC.  
PI Aabkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaldi CJ, Gurney AL, Kiljavin IO, Napier MA, Pan J, Paoni NF,  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;  
XX  
XX WPI: 2001-032160/04.  
DR P-PSDB; AAB55204.  
XX  
XX PRO polynucleotides used to produce polypeptides used to target  
PT bioactive molecules such as toxins, radiolabels or antibodies, to  
PT specific cells, to cause targeted cell death -  
XX  
XX Claim 2; Fig 128; 935bp; English.  
XX  
XX The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins  
CC can be used for targeted delivery of bioactive molecules, such as  
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
CC and DNA. They may also be used to produce transgenic animals which are  
CC used to develop and screen therapeutically useful reagents. The PRO  
CC nucleotide and protein sequence can be used for tissue typing and in  
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used  
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.  
XX  
XX Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
SQ  
Alignment Scores:  
Pred. No.: 7.89e-47 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x AAF44164 (1-415)  
QY 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20  
DB 97 GAGGAGAAAGCACCATTGAGAAATTATGCTCAGACGCCGAGCTTTAAACCCCGTTC 156  
QY 21 LeuAsnIleAspIleLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTyrPheAla 40  
DB 157 CTGAACATCGCAAAATTCGATCGCTTAAAGCTGATGATGCTTCTGAACGACACGCC 216  
QY 41 LeuPheGluSerIleValArgIleValLeuProPheLeuAsnThrPAPAAlaPheProLysIleu 60  
DB 217 CTTTGTAGTCTATCAAAAAGAACTTCTCTTCCCAACTGGAGATGCCCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGGACTGAGGAGGCGCAACTCTGATGCCGAG 309  
RESULT 6  
AAC97491  
ID AAC97491 standard; cDNA; 415 BP.  
XX AAC97491;  
AC AAC97491;  
XX  
DT 28-FEB-2001 (first entry)  
XX

DE Human angiogenesis-associated protein PRO826 cDNA, SEQ ID NO:157.  
XX  
XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal; ss.  
XX  
XX Homo sapiens.  
XX  
XX MO200053753-A2.  
XX  
XX 14-SEP-2000.  
XX  
XX 05-JAN-2000; 2000MO-US00219.  
XX  
XX 08-MAR-1999; 99MO-US05028.  
XX 12-MAR-1999; 99US-0123957.  
XX 14-MAY-1999; 99US-0134287.  
XX 02-JUN-1999; 99MO-US12252.  
XX 23-JUN-1999; 99US-0141037.  
XX 26-JUL-1999; 99US-0144758.  
XX 01-SEP-1999; 99MO-US20111.  
XX 08-SEP-1999; 99MO-US20594.  
XX 15-SEP-1999; 99MO-US21090.  
XX 15-SEP-1999; 99MO-US21547.  
XX 05-OCT-1999; 99MO-US23089.  
XX 30-NOV-1999; 99MO-US28313.  
XX 30-NOV-1999; 99MO-US28409.  
XX 02-DEC-1999; 99MO-US28564.  
XX 02-DEC-1999; 99MO-US28565.  
XX  
XX (GENTH ) GENENTECH INC.  
XX  
XX Aabkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Masters SA;  
PI Paoni NF, Pletel RW, Watanabe CK, Williams PM, Wood WI;  
XX  
XX WPI: 2001-090793/10.  
DR P-PSDB; AAB53094.  
XX  
XX New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
XX  
XX Claim 58; Fig 61; 293bp; English.  
XX  
XX The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's

CC disease, or stroke. PRO nucleic acids are additionally useful in the  
 CC recombinant production of PRO proteins, as hybridisation probes to  
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
 CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
 CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
 CC animals useful for the development and screening of potential  
 CC therapeutic agents. The present sequence represents a cDNA encoding a PRO  
 CC protein of the invention.

XX SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

# Alignment Scores:

| Pred. No.:             | 7,899-47 | Length:       | 415 |
|------------------------|----------|---------------|-----|
| Score:                 | 375.00   | Matches:      | 71  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 22       | Gaps:         | 0   |

US-10-059-395-142\_COPY\_29\_99 (1-71) x AAC97491 (1-415)

QY 1 GIUGIUGIUSERTHRIEGLUSNTYRRAASERARPGIUAIAAPheantHrophe 20

DB 97 GAGGAAGAAAGACCAATGAGATTATGCGTACACAGCCGAGCCCTTAAACCCCGCTTC 156

QY 21 LeuAniIleAPlyleuArgSerAlaPheIysAlaAPGluPheIysAntHphIAla 40

DB 157 CTGAACATCGACAAATGGATCTGCGTTTAGCGCTGATGATTCCTGACTGCGACGCGC 216

QY 41 LeupheIuSerIleIysArgIysleuProPheIysAntHrPaspAlaPheProIysIeu 60

DB 217 CTTCTTGAAGTCTATCAAAAGAACTCTTCTTCAACTGAGATGCCCTTCTTAAGCG 276

QY 61 LysGIyleuArgSerAlaThrProAPAlaIgin 71

DB 277 AAAGACTGAGAGGAGCACTCTGATGCCAG 309

## RESULT 7

ABL95626 ID ABL95626 standard; cDNA; 415 BP.

AC ABL95626;

DT 19-JUL-2002 (first entry)

DE Human angiogenesis related cDNA PRO826 SEQ ID NO: 131.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;

KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;

KW cardiac; cytosolic; antiangiogenic; hypotensive; vulnary;

XX antiarteriosclerotic; gene; ss.

OS Homo sapiens.

XX WO200208284-A2.

PD 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 28-JUL-2000; 2000US-220644P.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-0643657.

XX 23-AUG-2000; 2000WO-US23522.

XX 24-AUG-2000; 2000US-233328P.

XX 07-SEP-2000; 2000US-230978P.

XX 15-SEP-2000; 2000US-000000P.

XX 18-SEP-2000; 2000US-0664610.

XX 18-SEP-2000; 2000US-0665350.

XX 24-OCT-2000; 2000US-242922P.

PR 08-NOV-2000; 2000US-0709238.

PR 08-NOV-2000; 2000WO-US30952.

PR 10-NOV-2000; 2000WO-US30873.

PR 01-DEC-2000; 2000WO-US32678.

PR 20-DEC-2000; 2000US-0747259.

PR 20-DEC-2000; 2000WO-US34956.

PR 22-JAN-2001; 2001US-0767609.

PR 28-FEB-2001; 2001US-0796498.

PR 28-FEB-2001; 2001WO-US06520.

PR 01-MAR-2001; 2001WO-US06666.

PR 09-MAR-2001; 2001US-0802706.

PR 14-MAR-2001; 2001US-0808689.

PR 22-MAR-2001; 2001US-0816744.

PR 05-APR-2001; 2001US-0828366.

PR 10-MAY-2001; 2001US-0854208.

PR 10-MAY-2001; 2001US-0854280.

PR 25-MAY-2001; 2001US-0866028.

PR 25-MAY-2001; 2001US-0866034.

PR 25-MAY-2001; 2001WO-US17092.

PR 30-MAY-2001; 2001US-0870574.

PR 30-MAY-2001; 2001WO-US17443.

PR 01-JUN-2001; 2001WO-US17800.

PR 20-JUN-2001; 2001WO-US19692.

PR 28-JUN-2001; 2001WO-US00000.

XX (GERTH ) GENENTECH INC.

PA (BAKE) BAKER K P.

PA (FERR) FERRARA N.

PA (GERB) GERBER H.

PA (GERR) GERRITSEN M E.

PA (GODD) GODDARD A.

PA (GODO) GODOWSKI P J.

PA (GRUN) GRUNEY A L.

PA (HILL) HILLMAN K J.

PA (MARS) MARSTERS S A.

PA (PANU) PAN J.

PA (PAON) PAONI N F.

PA (STEP) STEPHAN J F.

PA (WATA) WATANABE C K.

PA (WILL) WILLIAMS P W.

PA (WOOD) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,

PI Stephan JF, Watanabe CK, Williams PW, Wood WI, Ye W,

XX WPI; 2002-171999/22.

DR P-PSDB; ABB95486.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial

XX infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 1; Fig 131; 567pp; English.

XX The present invention provides the protein and coding sequences of human

CC PRO proteins. These are useful for treating or diagnosing a

CC cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound

CC healing. The present sequence is a coding sequence of the invention.

SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

# Alignment Scores:

| Pred. No.:             | 7,899-47 | Length:       | 415 |
|------------------------|----------|---------------|-----|
| Score:                 | 375.00   | Matches:      | 71  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 24       | Gaps:         | 0   |

us-10-059-395-142\_copy\_29\_99 (1-71) x ABL95626 (1-415)

```
Qy 1 GIUGLUGUSETTIRIIEGLIUAANTYRALASERARPGIOUAIAPHEAENTHPRophe 20
Db 97 GAGAGAGAAACACCATTTGAGAAATTATGCTGACAGACCCGAGGCTTTAAACCCCGTTC 156
Qy 21 LeuAnniLeaPlyLeuAArgSerAlaPheLysAlaAspGluPheLeuAsnTriPhisAla 40
Db 157 CTGAACATCGACAAATTCGATCGCTTTAAGGCTGATGAGTCTTCTGAACCTGGACGCC 216
Qy 41 LeuPhegluSerIleLysArgLysLeuProPheLeuAsnTriPaspAlaPheProLysLeu 60
Db 217 CTCCTTGAGTCTATCAAAAGAACTTCTTTCCTCAACTGGAGTGCCTTTCCTTAAGCTG 276
Qy 61 LysGlyLeuAArgSerAlaThrProAspAlaGln 71
Db 277 AAAGGACTGAGAGGCGCAACTCTGATGCCAG 309
RESULT 8
ABK69971
ID ABK69971 standard; DNA; 415 BP.
XX
AC ABK69971;
XX
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human Pro peptide #11.
XX
KW Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW genetic disorder; tumour; cancer.
XX
OS Homo sapiens.
XX
FN WO200224888-A2.
XX
PD 28-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US27099.
XX
PR 01-SEP-2000; 2000US-229896P.
XX
PR 05-SEP-2000; 2000US-230621P.
XX
PR 22-SEP-2000; 2000US-235147P.
XX
PR 10-NOV-2000; 2000WO-US30873.
XX
PR 12-JAN-2001; 2001US-261878P.
XX
PR 16-JAN-2001; 2001US-261910P.
XX
PR 16-JAN-2001; 2001US-261939P.
XX
PR 16-JAN-2001; 2001US-262150P.
XX
PR 25-JAN-2001; 2001US-264395P.
XX
PR 02-FEB-2001; 2001US-266421P.
XX
PR 09-FEB-2001; 2001US-267623P.
XX
PR 28-FEB-2001; 2001WO-US06520.
XX
PR 09-MAR-2001; 2001US-274399P.
XX
PR 03-APR-2001; 2001US-280982P.
XX
PR 04-APR-2001; 2001US-282129P.
XX
PR 09-MAY-2001; 2001US-282199P.
XX
PR 25-MAY-2001; 2001WO-US17092.
XX
PR 01-JUN-2001; 2001WO-US17800.
XX
PR 20-JUN-2001; 2001WO-US19692.
XX
PR 29-JUN-2001; 2001WO-US21066.
XX
PR 09-JUL-2001; 2001WO-US21735.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z,
PI Fong S;
XX
XX WPI; 2002-362426/39.
XX
XX P-PSDB; ABG34040.
XX
PT New PRO polypeptides and polynucleotides encoding the polypeptides,
```

PT useful in gene therapy, chromosome identification, tissue typing, or  
PT for genetic analysis of individuals with genetic disorders -  
XX  
XX  
PS Claim 2; Figure 21, 218pp; English.

CC This invention relates to the cDNA and protein sequences of novel  
CC secreted and transmembrane polypeptides PRO polypeptides. The  
CC invention also comprises a method for producing the proteins of the  
CC invention by recombinant means and antibodies specific for the protein  
CC of the invention. The antibody may be used for detecting the PRO  
CC proteins of the invention and may be used to modify their activity.  
CC polynucleotides may be used as hybridisation probes for a cDNA library  
CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to  
CC construct hybridisation probes for mapping the gene which encodes that  
CC PRO and for genetic analysis of individuals with genetic disorders, in  
CC assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knock-out animals which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides are useful in gene therapy, and as molecular weight  
CC markers for protein electrophoresis purposes. The sequences may  
CC also be used to detect overexpression on PRO polypeptides in cancerous  
CC tumours and for screening for differentially expressed genes using  
CC microarray technology. The present sequence represents a cDNA encoding  
XX a human PRO protein of the invention.

XX SO Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

#### Alignment Scores:

|                        |          |               |     |
|------------------------|----------|---------------|-----|
| Pred. No.:             | 7,896-47 | Length:       | 415 |
| Score:                 | 375.00   | Matches:      | 71  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 24       | Gaps:         | 0   |

us-10-059-395-142\_copy\_29\_99 (1-71) x ABK69971 (1-415)

```
Qy 1 GIUGLUGUSETTIRIIEGLIUAANTYRALASERARPGIOUAIAPHEAENTHPRophe 20
Db 97 GAGAGAGAAACACCATTTGAGAAATTATGCTGACAGACCCGAGGCTTTAAACCCCGTTC 156
Qy 21 LeuAnniLeaPlyLeuAArgSerAlaPheLysAlaAspGluPheLeuAsnTriPhisAla 40
Db 157 CTGAACATCGACAAATTCGATCGCTTTAAGGCTGATGAGTCTTCTGAACCTGGACGCC 216
Qy 41 LeuPhegluSerIleLysArgLysLeuProPheLeuAsnTriPaspAlaPheProLysLeu 60
Db 217 CTCCTTGAGTCTATCAAAAGAACTTCTTTCCTCAACTGGAGTGCCTTTCCTTAAGCTG 276
Qy 61 LysGlyLeuAArgSerAlaThrProAspAlaGln 71
Db 277 AAAGGACTGAGAGGCGCAACTCTGATGCCAG 309
```

#### RESULT 9

ABL88137  
ID ABL88137 standard; cDNA; 415 BP.

XX ABL88137;

XX 16-MAY-2002 (first entry)

XX Human PRO826 cDNA sequence SEQ ID NO:131.

XX Human; angiogenesis; cardiac; cytotactic; antiangiogenic; hypotensive;  
XX vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
XX age-related macular degeneration; arterial restenosis; angina;  
XX rheumatoid arthritis; myocardial infarction; thrombophilicities;  
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
XX wound healing; chromosome mapping; gene mapping; gene; ss.





XX (GETH ) GENENTECH INC.  
PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,  
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI,  
XX WPI; 2002-172001/22.  
DR P-PSDB; AA063664.  
XX  
PI One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for treating a PRO related disorder and for diagnosing tumours  
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
PT tumour or liver tumour -  
XX  
PS Claim 2; Figure 145; 359pp; English.  
XX  
CC The invention relates to one hundred and twenty two nucleic acids  
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
CC agonists and antagonists are useful for treating a PRO related disorder.  
CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
CC liver tumour. The PRO polypeptides are useful for stimulating the  
CC proliferation of, or gene expression, in pericyte cells, for stimulating  
CC the proliferation or differentiation of chondrocyte cells, for  
CC stimulating the release of tumour necrosis factor-alpha from human blood,  
CC for stimulating or inhibiting the proliferation of normal human dermal  
CC fibroblast cells. The PRO polypeptide may also be used as molecular  
CC weight markers and for tissue typing. The PRO nucleic acids have  
CC applications in molecular biology, including use as hybridisation probes,  
CC and in chromosome and gene mapping. ABK3536-ABK3657 represent human  
CC PRO protein coding sequences of the invention.  
XX  
SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 7.89e-47 Length: 415  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x ABK3608 (1-415)  
  
QY 1 GluGluIuSerTrpTrpIleGluAsnTrpAlaSerArgProGluAlaPheAsnTrpPhe 20  
Db 97 GAGGAGAAAGACACATTGAGATTATGCGTCACGAGCCCGAGGCTTTAACACCCCGTTC 156  
QY 21 LeuAsnIleApyLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40  
Db 157 CTGAACATCGACAAATTCGATCGCGTTTAAGGCTATGATGATTCCTGAACCTGACAGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAlaPheProLysLeu 60  
Db 217 CTCTTGAAGTCTATCAAAAGGAACTTCCTTCTCTCAACGTGGATGCTTCTTAAGCTG 276  
QY 61 LysGlyLeuArgSerAlaTrpProAspAlaGln 71  
Db 277 AAAGGACTGAGAGGAGGACACTCTGATGCCAG 309  
  
RESULT 11  
ABX80255  
ID ABX80255 standard; DNA; 415 BP.  
XX  
AC ABX80255;  
XX  
XX 28-APR-2003 (first entry)  
DT  
XX  
XX Novel human secreted or transmembrane protein PRO819 DNA.  
DB  
XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;

KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ds.  
XX  
OS Homo sapiens.  
XX  
XX US2002132252-A1.  
XX  
PD 19-SEP-2002.  
XX  
PF 14-NOV-2001; 2001US-0990442.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
XX 16-SEP-1998; 98WO-US19330.  
XX 17-SEP-1998; 98WO-US19437.  
XX 07-OCT-1998; 98WO-US21141.  
XX 01-DEC-1998; 98WO-US25108.  
XX 05-JAN-1999; 99WO-US00106.  
XX 08-MAR-1999; 99WO-US05028.  
XX 02-JUN-1999; 99WO-US12252.  
XX 15-SEP-1999; 99WO-US21090.  
XX 15-SEP-1999; 99WO-US21547.  
XX 30-NOV-1999; 99WO-US28313.  
XX 01-DEC-1999; 99WO-US28301.  
XX 01-DEC-1999; 99WO-US28634.  
XX 16-DEC-1999; 99WO-US30095.  
XX 20-DEC-1999; 99WO-US30911.  
XX 06-JAN-2000; 2000WO-US00219.  
XX 06-JAN-2000; 2000WO-US00376.  
XX 11-FEB-2000; 2000WO-US03565.  
XX 18-FEB-2000; 2000WO-US04341.  
XX 22-FEB-2000; 2000WO-US04414.  
XX 24-FEB-2000; 2000WO-US04914.  
XX 24-FEB-2000; 2000WO-US05004.  
XX 02-MAR-2000; 2000WO-US05841.  
XX 10-MAR-2000; 2000WO-US06319.  
XX 15-MAR-2000; 2000WO-US06884.  
XX 20-MAR-2000; 2000WO-US07377.  
XX 30-MAR-2000; 2000WO-US08439.  
XX 15-MAY-2000; 2000WO-US13358.  
XX 17-MAY-2000; 2000WO-US13705.  
XX 22-MAY-2000; 2000WO-US14042.  
XX 30-MAY-2000; 2000WO-US14941.  
XX 02-JUN-2000; 2000WO-US15264.  
XX 28-JUL-2000; 2000WO-US20710.  
XX 11-AUG-2000; 2000WO-US22031.  
XX 23-AUG-2000; 2000WO-US23522.  
XX 24-AUG-2000; 2000WO-US23328.  
XX 08-NOV-2000; 2000WO-US30952.  
XX 01-DEC-2000; 2000WO-US32678.  
XX 28-FEB-2001; 2001WO-US06520.  
XX 01-JUN-2001; 2001WO-US17800.  
XX 20-JUN-2001; 2001WO-US16992.  
XX 29-JUN-2001; 2001WO-US21066.  
XX 09-JUL-2001; 2001WO-US21735.  
XX 16-JUN-1997; 97US-049787P.  
XX 17-OCT-1997; 97US-062250P.  
XX 12-NOV-1997; 97US-065186P.  
XX 13-NOV-1997; 97US-065311P.  
XX 24-NOV-1997; 97US-066770P.  
XX 25-FEB-1998; 98US-075945P.  
XX 20-MAR-1998; 98US-078910P.  
XX 28-APR-1998; 98US-083322P.  
XX 07-MAY-1998; 98US-084600P.  
XX 28-MAY-1998; 98US-087106P.  
XX 02-JUN-1998; 98US-087607P.  
XX 02-JUN-1998; 98US-087609P.  
XX 02-JUN-1998; 98US-087753P.

PR 03-JUN-1998; 98US-087827P.  
 PR 04-JUN-1998; 98US-088021P.  
 PR 04-JUN-1998; 98US-088025P.  
 PR 04-JUN-1998; 98US-088026P.  
 PR 04-JUN-1998; 98US-088029P.  
 PR 04-JUN-1998; 98US-088030P.  
 PR 04-JUN-1998; 98US-088033P.  
 PR 04-JUN-1998; 98US-088326P.  
 PR 05-JUN-1998; 98US-088167P.  
 PR 05-JUN-1998; 98US-088202P.  
 PR 05-JUN-1998; 98US-088212P.  
 PR 05-JUN-1998; 98US-088217P.  
 PR 09-JUN-1998; 98US-088555P.  
 PR 10-JUN-1998; 98US-088734P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088742P.  
 PR 10-JUN-1998; 98US-088810P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088826P.  
 PR 11-JUN-1998; 98US-088858P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088876P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089440P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 17-JUN-1998; 98US-089532P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089588P.  
 PR 17-JUN-1998; 98US-089599P.  
 PR 17-JUN-1998; 98US-089600P.  
 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089801P.  
 PR 18-JUN-1998; 98US-089907P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 28-AUG-2001; 2001US-0941392.

(GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers J, Eaton DJ,  
 PI Ferreira N, Fong S, Gerber H, Gertlesen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AL, Kijavrin TJ, Napier MA, Pan J, Peoni NP,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;

XX WPI; 2003-247083/24.  
 DR P-PSDB; ABUS9098.

PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 PT are therapeutically useful for enhancing immune response and in cancer  
 PT treatments

XX Claim 2; Fig 130; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
 CC PRO943, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and angiogenesis of this polypeptide are  
 CC useful for treating cancerous tumours. PRO812 inhibits vascular  
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 CC cells and is thus useful for inhibiting endothelial cell growth in  
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing

CC immune response. PRO826, PRO826, PRO1068 or PRO1132 enhance survival of  
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
 CC disease. PRO1310, PRO844, PRO1312, PRO1387 and PRO1387 induce the  
 CC proliferation and/or redifferentiation of chondrocytes in culture and  
 CC are thus useful for treating sports injuries, and arthritis. This  
 CC sequence represents a novel human PRO protein polynucleotide.

XX SQ Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;

Alignment Scores:  
 Pred. No.: 7,89e-47 Length: 415  
 Score: 375.00 Matches: 71  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 25 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x ABX80255 (1-415)

QY 1 GiugliuSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrPrope 20  
 DB 97 GAGAAAGAAAGACCATTCAGATTATGGCTACGACCGGACGCTTTAAACCCCGCTTC 156

QY 21 LeuAnIleAspIleuArgSerAlaPheIleAlaAspGluPheLeuAsnTrpHisAla 40  
 DB 157 CTGAACATCGACAAATGCGATCTCGTTAAAGCTGATGATCTCTGAACGCGACGCC 216

QY 41 LeupheGluSerIleuArgIleuProPheLeuAsnTrpAspAlaPheProIleu 60  
 DB 217 CTTCTTGACTCTATCAAAAGAACTCTCTTCCCTCACTGGAATGCCCTTCTTAAGCTG 276

QY 61 IySGIlyLeuArgSerAlaThrProAspAlaGln 71  
 DB 277 AAAGCACTGAGGAGCGCAACTCCTGATGCCAG 309

RESULT 12  
 ABX80759  
 ID ABX80759 standard; CDNA; 415 BP.

XX AC ABX80759;

DT 22-APR-2003 (first entry)

XX Human secreted/transmembrane protein CDNA, #78.

XX Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical;

KW diagnostic; biosensor; bioindicator; tumour; therapeutic; TAT; ADAPT;

KW gene therapy; tumour-associated antigenic target; TAT; ADAPT;

XX antibody-dependent enzyme mediated prodrug therapy; cytoabatic.

XX Homo sapiens.

XX US2003027162-A1.

XX 06-FEB-2003.

XX 15-NOV-2001; 2001US-0997428.

XX 05-NOV-1997; 97WO-US20069.

XX 16-SEP-1998; 98WO-US19330.

XX 17-SEP-1998; 98WO-US19437.

XX 07-OCT-1998; 98WO-US21141.

XX 01-DEC-1998; 98WO-US25108.

XX 05-JAN-1999; 99WO-US00106.

XX 08-MAR-1999; 99WO-US05028.

XX 02-JUN-1999; 99WO-US12252.

XX 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.  
PR 30-NOV-1999; 99WO-US28313.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 15-MAY-2000; 2000WO-US13358.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 16-JUN-1997; 97US-049787P.  
PR 17-OCT-1997; 97US-062250P.  
PR 13-NOV-1997; 97US-065186P.  
PR 12-NOV-1997; 97US-065311P.  
PR 24-NOV-1997; 97US-066770P.  
PR 25-FEB-1998; 98US-075945P.  
PR 20-MAR-1998; 98US-078910P.  
PR 28-APR-1998; 98US-083222P.  
PR 07-MAY-1998; 98US-084600P.  
PR 28-MAY-1998; 98US-087106P.  
PR 02-JUN-1998; 98US-087607P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-087827P.  
PR 04-JUN-1998; 98US-088021P.  
PR 04-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.  
PR 04-JUN-1998; 98US-088028P.  
PR 04-JUN-1998; 98US-088029P.  
PR 04-JUN-1998; 98US-088030P.  
PR 04-JUN-1998; 98US-088033P.  
PR 04-JUN-1998; 98US-088126P.  
PR 05-JUN-1998; 98US-088167P.  
PR 05-JUN-1998; 98US-088202P.  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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DB 157 CTGAACATCGACAAATTCGATCGCTTAAAGCTGATGATCTTCTGAACCTGGACGCC 216  
QY 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60  
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DT 01-MAY-2003 (first entry)  
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XX Human secreted/transmembrane protein cDNA, #78.  
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XX pharmaceutical; diagnostic; therapeutic; gene therapy.  
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XX Homo sapiens.
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XX US2002160384-A1.
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XX 05-NOV-1997; 97WO-US20069.
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XX 01-DEC-2000; 2000WO-US32678.
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XX 01-JUN-2001; 2001WO-US17800.
XX 20-JUN-2001; 2001WO-US19692.
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XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Baton DL;
XX Ferrazzi N, Fong S, Garbar H, Gerritsen ME, Goddard A, Godowski PJ,
XX Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW, Wood WI;
XX Zhang Z;
XX
XX WPI, 2003-288106/28.
XX P-PSDB; ABU60528.
XX
XX New transmembrane polypeptides and nucleic acids encoding the
XX polypeptides, useful in gene therapy, in chromosome identification, as
XX chromosome markers, or in generating probes -
XX
XX Claim 2; Fig 128; 650pp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
XX comprising a sequence without signal peptide and the nucleic acid
XX encoding them. The polypeptides can be used to raise antibodies that
XX specifically bind to the PRO polypeptide, for linking a bioactive
XX molecule to a cell expressing a PRO protein and for modulating at least
XX one biological activity of a cell. The PRO polypeptides or
XX polynucleotides are also useful in gene therapy, in chromosome
XX identification, as chromosome markers, or in generating probes. The PRO
XX polypeptides are useful as molecular markers for protein
XX electrophoresis, and the isolated nucleic acids may be used for
XX recombinantly expressing those markers. The PRO polypeptides and nucleic
XX acids may also be used in tissue typing. Anti-PRO antibodies are useful
XX in diagnostic assays for PRO, and in affinity purification of PRO from
XX recombinant cell culture or natural sources. The sequences presented in
XX CC ABX90083-ABX90468 are the genes encoding, the primers amplifying and the
XX CC probes detecting the PRO polynucleotides of the invention.
XX CC Note: The sequence data for this patent is also available in electronic
XX CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 415 BP; 99 A; 126 C; 92 G; 98 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 7,896-47 Length: 415
XX Score: 375.00 Matches: 71
XX Percent Similarity: 100.00% Conservative: 0
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KW liver; horse; cow; dog; sheep; pig; goat; rabbit; ADERT;  
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OS Homo sapiens.  
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XX 15-NOV-2001; 2001US-0997666.  
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PR 24-JUN-1998; 98US-090435P.



PR 24-JUN-1998; 98US-090444P.  
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PR 18-AUG-1998; 98US-096949P.  
PR 18-AUG-1998; 98US-096950P.  
PR 18-AUG-1998; 98US-096959P.  
PR 18-AUG-1998; 98US-096960P.  
PR 18-AUG-1998; 98US-097022P.  
PR 19-AUG-1998; 98US-097141P.  
PR 20-AUG-1998; 98US-097218P.  
PR 24-AUG-1998; 98US-097661P.  
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PR 26-AUG-1998; 98US-097986P.  
PR 26-AUG-1998; 98US-098014P.  
PR 31-AUG-1998; 98US-098525P.  
PR 16-SEP-1998; 98US-100634P.  
PR 17-SEP-1998; 98US-100858P.

PR 22-DEC-1998; 98US-113296P.  
PR 12-MAR-1999; 98US-123957P.  
PR 23-JUN-1999; 98US-141037P.  
PR 07-JUL-1999; 98US-143048P.

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| Score:                 | 375.00   | Matches:      | 71  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 25       | Gaps:         | 0   |

US-10-059-395-142\_COPY\_29\_99 (1-71) x ABX77843 (1-415)

|    |     |  |                 |     |
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| Db | 97  | GAGGAGAGAAACACCATTTGAGATTATTCGTCACGACCCGAGCCTTTAAACCCCGTTC   |                 | 156 |
| Qy | 21  | LeuAsnIleAspIysLeuArgSerAlaPheIysAlaAspGIuPheLeuAsnTrpHisAla |                 | 40  |
| Db | 157 | CTGAACATCGACAATTGCGATCGCTTTAAGGCTGATGAGTTCGAACTGCGACACCC     |                 | 216 |
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| Db | 217 | CTCTTGAGTCTATCAAAAGAACTTCCTTCTCAACTGAGATGCTTCTTAAGCTG        |                 | 276 |
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| Db | 277 | AAAGACTGAGAGAGCGCACTCTGATGCCAG                               |                 | 309 |

Search completed: November 28, 2003, 14:33:08  
Job time : 221 secs

GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 13:45:19 / Search time 252 Seconds

(without alignments)  
928.266 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99

Perfect score: 375  
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Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

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-FAPOP=6 -FAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database: Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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| 1          | 375   | 100.0              | 415 9 | US-09-989-722-200 Sequence 200, App |

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| 2  | 375 | 100.0 | 415 9  | US-09-989-723-200 Sequence 200, App  |
| 3  | 375 | 100.0 | 415 9  | US-09-989-279-200 Sequence 200, App  |
| 4  | 375 | 100.0 | 415 9  | US-09-989-727-200 Sequence 200, App  |
| 5  | 375 | 100.0 | 415 10 | US-09-989-731-200 Sequence 200, App  |
| 6  | 375 | 100.0 | 415 10 | US-09-989-732-200 Sequence 200, App  |
| 7  | 375 | 100.0 | 415 10 | US-09-991-073-200 Sequence 200, App  |
| 8  | 375 | 100.0 | 415 10 | US-09-990-442-200 Sequence 200, App  |
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| 45 | 375 | 100.0 | 415 11 | US-09-997-440-200 Sequence 200, App  |

## ALIGNMENTS

RESULT 1  
US-09-989-722-200  
Sequence 200, Application US/09989722  
Patent No. US20020072067A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavina, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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;; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey

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;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
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APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
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APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
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PRIOR FILING DATE: 1998-07-09

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Pred. No.: 6.08e-48 Length: 415  
Score: 375.00 Matches: 71  
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Query Match: 100.00% Indels: 0  
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US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-989-727-200 (1-415)

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;; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

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;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerltsen, Mary B.  
;; APPLICANT: Goddard, Audrey  
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;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
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PRIOR FILING DATE: 1998-07-09

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DB 217 CTTTGAGTCTATCAAAAGAACTTCCTTCCCTCACTGGAGGCTTCTTAAGCTG 276  
QY 61 LYGIGLYLEUARGSERIALPHELYSALIAAPGILUPHELEUASRTTPTISALA 71  
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## RESULT 8

US-09-990-442-200  
Sequence 200, Application US/09990442  
Patent No. US20020132252A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Fong, Sherman  
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APPLICANT: Napier, Mary A.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P18  
CURRENT APPLICATION NUMBER: US/09/990,442  
PRIOR FILING DATE: 2001-11-14  
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

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DB 157 CTGAACATGACAAATTTGCGATCTGCGTTTAAAGCTGATGAGTTCCTGAACGCGACGCC 216  
QY 41 LeuPheGluSerIleIleArgIleuProPheLeuAsnThrAspAlaPheProIleu 60  
DB 217 CTCTTGAAGTCTATCAAAAGGAACCTTCTTCTCACTGGGATGCTTCTCTAAGCTG 276  
QY 61 LyeGlyLeuArgSerAlaThrProAspAlaGln 71  
DB 277 AAAGACTGAGGAGCGCACTCTGATGCCGAG 309

RESULT 9  
US-09-991-163-200  
; Sequence 200, Application US/09991163  
; Patent No. US20020132253A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashtkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; TITLE OF INVENTION: Acids Encoding the Same  
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Alignment Scores:
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Query Match: 100.00% Indels: 0
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QY 61 LVEG1VLEUARGSERALATHRPROASAPALAG1N 71
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
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; APPLICANT: Botstein, David

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APPLICANT: Eaton, Dan L.  
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;; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

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| Score:                 | 375.00   | Matches:      | 71  |
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Db 277 AAGGACTGAGAGCGCACTCTGATGCCCG 309  
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US-09-989-721-200  
; Sequence 200, Application US/09989721  
; Patent No. US20020142961A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Guiney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumaas, Daniel  
; APPLICANT: Tumaas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC55  
; CURRENT APPLICATION NUMBER: US/09/989,721  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
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 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

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 Conservative: 0

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 Mismatches: 0  
 Indels: 0

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RESULT 13  
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 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Baton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C20  
 CURRENT APPLICATION NUMBER: US/09/992,598  
 CURRENT FILING DATE: 2001-11-14  
 PRIOR APPLICATION NUMBER: 60/045787  
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

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US-09-989-293A-200  
; Sequence 200, Application US/09989293A  
; Patent No. US20020177164A1

## GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Geritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
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;; APPLICANT: K1javin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tamas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730PLC66  
;; CURRENT APPLICATION NUMBER: US/09/989,293A  
;; PRIOR FILING DATE: 2001-11-20  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
;; PRIOR FILING DATE: 1997-11-12  
;; PRIOR APPLICATION NUMBER: 60/065311

;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/066770  
;; PRIOR FILING DATE: 1997-11-24  
;; PRIOR APPLICATION NUMBER: 60/075945  
;; PRIOR FILING DATE: 1998-02-25  
;; PRIOR APPLICATION NUMBER: 60/078910  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/084600  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/087106  
;; PRIOR FILING DATE: 1998-05-28  
;; PRIOR APPLICATION NUMBER: 60/087607  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087609  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087759  
;; PRIOR FILING DATE: 1998-06-02  
;; PRIOR APPLICATION NUMBER: 60/087827  
;; PRIOR FILING DATE: 1998-06-03  
;; PRIOR APPLICATION NUMBER: 60/088021  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088025  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088026  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088028  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088029  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088030  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088033  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088326  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088167  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088202  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088212  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088217  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088655  
;; PRIOR FILING DATE: 1998-06-09  
;; PRIOR APPLICATION NUMBER: 60/088734  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088738  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088742  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088810  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088824  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088826  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088858  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088861  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088876  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/089105  
;; PRIOR FILING DATE: 1998-06-12  
;; PRIOR APPLICATION NUMBER: 60/089440  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089512  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089514  
;; PRIOR FILING DATE: 1998-06-16





|  |                                 |
|--|---------------------------------|
| FILE REFERENCE: P2730PC66              | FILE REFERENCE: US/09/989,735   |
| CURRENT APPLICATION NUMBER: 2001-11-19 | CURRENT FILING DATE: 2001-11-19 |
| PRIOR APPLICATION NUMBER: 1997-06-16   | PRIOR FILING DATE: 1997-06-16   |
| PRIOR APPLICATION NUMBER: 60/062250    | PRIOR FILING DATE: 1997-10-17   |
| PRIOR APPLICATION NUMBER: 60/065186    | PRIOR FILING DATE: 1997-11-12   |
| PRIOR APPLICATION NUMBER: 60/065311    | PRIOR FILING DATE: 1997-11-13   |
| PRIOR APPLICATION NUMBER: 60/066770    | PRIOR FILING DATE: 1997-11-24   |
| PRIOR APPLICATION NUMBER: 60/075945    | PRIOR FILING DATE: 1998-02-25   |
| PRIOR APPLICATION NUMBER: 60/078910    | PRIOR FILING DATE: 1998-03-20   |
| PRIOR APPLICATION NUMBER: 60/083322    | PRIOR FILING DATE: 1998-04-28   |
| PRIOR APPLICATION NUMBER: 60/084600    | PRIOR FILING DATE: 1998-05-07   |
| PRIOR APPLICATION NUMBER: 60/087106    | PRIOR FILING DATE: 1998-05-28   |
| PRIOR APPLICATION NUMBER: 60/087607    | PRIOR FILING DATE: 1998-06-02   |
| PRIOR APPLICATION NUMBER: 60/087609    | PRIOR FILING DATE: 1998-06-02   |
| PRIOR APPLICATION NUMBER: 60/087759    | PRIOR FILING DATE: 1998-06-02   |
| PRIOR APPLICATION NUMBER: 60/087827    | PRIOR FILING DATE: 1998-06-03   |
| PRIOR APPLICATION NUMBER: 60/088021    | PRIOR FILING DATE: 1998-06-04   |
| PRIOR APPLICATION NUMBER: 60/088025    | PRIOR FILING DATE: 1998-06-04   |
| PRIOR APPLICATION NUMBER: 60/088026    | PRIOR FILING DATE: 1998-06-04   |
| PRIOR APPLICATION NUMBER: 60/088028    | PRIOR FILING DATE: 1998-06-04   |
| PRIOR APPLICATION NUMBER: 60/088029    | PRIOR FILING DATE: 1998-06-04   |
| PRIOR APPLICATION NUMBER: 60/088030    | PRIOR FILING DATE: 1998-06-04   |
| PRIOR APPLICATION NUMBER: 60/088033    | PRIOR FILING DATE: 1998-06-04   |
| PRIOR APPLICATION NUMBER: 60/088326    | PRIOR FILING DATE: 1998-06-04   |
| PRIOR APPLICATION NUMBER: 60/088167    | PRIOR FILING DATE: 1998-06-05   |
| PRIOR APPLICATION NUMBER: 60/088202    | PRIOR FILING DATE: 1998-06-05   |
| PRIOR APPLICATION NUMBER: 60/088212    | PRIOR FILING DATE: 1998-06-05   |
| PRIOR APPLICATION NUMBER: 60/088217    | PRIOR FILING DATE: 1998-06-05   |
| PRIOR APPLICATION NUMBER: 60/088655    | PRIOR FILING DATE: 1998-06-09   |
| PRIOR APPLICATION NUMBER: 60/088734    | PRIOR FILING DATE: 1998-06-10   |
| PRIOR APPLICATION NUMBER: 60/088738    | PRIOR FILING DATE: 1998-06-10   |
| PRIOR APPLICATION NUMBER: 60/088742    | PRIOR FILING DATE: 1998-06-10   |
| PRIOR APPLICATION NUMBER: 60/088810    | PRIOR FILING DATE: 1998-06-10   |
| PRIOR APPLICATION NUMBER: 60/088824    | PRIOR FILING DATE: 1998-06-10   |
| PRIOR APPLICATION NUMBER: 60/088826    | PRIOR FILING DATE: 1998-06-10   |
| PRIOR APPLICATION NUMBER: 60/088858    | PRIOR FILING DATE: 1998-06-11   |
| PRIOR APPLICATION NUMBER: 60/088861    | PRIOR FILING DATE: 1998-06-11   |

[illegible]

/ PRIOR FILING DATE: 1998-06-25  
/ PRIOR APPLICATION NUMBER: 60/090696  
/ PRIOR FILING DATE: 1998-06-25  
/ PRIOR APPLICATION NUMBER: 60/090862  
/ PRIOR FILING DATE: 1998-06-26  
/ PRIOR APPLICATION NUMBER: 60/090863  
/ PRIOR FILING DATE: 1998-06-26  
/ PRIOR APPLICATION NUMBER: 60/091360  
/ PRIOR FILING DATE: 1998-07-01  
/ PRIOR APPLICATION NUMBER: 60/091478  
/ PRIOR FILING DATE: 1998-07-02  
/ PRIOR APPLICATION NUMBER: 60/091544  
/ PRIOR FILING DATE: 1998-07-01  
/ PRIOR APPLICATION NUMBER: 60/091519  
/ PRIOR FILING DATE: 1998-07-02  
/ PRIOR APPLICATION NUMBER: 60/091626  
/ PRIOR FILING DATE: 1998-07-02  
/ PRIOR APPLICATION NUMBER: 60/091633  
/ PRIOR FILING DATE: 1998-07-02  
/ PRIOR APPLICATION NUMBER: 60/091978  
/ PRIOR FILING DATE: 1998-07-07  
/ PRIOR APPLICATION NUMBER: 60/091982  
/ PRIOR FILING DATE: 1998-07-07  
/ PRIOR APPLICATION NUMBER: 60/092182  
/ PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

| Pred. No.:             | 6,08e-48 | Length:       | 415 |
|------------------------|----------|---------------|-----|
| Score:                 | 375.00   | Matches:      | 71  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 10       | Gaps:         | 0   |

US-10-059-395-142\_COPY\_29\_99 (1-71) x US-09-989-735-200 (1-415)

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | GIUGLUGLuserThrIleGlubentYrAlaSerArgProGluAlaPheAsnThrProPhe  | 20  |
| Db | 97  | GAGGAAGAAGACCACTTGAATATGCGTCACGACCCGAGCCCTTTAAACCCCGTTC       | 156 |
| Qy | 21  | LeuAsnIleAspIleuArgSerAlaPheIleAlaAspGluPheLeuAsnThrPheIleAla | 40  |
| Db | 157 | CTGAACATCGACAAATTCGATCGCTTAAAGGCTGATGAGTTCCTGAACCTGGCACGCC    | 216 |
| Qy | 41  | LeuPheGluSerIleIleArgIleuProPheLeuAsnThrAspAlaPheProIleu      | 60  |
| Db | 217 | CTCTTGAGTCATCAAAAGAAACTTCCTTCCTCAACTGGAGTCCCTTCTTAAGCTG       | 276 |
| Qy | 61  | IysGlyLeuArgSerAlaThrProAspAlaGln                             | 71  |
| Db | 277 | AAAGACTGAGGAGCGCACTCTGATGCCCGAG                               | 309 |

Search completed: November 28, 2003, 15:05:24  
Job time : 258 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 13:44:14 / Search time 1605 Seconds

(without alignments)  
1075.151 Million cell updates/sec

Title: US-10-059-395-142\_COPY\_29\_99  
Perfect score: 375  
Sequence: 1 EESTIENYASRPEAFNTFP.....LNMWAFPKLGRSATPDQA 71

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODE=frame\_plus\_p2n.model -DEV=klh  
-Q=/cgn2\_1/USPTO.spool/US1005395/runat\_25112003\_141913\_11706/app\_query.fasta\_1.263  
-DB=EST-QFMT=fastap -SUFIX=rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US1005395.OCEN\_1\_1\_2810@runat\_25112003\_141913\_11706 -NCPU=6 -ICPU=3  
-NO\_MAP -LARGEOUERY -NEG SCORES=0 -WAIT -OSPBLOCK=100 -LONGLOC  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST.\*  
1: em\_estba.\*  
2: em\_estchum.\*  
3: em\_estcin.\*  
4: em\_estcmu.\*  
5: em\_estcov.\*  
6: em\_estcpl.\*  
7: em\_estcro.\*  
8: em\_hcc.\*  
9: gb\_estcl.\*  
10: gb\_estl2.\*  
11: gb\_hcc.\*  
12: gb\_estl3.\*  
13: gb\_estl4.\*  
14: gb\_estl5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_ges\_hum.\*  
18: em\_ges\_luv.\*  
19: em\_ges\_pin.\*  
20: em\_ges\_vrt.\*  
21: em\_ges\_fun.\*  
22: em\_ges\_mam.\*  
23: em\_ges\_mus.\*  
24: em\_ges\_pro.\*  
25: em\_ges\_rnd.\*  
26: em\_ges\_ping.\*  
27: em\_ges\_vrl.\*  
28: gb\_gesl.\*

29: gb\_ges2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID     | Description         |
|------------|-------|---------|--------------|-----------|---------------------|
| 1          | 375   | 100.0   | 318          | AA586846  | AA586846 nm7e11.s   |
| 2          | 375   | 100.0   | 334          | AA297512  | AA297512 EST113061  |
| 3          | 375   | 100.0   | 339          | AA778414  | AA778414 zf39e05.s  |
| 4          | 375   | 100.0   | 359          | AA238758  | AA238758 xp03e08.x  |
| 5          | 375   | 100.0   | 359          | BE466728  | BE466728 h224g06.x  |
| 6          | 375   | 100.0   | 362          | AA140605  | AA140605 qe05f03.x  |
| 7          | 375   | 100.0   | 373          | AA722694  | AA722694 z982b06.s  |
| 8          | 375   | 100.0   | 381          | W69108    | W69108 z444c04.s1   |
| 9          | 375   | 100.0   | 394          | W60320    | W60320 z429g01.s1   |
| 10         | 375   | 100.0   | 412          | W60268    | W60268 z429g01.s1   |
| 11         | 375   | 100.0   | 424          | W69083    | W69083 z444b06.s1   |
| 12         | 375   | 100.0   | 432          | BX112106  | BX112106 BX112106   |
| 13         | 375   | 100.0   | 432          | W69233    | W69233 z444c04.r1   |
| 14         | 369   | 98.4    | 359          | BG150312  | BG150312 7j38g03.x  |
| 15         | 364   | 97.1    | 378          | AA184682  | AA184682 qd68b02.x  |
| 16         | 362   | 96.5    | 413          | AA393296  | AA393296 zc74f05.r  |
| 17         | 362   | 96.5    | 431          | W69227    | W69227 z444b06.r1   |
| 18         | 352   | 93.9    | 358          | AW003825  | AW003825 wq83f12.x  |
| 19         | 343   | 91.5    | 345          | AA1217565 | AA1217565 qd43d02.x |
| 20         | 341   | 90.9    | 377          | AA582988  | AA582988 nm72h02.s  |
| 21         | 328   | 87.5    | 334          | AI217587  | AI217587 qd43f04.x  |
| 22         | 323.5 | 86.3    | 326          | AA297513  | AA297513 EST113062  |
| 23         | 300   | 80.0    | 241          | AA595889  | AA595889 nm64g08.s  |
| 24         | 286   | 76.3    | 345          | AA583942  | AA583942 nm64f07.s  |
| 25         | 286   | 76.3    | 376          | W95920    | W95920 z608d01.r1   |
| 26         | 280   | 74.7    | 330          | W95883    | W95883 z608d01.s1   |
| 27         | 276.5 | 73.7    | 421          | AV618771  | AV618771 AV618771   |
| 28         | 258   | 68.8    | 339          | W52030    | W52030 z413b01.s1   |
| 29         | 252   | 67.2    | 436          | AV597545  | AV597545 AV597545   |
| 30         | 225   | 60.0    | 368          | AW260965  | AW260965 EQUK9243   |
| 31         | 222.5 | 59.3    | 444          | B1286103  | B1286103 UI-R-DDO-  |
| 32         | 219.5 | 58.5    | 394          | B1281142  | B1281142 UI-R-DDO-  |
| 33         | 219.5 | 58.5    | 446          | B1283220  | B1283220 UI-R-DDO-  |
| 34         | 219.5 | 58.5    | 448          | B1282568  | B1282568 UI-R-DDO-  |
| 35         | 219.5 | 58.5    | 452          | B1277693  | B1277693 UI-R-CZO-  |
| 36         | 219.5 | 58.5    | 454          | B128573   | B128573 UI-R-DDO-   |
| 37         | 219.5 | 58.5    | 461          | B1285632  | B1285632 UI-R-DDO-  |
| 38         | 219.5 | 58.5    | 466          | B1277761  | B1277761 UI-R-CZO-  |
| 39         | 218   | 58.1    | 239          | AA595930  | AA595930 nm66a07.s  |
| 40         | 214   | 57.1    | 344          | AA619595  | AA619595 v154g08.r  |
| 41         | 214   | 57.1    | 346          | B1137356  | B1137356 B1137356   |
| 42         | 214   | 57.1    | 382          | AA727573  | AA727573 v097a02.x  |
| 43         | 214   | 57.1    | 386          | AA169065  | AA169065 m821b01.r  |
| 44         | 214   | 57.1    | 409          | AA572239  | AA572239 v151g12.x  |
| 45         | 214   | 57.1    | 427          | AA726579  | AA726579 v093a07.x  |

#### ALIGNMENTS

RESULT 1  
AA586846/c  
LOCUS  
DEFINITION AA586846 318 bp mRNA linear EST 26-SRP-1997  
m7e11.81 NCT\_CGAP\_Lar1 Homo sapiens cDNA clone IMAGE:1088972 3',  
RNA sequence.  
AA586846  
ACCESSION  
VERSION AA586846.1 GI:2397660  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
EST.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
1 (bases 1 to 318)

**AUTHORS** NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
**JOURNAL** Tumor Gene Index  
**COMMENT** Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapdb-remail.nih.gov](mailto:cgapdb-remail.nih.gov)  
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.  
 Bmerer-Buck, M.D., Ph.D.  
 CDNA Library Preparation: Stratagene, Inc.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CCAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LMD at:  
[www-bio.liml.gov/bbrip/image/image.html](http://www-bio.liml.gov/bbrip/image/image.html)  
 Insert Length: 465 Std Error: 0.00  
 Seq primer: -40m13 fwd. RT from Amersham.

# FEATURES

Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1088972"  
 /tissue\_type="larynx"  
 /lab\_host="SQR (kanamycin resistant)"  
 /clone\_lib="NCI-CCAP Lat1"  
 /note="Organ: larynx; Vector: Bluescript SK-; Site: 1:  
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:  
 Oligo dt. larynx. 5' adaptor sequence: 5' GAATTCGACGACG  
 3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'  
 Average insert size: 0.9 kb."

**BASE COUNT** 76 a 67 c 90 g 85 t  
**ORIGIN**

## Alignment Scores:

| Pred. No.:             | 4,666-44 | Length:       | 318 |
|------------------------|----------|---------------|-----|
| Score:                 | 375.00   | Matches:      | 71  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 9        | Gaps:         | 0   |

US-10-059-395-142\_COPY\_29\_99 (1-71) x AA586846 (1-318)

**QY** 1 GUGUGUGUSeThrlleGluAenTyralaSeArpProGluAlaPheAenThrProPhe 20  
**DB** 316 GAGGAGAAGAACCACTGAGATTATGCTCAGACCGAGGCTTTAAACCCCGTTT 257  
**QY** 21 LeuAnllleaplyleuArgSerAlaPheIysAlaAapGluPheLeuAenThrPheAla 40  
**DB** 256 CTGAACATCGACAAATTCGATCTCGTTTAAAGCTGATGAGTTCTTGAACCTGCACGCC 197  
**QY** 41 LeupheGluSerllelyeArglyleuProPheLeuAenThrPAPAlaPheProlyleu 60  
**DB** 196 CTCCTTGAGTCTATCAAAAGAACTCTTCTTCCCACTGAGAGCCCTTCTTAAGCTG 137  
**QY** 61 LygGlyleuArgSerAlaThrProAapAlaGln 71  
**DB** 136 AAAGACTGAGGAGCGCAACTCTGATGCCAG 104

**RESULT 2** AA297512 334 bp mRNA linear EST 18-APR-1997  
**LOCUS** EST113061 Petal skin Homo sapiens cdna 5' end, mRNA sequence.  
**ACCESSION** AA297512  
**VERSION** AA297512.1 GI:1949666  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 334)  
**AUTHORS** Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., Bult  
 C.J., Lee N.H., Kirschner E.F., Weinstein K.G., Gocayne J.D., White

**TITLE** Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
**JOURNAL** Nature 377 (6547 Suppl), 3-174 (1995)  
**MEDLINE** 96026280  
**PUBMED** 7566098  
**COMMENT** Other ESTs: THC151622  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: [arketav@tigr.org](mailto:arketav@tigr.org)  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/cdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.

## FEATURES

Location/Qualifiers  
 1..334  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="ATCC (Inhost):141532"  
 /db\_xref="taxon:9606"  
 /tissue\_type="epithelium"  
 /cell\_type="epithelial cell"  
 /dev\_stage="fetus"  
 /clone\_lib="Petal skin"  
 /note="Organ: skin; Vector: pBluescript SK-; Site: 1:  
 EcoRI; Site 2: XhoI"

**BASE COUNT** 77 a 100 c 78 g 78 t 1 others  
**ORIGIN**

| Pred. No.:             | 4,996-44 | Length:       | 334 |
|------------------------|----------|---------------|-----|
| Score:                 | 375.00   | Matches:      | 71  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 9        | Gaps:         | 0   |

US-10-059-395-142\_COPY\_29\_99 (1-71) x AA297512 (1-334)

**QY** 1 GUGUGUGUSeThrlleGluAenTyralaSeArpProGluAlaPheAenThrProPhe 20  
**DB** 98 GAGGAGAAGAACCACTGAGATTATGCTCAGACCGAGGCTTTAAACCCCGTTT 157  
**QY** 21 LeuAnllleaplyleuArgSerAlaPheIysAlaAapGluPheLeuAenThrPheAla 40  
**DB** 158 CTGAACATCGACAAATTCGATCTCGTTTAAAGCTGATGAGTTCTTGAACCTGCACGCC 217  
**QY** 41 LeupheGluSerllelyeArglyleuProPheLeuAenThrPAPAlaPheProlyleu 60  
**DB** 218 CTCCTTGAGTCTATCAAAAGAACTCTTCTTCCCACTGAGAGCCCTTCTTAAGCTG 277  
**QY** 61 LygGlyleuArgSerAlaThrProAapAlaGln 71  
**DB** 278 AAAGACTGAGGAGCGCAACTCTGATGCCAG 310

|  |
|--|
| RESULT 3   |
| AA778414/c   |
| LOCUS AA778414 339 bp mRNA linear EST 05-FEB-1996  |
| DEFINITION zif39e05.s1 Soares_fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:379328 3', mRNA sequence.  |
| ACCESSION AA778414   |
| VERSION AA778414.1 GI:2837745  |
| KEYWORDS EST.  |
| SOURCE Homo sapiens (human)  |
| ORGANISM Homo sapiens  |
| REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  |
| AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lemon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Stepcevic,M., Tan,F., Thelsting,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.  |
| TITLE Mashu-NCI human EST Project  |
| JOURNAL Unpublished  |
| COMMENT Contact: Wilson RK<br>Washington University School of Medicine<br>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108<br>Tel.: 314 286 1800<br>Fax: 314 286 1810<br>Email: est@watson.wustl.edu<br>This clone is available royalty-free through LMLT ; contact the IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information.<br>Seq primer: -40mJ fwd. ET from Amerham.   |
| FEATURES   |
| Source   |
| Location/Qualifiers  |
| 1..339   |
| /organism="Homo sapiens"   |
| /mol_type="mRNA"   |
| /db_xref="GDB:1287584"   |
| /db_xref="taxon:9606"  |
| /clone="IMAGE:379328"  |
| /sex="unknown"   |
| /dev_stage="19 weeks"  |
| /lab_host="DH10B (ampicillin resistant)"   |
| /clone_lib="Soares fetal heart NbHH19W"  |
| /note="Organ: heart; Vector: pUT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTAACAATCGAAGTGGAAGCCGCCCATCTTTTTTTT 3'] , double-stranded cDNA was site selected, ligated to Eco RI adapters (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pUT3 vector (Pharmacia). Library went through one round of normalization to a C <sub>ot</sub> = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHH19W." |
| BASE COUNT 79 a 77 c 96 g 87 t   |
| ORIGIN   |
| Alignment Scores:  |
| Pred. No.: 5.le-44 Length: 339   |
| Score: 375.00 Matches: 71  |
| Percent Similarity: 100.00% Conservative: 0  |
| Best Local Similarity: 100.00% Mismatch: 0   |
| Query Match: 100.00% Indels: 0   |
| DB: Gaps: 0  |
| US-10-059-395-142_COPY_29_99 (1-71) x AA778414 (1-339)   |
| OY 1 GluglugusertThillegluasentYrAlaserarPProglualaphesantThroPhe 20   |
| Dd 316 GAGGAAGAAGACCAATTGAGATTAATGTGCACAGACCAGGGCCTTTAACACCCCCTTC 257  |
| OY 21 leuananileapyleueuarGserLapeleyaalaaRgUlpuhEleuasntThptla 40   |
| Dd 256 CTGAACATCGAANAATTCGATCTCGCTTAAAGGCTGAATGAATTCCTGAACAGCACGCC 197   |
| OY 41 leupneglusertillelyearglylsleupTrophenelusAsntripAspalaphetrolysenu 60   |

[illegible]

Db 141 CTGAACATCGAACAAATTCGATCTGCTTTAAGCGTGAATGATTCCTGAACTGGACGCC 200  
Oy LeuphegiusserielysarylsleuProphleuauantTpaapalaPhapProlyseu 60  
Db 201 CTTTGTAGTCTATCAAAAGAAAGAACTTCTTCCCAACTGAGATGCTTTCTTAAGCTG 260  
Oy 61 LyegilyleuargserialatThrProapalagin 71  
Db 261 AAAGACTGAGGAGCGCAACTCTGATGCCAG 293

RESULT 5  
BE466728/c 359 bp mRNA linear EST 27-JUL-2000  
LOCUS h224906.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:3208954 3',  
DEFINITION mRNA sequence.  
ACCESSION BE466728  
VERSION BE466728.1 GI:9512503  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 359)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLT, send email to:  
info@image.llnl.gov  
Seg primer: -40UP from Glibco.  
Location/Qualifiers  
FEATURES  
source  
1..359  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3208954"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_GC6"  
/note="Vector: p773D-Pac (pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA  
from the normalized library NCI\_CGAP GC4 was prepared, and  
as circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (cloneids  
1257096-1258631, 1469064-1470983, and 1475592-1476743).  
Subtraction by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 77 a 80 c 96 g 106 t  
ORIGIN  
Alignment Scores: 5.54e-44 Length: 359  
Pred. No.: 375.00 Matches: 71  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x BE466728 (1-359)  
Oy 1 GluglugluserThrillegiueantYralaserArgProglualAphaenanthProphe 20  
Db 332 GAGGAGAAAGCACTTATGAGATTTATGCTCAAGACCCGAGGCTTTAAACACCCCTTC 273

Oy 21 LeuansilleaplysleuAargserialAphelyalAapglupheleuAantTphila 40  
Db 272 CTGAACATCGAACAAATTCGATCTGCTTTAAGCGTGAATGATTCCTGAACTGGACGCC 213  
Oy 41 LeuphegiusserielysarylsleuProphleuauantTpaapalaPhapProlyseu 60  
Db 212 CTTTGTAGTCTATCAAAAGAAAGAACTTCTTCCCAACTGAGATGCTTTCTTAAGCTG 153  
Oy 61 LyegilyleuargserialatThrProapalagin 71  
Db 152 AAAGACTGAGGAGCGCAACTCTGATGCCAG 120

RESULT 6  
A1140605/c 362 bp mRNA linear EST 29-OCT-1998  
LOCUS ge05f03.x1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1738109  
DEFINITION 3', mRNA sequence.  
ACCESSION A1140605  
VERSION A1140605.1 GI:3648062  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 362)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLT at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert length: 425 Std Error: 0.00  
Seg primer: -40m13 fwd, 5' from Amersham.  
Location/Qualifiers  
FEATURES  
source  
1..362  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:1738109"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_testis NHT"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech Laboratories  
, Inc., and primed with a Not I - oligo(dT) primer 3'.  
TGTTCACATCTGAAATGAGGAGCGCGCCCAATTTTCTTTTCTTTT 3'.  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p773 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 77 a 81 c 99 g 105 t  
ORIGIN  
Alignment Scores: 5.6e-44 Length: 362  
Pred. No.: 375.00 Matches: 71  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
US-10-059-395-142\_COPY\_29\_99 (1-71) x A1140605 (1-362)

|                   |   |   |                             |
|-------------------|---|---|-----------------------------|
| QY                | 1   | GluglugluserTh11GluabentVyr1aseraGPproGUa1aPhaasnthProbe  | 20                          |
| Db                | 331   | GAGAGAGAAACACCATTCAGATTATGGTCACACCCGAGCCCTTTAAACCCCGTTC   | 272                         |
| QY                | 21  | Leubani1aaplyleAurSer1aPheylsalaAepGluPheLeuAantRph1sAla  | 40                          |
| Db                | 271   | CTGAACATCGACAATTCCGATCTCGTTTAAGCTGATGAGTTCCTAACTGGACACC   | 212                         |
| QY                | 41  | Leuphegluser11aLyarglyleuProPheLeuAantTPAspAlaPheProlyleu | 60                          |
| Db                | 211   | CTCTTGGAGTCTATCAAAAGGAACCTCTTCCCTCAACTGGAGACCTTCTTAAGCTG  | 152                         |
| QY                | 61  | Lyg1yLeuAurSer1aThProspAlaGin                             | 71                          |
| Db                | 151   | AAAGACTGAGAGCGCCAACTCTGATGCCAG                            | 119                         |
| RESULT 7          |   |   |                             |
| LOCUS             | AA722694/c  |   |                             |
| DEFINITION        | zgc2b06.61 Soares_fetal_heart_NbHh19w   | 373 bp  | mRNA linear EST 02-JAN-1998 |
| ACCESSION         | AA722694  |   |                             |
| VERSION           | AA722694.1  |   |                             |
| KEYWORDS          | EST.  |   |                             |
| SOURCE            | Homo sapiens (human)  |   |                             |
| ORGANISM          | Homo sapiens  |   |                             |
| REFERENCE         | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.   |   |                             |
| AUTHORS           | 1 (bases 1 to 373)<br>Hillier,L., Allen,M., Bowles,L., Dubuque,T., Giesel,G., Jost,S., Kitzman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Matris,M., Martin,J., Moore,B., Schellenberg,K., Stepec,N., Tan,F., Theisling,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.  |   |                             |
| TITLE             | WashU-NCI human EST Project   |   |                             |
| JOURNAL           | Unpublished   |   |                             |
| COMMENT           | Contact: Wilson RX<br>Washington University School of Medicine<br>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108<br>Tel: 314 286 1800<br>Fax: 314 286 1810<br>Email: est@watson.wustl.edu<br>This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.<br>Seq primer: -40m13 fwd. ET from Amersham.<br>Location/Qualifiers<br>1..373<br>/organism="Homo sapiens"<br>/mol_type="mRNA"<br>/db_xref="GDB:1307650"<br>/db_xref="taxon:9606"<br>/clone="IMAGE:399827"<br>/sex="unknown"<br>/dev_stage="19 weeks"<br>/lab_host="NBH19w (ampicillin resistant)"<br>/clone_lib="Soares_fetal_heart_NbHh19w"<br>/note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCGAAGGAGGAGCGCGCCGACATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Falini Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHh19w." |   |                             |
| BASE COUNT        | 89 a  | 81 c  | 113 g 90 t                  |
| ORIGIN            |   |   |                             |
| Alignment Scores: |   |   |                             |
| Pred. No.:        | 5.85e-44  | Length:   | 373                         |
| Score:            | 375.00  | Matches:  | 71                          |

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-059-395-142_COPY_29_99 (1-71) x AA222694 (1-373)

OY      1 GluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20
Db      319 GAGGAMAAAGACCACTTGAGAATTATTCGTCCACGACCAGGGCCTTTAACACCCCGTTC 260
OY      21 LeuSntIleApIysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40
Db      259 CTGAACATCCAGCAAAATTCGATCGCGCTTTAAGCGTAGTAATGCCTCAACTGCGCACGCC 200
OY      41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60
Db      199 CTTTBAAGCTACCAAAAGAAATCTCTTCTCCTCACTGGAGATGCTTTCCTAAGCTG 140
OY      61 LysGlyLeuArgSerAlaThrProAspAlaGln 71
Db      139 AAAGACTGAGAGAGCGCACTCTCGATGCCAG 107

RESULT 8
W69108/c W69108 381 bp mRNA linear EST 16-OCT-1996
LOCUS z44c04.g1 Soares fetal heart NBH19W Homo sapiens cDNA clone
DEFINITION IMAGE:343494 3', mRNA sequence.
ACCESSION W69108
VERSION W69108.1 GI:1378389
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 381)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
,M., Hultman,M., Kucaba,T., Le,M., Lemmon,G., Mayra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaakie,B., Waterston
,R., Williamson,A., Wohlmann,P. and Wilson,R.
The Wash-Merck EST Project
Unpublished
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 442 Std Error: 0.00
Seq primer: mob.REGA+RT
High quality sequence stop: 347.
Location/Qualifiers
1. 381
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/db_xref="GDB:126869"
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/clone="IMAGE:343494"
/sex="unknown"
/dev stage="19 weeks"
/lab host="DH10B (ampicillin resistant)"
/clone_lhb="Soares_fetal_heart_NBH19W"
/note="Organ: heart; Vector: pTZ19D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - Oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCATCTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTZ19 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
```

M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBH19W."

BASE COUNT 91 a 86 c 114 g 89 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 6.03e-44 Length: 381

Score: 375.00 Matches: 71

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 14 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x W69108 (1-381)

QY 1 GUGUGUGUSeThrlleGUaenTYrAlaSerArpProGUaLaphaenThrPrope 20

DB 317 GAGGAAGAAACACCAATTGAGATATGCGTCACGACCGAGCCCTTTAACACCCCGTTTC 258

QY 21 LeuAnllleApplYleuArSeSerAlaPheLYsAlaApGluPheLeuAnTrpHisAla 40

DB 257 CTGAACATCGACAATTGCGATCTGCTTTAAGCTGATGAGTCTCTGAACCTGGACCGCC 198

QY 41 LeupheGluSeRllyeArGlYsLeuPProPheLeuAnTrpAspAlaPheProLYsLeu 60

DB 197 CTTTGGATCTATCAAAAGAAACTCTCTTCCCTCAATGGAGATGCCCTTCTTAAGCTG 138

QY 61 LYsGlyLeuArSeSerAlaThrProAspAlaGln 71

DB 137 AAAGGACTGAGAGCGCAACTCTGATGCCAG 105

RESULT 9

LOCUS W60320 394 bp mRNA linear EST 15-OCT-1996

DEFINITION z239g01.s1 Soares fetal heart NBH19W Homo sapiens cDNA clone

ACCESSION W60320

VERSION W60320.1 GI:1367079

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lemmon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.

ORGANISM The WashU-Merck EST Project

UNPUBLISHED

CONTACT: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 476 Std Error: 0.00

Seq primer: mob.REGA+ET.

FEATURES

source

1..394

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:1267471"

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/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares\_fetal\_heart\_NBH19W"

/note="Organ: heart; Vector: pT73D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTACCAATCTGAAGGAGCGCGCGGACTTTTCTTTTCTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBH19W."

BASE COUNT 94 a 88 c 119 g 91 t 2 others

ORIGIN

Alignment Scores:

Pred. No.: 6.32e-44 Length: 394

Score: 375.00 Matches: 71

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 14 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x W60320 (1-394)

QY 1 GUGUGUGUSeThrlleGUaenTYrAlaSerArpProGUaLaphaenThrPrope 20

DB 320 GAGGAAGAAACACCAATTGAGATATGCGTCACGACCGAGCCCTTTAACACCCCGTTTC 261

QY 21 LeuAnllleApplYleuArSeSerAlaPheLYsAlaApGluPheLeuAnTrpHisAla 40

DB 260 CTGAACATCGACAATTGCGATCTGCTTTAAGCTGATGAGTCTCTGAACCTGGACCGCC 201

QY 41 LeupheGluSeRllyeArGlYsLeuPProPheLeuAnTrpAspAlaPheProLYsLeu 60

DB 200 CTTTGGATCTATCAAAAGAAACTCTCTTCCCTCAATGGAGATGCCCTTCTTAAGCTG 141

QY 61 LYsGlyLeuArSeSerAlaThrProAspAlaGln 71

DB 140 AAAGGACTGAGAGCGCAACTCTGATGCCAG 108

RESULT 10

LOCUS W60268 412 bp mRNA linear EST 15-OCT-1996

DEFINITION z239g01.r1 Soares fetal heart NBH19W Homo sapiens cDNA clone

ACCESSION W60268

VERSION W60268.1 GI:1367169

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lemmon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.

ORGANISM The WashU-Merck EST Project

UNPUBLISHED

CONTACT: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 476 Std Error: 0.00

Seq primer: mob.REGA+ET

High quality sequence strop: 385.

FEATURES

source

1..412

/organism="Homo sapiens"

/mol\_type="mRNA"

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/clone="IMAGE:342096"

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/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares\_fetal\_heart\_NBH19W"

/note="Organ: heart; Vector: pT73D (Pharmacia) with a



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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1267471"
/db_xref="taxon:9606"
/clone="IMAGE:342096"
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/notes="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCCGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbH19W."
```

```
BASE COUNT      96 a      127 c      88 g      98 t      3 others
ORIGIN
```

Alignment Scores:

|                        |          |               |     |
|------------------------|----------|---------------|-----|
| Pred. No.:             | 6,74e-44 | Length:       | 412 |
| Score:                 | 375.00   | Matches:      | 71  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 14       | Gaps:         | 0   |

US-10-059-395-142\_COPY\_29\_99 (1-71) x W60268 (1-412)

```
QY      1  G G I G U G U S E R T H I L E G I U A N T Y R A L A S E R A T P R O G I U A L A P H A S N T H P R O P H E
      97  G A G G A G A A A C C A C C A T T A G C G T C A C G A C C G A G C C C T T T A A C C C C G T T C
      21  L E U A N T L E A P L Y L E U A R G S E R A L A P H E L Y S A L A S P G I U P H E L E U A N T T P H I S A L A
      157 C T G A A C A T C G A C A A T T G C A T C T G C T T T A A G C G A G A G T T C C T G A A C T G G C A C G C C
      41  L E U P H E G I U S E R I L E Y S A R G L Y S L E U P R O P H E L E U A N T T P A S P A L A P H E P R O L Y S L E U
      217 C T C T T G A C T C A T C A A A G A A A C T C T T T C C T C A C T G G A G A T C C T T C T T A G C T G
      61  L Y S G I L E U A R G S E R A L A T H R P R O A P A L A G I N 71
      277 A A A G A C T G A G G A G C C A A C T C C T G A T G C C A G 309
```

RESULT 11  
W69083/c 424 bp mRNA linear EST 16-OCT-1996  
LOCUS z44b06.s1 Soares fetal heart NbH19W Homo sapiens cDNA clone  
DEFINITION IMAGE:343475.3', mRNA sequence.  
ACCESSION W69083  
VERSION W69083.1 GI:1378383  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maita, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.  
TITLE The Maabu-Werck EST Project  
JOURNAL Unpublished  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800

Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert Length: 466 Std Error: 0.00  
Seq primer: mob.REGA+ET  
High quality sequence stop: 339.  
Location/Qualifiers

#### FEATURES

source

1..424

```
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1268850"
/db_xref="taxon:9606"
/clone="IMAGE:343475"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_11b="Soares_fetal_heart_NbH19W"
/notes="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCCGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbH19W."
```

BASE COUNT 98 a 100 c 129 g 97 t

ORIGIN

Alignment Scores:

|                        |          |               |     |
|------------------------|----------|---------------|-----|
| Pred. No.:             | 7.02e-44 | Length:       | 424 |
| Score:                 | 375.00   | Matches:      | 71  |
| Percent Similarity:    | 100.00%  | Conservative: | 0   |
| Best Local Similarity: | 100.00%  | Mismatches:   | 0   |
| Query Match:           | 100.00%  | Indels:       | 0   |
| DB:                    | 14       | Gaps:         | 0   |

US-10-059-395-142\_COPY\_29\_99 (1-71) x W69083 (1-424)

```
QY      1  G G I G U G U S E R T H I L E G I U A N T Y R A L A S E R A T P R O G I U A L A P H A S N T H P R O P H E
      317  G A G G A G A A A C C A C C A T T A G C G T C A C A C A C C G A G C C C T T T A A C C C C G T T C
      21  L E U A N T L E A P L Y L E U A R G S E R A L A P H E L Y S A L A S P G I U P H E L E U A N T T P H I S A L A
      257 C T G A A C A T C G A C A A T T G C A T C T G C T T T A A G C T G A T G A G T T C C T G A A C T G G C A C G C C
      41  L E U P H E G I U S E R I L E Y S A R G L Y S L E U P R O P H E L E U A N T T P A S P A L A P H E P R O L Y S L E U
      197 C T C T T G A C T C A T C A A A G A A A C T C T T T C C T C A C A C T G G A G A G C C T T T C T T A G C T G
      61  L Y S G I L E U A R G S E R A L A T H R P R O A P A L A G I N 71
      137 A A A G A C T G A G A G C C A A C T C C T G A T G C C A G 105
```

RESULT 12  
BX112106 432 bp mRNA linear EST 07-FEB-2003  
LOCUS BX112106 Soares\_fetal\_heart\_NbH19W Homo sapiens cDNA clone  
DEFINITION IMAGE:998DD01781; IMAGE:342096, mRNA sequence.  
ACCESSION BX112106  
VERSION BX112106.1 GI:27878783  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Parsch, E., Peters, M.,  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 432)

TITLE  
JOURNAL  
COMMENT

Radelof, U., Schneider, D. and Korn, B.  
Human Unigeneset - RZPD3  
Unpublished  
Contact: Ina Rolfe  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGp98D01781.  
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
http://www.rzpd.de/CloneCards/cgi-  
bit/showlib.pl.cgi?response2libNo=972 Contact: Ina Rolfe  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de  
This clone is available royalty-free from RZPD,  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r, primer sequence: TTTCACACAGAAACACCTATGAC.  
Location/Qualifiers

## FEATURES

source

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1..432
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp98D01781 ; IMAGB:342096"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NBHL19W"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGAGGAGCGCGCCGACCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHL19W."
```

BASE COUNT 113 a 129 c 92 g 98 t  
ORIGIN

Alignment Scores:  
Pred. No.: 7.21e-44 Length: 432  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x BX112106 (1-432)

QY 1 GUGUGUGUSeThriIleGIUASeNTyRAlaSeArpProGIUAAlaPheAsnThProPhe 20  
DB 99 GAGGAGAAAGCAACATTGAGATTAATGCGTCACACACCGGCTTTAAACACCCCGTTC 158  
QY 21 LeuAenIleApIySeLeuArgeSerAlaPheIySaIaAaPgiUpheLeuAsnTriPHisAla 40  
DB 159 CTGAACATCGACAAATTCGATTCGCTTTAAGGCTGATGACTTCTTAACCTGGACACCC 218  
QY 41 LeuphegiuSeTilIeYArGIySeLeuProPheLeuAsnTriPaspAlaPheProIyLeu 60  
DB 219 CTCTTGAAGTATCAAAAGAACTTCCTTCTCAACTGGAGGCTTTCTTAAGCTG 278  
QY 61 LySGIyLeuArgeSerAlaThProAspAlaGln 71  
DB 279 AAAAGACTGAGAGCGCAACTCTGATGCCAG 311  
RESULT 13  
W69233 M69233 432 bp mRNA linear EST 16-OCT-1996

## DEFINITION

z444c04.r1 Soares fetal heart NBHL19W Homo sapiens cDNA clone  
IMAGB:343494 5', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

## REFERENCE

AUTHORS

1 (bases 1 to 432)  
Mammalia; Euteleostomi; Primates; Catarrhini; Homnidae; Homo.  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,  
'M., Hulman, M., Kucaba, T., Le, M., Lemon, G., Marra, M., Parsons, J.,  
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaekis, E., Waterston,  
'R., Williamson, A., Wohlmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished

## TITLE

JOURNAL

COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LINL; contact the  
IMAGS Consortium (info@image.liml.gov) for further information.  
Insert Length: 442 Std Error: 0.00  
Seq primer: mob.REGA+ET  
High quality sequence stop: 341.  
Location/Qualifiers

## FEATURES

source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1268869"
/db_xref="taxon:9606"
/clone="IMAGB:343494"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NBHL19W"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGAGGAGCGCGCCGACCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHL19W."
```

BASE COUNT 106 a 127 c 94 g 102 t 3 others  
ORIGIN

Alignment Scores:  
Pred. No.: 7.21e-44 Length: 432  
Score: 375.00 Matches: 71  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x W69233 (1-432)

QY 1 GUGUGUGUSeThriIleGIUASeNTyRAlaSeArpProGIUAAlaPheAsnThProPhe 20  
DB 96 GAGGAGAAAGCAACATTGAGATTAATGCGTCACACACCGGCTTTAAACACCCCGTTC 155  
QY 21 LeuAenIleApIySeLeuArgeSerAlaPheIySaIaAaPgiUpheLeuAsnTriPHisAla 40  
DB 156 CTGAACATCGACAAATTCGATTCGCTTTAAGGCTGATGACTTCTTAACCTGGACACCC 215  
QY 41 LeuphegiuSeTilIeYArGIySeLeuProPheLeuAsnTriPaspAlaPheProIyLeu 60

Db 216 CTCCTTGAGTCATCAAGAAAGAACTCTTCTCTCACTGGAGTCCCTTCTTAAGCTG 275

Qy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71

Db 276 AAAGACTGAGAGCGCAACTCTGATGCCCA 308

RESULT 14

LOCUS BG150312/c 359 bp mRNA linear EST 05-FEB-2001

DEFINITION 7398903.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:3443116 3', mRNA sequence.

ACCESSION BG150312

VERSION BG150312.1 GI:12662342

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 359)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/BLND, send email to: [info@image.llnl.gov](mailto:info@image.llnl.gov)

Seq primer: -40UP from GIBCO.

FEATURES

source

1.359

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3443116"

/tissue\_type="pooled germ cell tumors"

/lab\_host="DH10B"

/clone\_11b="NCI\_CGAP\_GC6"

/note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP GC4 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 78 a 80 c 96 g 105 t

ORIGIN

Alignment Scores:

Pred. No.: 4.08e-43 Length: 359

Score: 369.00 Matches: 70

Percent Similarity: 98.59% Conservative: 0

Best Local Similarity: 98.59% Mismatches: 1

Query Match: 98.40% Indels: 0

DB: 10 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x BG150312 (1-359)

Qy 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20

Db 332 GAGGAAGAAAGCAACATTTGAGATTCGTCACGACCGAGGCTTTAAACCCCGCTTC 273

Qy 21 LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnThrPheAsn 40

Db 272 TTGAACATGCAACAATTGGCATCTGCGTTTAAGGCTGATGATGATTCCTGAACCTGGACGCG 213

Qy 41 LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTyrAspAlaPheProLysLeu 60

Db 212 CTCCTTGAGTCATCAAGAAAGAACTCTTCTCTCACTGGAGTCCCTTCTTAAGCTG 153

Qy 61 LysGlyLeuArgSerAlaThrProAspAlaGln 71

Db 152 AAAGACTGAGAGCGCAACTCTGATGCCCA 120

RESULT 15

LOCUS A1184682/c 378 bp mRNA linear EST 28-OCT-1998

DEFINITION qd68b02.x1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1734603 3', mRNA sequence.

ACCESSION A1184682

VERSION A1184682.1 GI:3735320

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 378)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/BLND, at: [www-bio.llnl.gov/bdrrp/image/image.html](http://www-bio.llnl.gov/bdrrp/image/image.html)

Insert length: 419 Std Error: 0.00

Seq primer: -40UP from GIBCO.

FEATURES

source

1.378

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1734603"

/sex="male"

/lab\_host="DH10B"

/clone\_11b="Soares\_testis\_NHT"

/note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAGTGGAGCGCGCCCAATTTTCTTTTCTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 80 a 89 c 105 g 104 t

ORIGIN

Alignment Scores:

Pred. No.: 2.32e-42 Length: 378

Score: 364.00 Matches: 69

Percent Similarity: 97.18% Conservative: 0

Best Local Similarity: 97.18% Mismatches: 2

Query Match: 97.07% Indels: 0

DB: 9 Gaps: 0

US-10-059-395-142\_COPY\_29\_99 (1-71) x A1184682 (1-378)

Qy 1 GluGluGluSerThrIleGluAsnTyrAlaSerArgProGluAlaPheAsnThrProPhe 20

Db 327 GAGGAAGAAAGCAACATTTGAGATTCGTCACGACCGAGGCTTTAAACCCCGCTTC 268

```
QY      21  LeuAsnIleAspLysLeuArgSerAlaPheLysAlaAspGluPheLeuAsnTrpHisAla 40
      267  CTGAACATCGACAAATTGCGATGCGCTTTAAGCTGATGAGTTCTGAACCTGGCAAGCC 208
QY      41  LeuPheGluSerIleLysArgLysLeuProPheLeuAsnTrpAspAlaPheProLysLeu 60
      207  CTCTTGAGTCTATCAAAAGGAACTTCCTTCTCAAGTGGGATGCCCTTCTTAAGCTG 148
QY      61  LysGlyLeuArgSerAlaTrpProAspAlaGln 71
      147  AAAGACTGAGAGCGCACTCTGATGCCAG 115
Db
```

Search completed: November 28, 2003, 15:00:00  
Job time : 1608 secs